NCBI Description



## Yer166wp [Saccharomyces cerevisiae]

224618 Seq. No. Seq. ID LIB3166-015-P1-K1-C2 Method BLASTX q548852 NCBI GI 347 BLAST score 8.0e-33 E value Match length 82 79 % identity 40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal NCBI Description protein S21 - rice >gi 303839 dbj BAA02158 (D12633) 40S subunit ribosomal protein [Oryza sativa] 224619 Seq. No. LIB3166-015-P1-K1-C5 Seq. ID BLASTX Method NCBI GI g3249064 BLAST score 325 E value 3.0e-30 119 Match length 55 % identity (AC004473) Strong similarity to trehalose-6-phosphate NCBI Description synthase homolog gb 2245136 from A. thaliana chromosome 4 contig gb Z97344. [Arabidopsis thaliana] 224620 Seq. No. Seq. ID LIB3166-015-P1-K1-C6 BLASTX Method NCBI GI q4218116 BLAST score 162 5.0e-11 E value 53 Match length 58 % identity NCBI Description (AL035353) putative protein [Arabidopsis thaliana] 224621 Seq. No. LIB3166-015-P1-K1-C8 Seq. ID BLASTX Method NCBI GI q1707364 BLAST score 636 E value 1.0e-66 Match length 137 % identity NCBI Description (X94626) AATP2 [Arabidopsis thaliana] Seq. No. 224622 LIB3166-015-P1-K1-D1 Seq. ID Method BLASTX NCBI GI g2911042 BLAST score 304 1.0e-27 E value Match length 75 % identity 80

31923

[Arabidopsis thaliana]

(AL021961) Phosphoglycerate dehydrogenase - like protein

Method

NCBI GI

BLASTX

q2493495



```
224623
Seq. No.
Seq. ID
                  LIB3166-015-P1-K1-D2
                  BLASTX
Method
NCBI GI
                  g2213425
BLAST score
                  596
                  6.0e-62
E value
                  143
Match length
                  43
% identity
                 (Z97064) hypothetical protein [Citrus x paradisi]
NCBI Description
                  224624
Seq. No.
Seq. ID
                  LIB3166-015-P1-K1-D3
Method
                  BLASTX
                  g2191135
NCBI GI
BLAST score
                  194
                  8.0e-15
E value
Match length
                  92
% identity
                  38
NCBI Description
                  (AF007269) A IG002N01.14 gene product [Arabidopsis
                  thaliana]
                  224625
Seq. No.
Seq. ID
                  LIB3166-015-P1-K1-D8
                  BLASTX
Method
NCBI GI
                  g2791834
BLAST score
                  604
                  7.0e-63
E value
Match length
                  117
                  98
% identity
NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta]
                  224626
Seq. No.
                  LIB3166-015-P1-K1-D9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4262236
BLAST score
                  458
E value
                  9.0e-46
Match length
                  123
                  69
% identity
NCBI Description (AC006200) putative ribose 5-phosphate isomerase
                  [Arabidopsis thaliana]
Seq. No.
                  224627
                  LIB3166-015-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3738259
BLAST score
                  472
E value
                  4.0e-49
Match length
                  135
% identity
                  79
                  (AB018411) cytosolic phosphoglycerate kinase 1 [Populus
NCBI Description
                  nigra]
                  224628
Seq. No.
                  LIB3166-015-P1-K1-E2
Seq. ID
```

Seq. ID Method

NCBI GI

BLAST score



```
BLAST score
                   499
E value
                   1.0e-50
Match length
                   116
                   78
% identity
                   SERINE CARBOXYPEPTIDASE-LIKE >gi 2129878 pir S72370
NCBI Description
                   carboxypeptidase - garden pea (fragment)
                   >gi_1089904_emb_CAA92216_ (Z68130) carboxypeptidase [Pisum
sativum] >gi_1587217_prf__2206338A Ser carboxypeptidase
                   [Pisum sativum]
                   224629
Seq. No.
Seq. ID
                   LIB3166-015-P1-K1-E3
                   BLASTX
Method
                   g4204697
NCBI GI
BLAST score
                   340
E value
                   6.0e-32
                   98
Match length
                   68
% identity
                   (AF117063) putative inositol polyphosphate 5-phosphatase
NCBI Description
                   At5P2 [Arabidopsis thaliana]
                   224630
Seq. No.
Seq. ID
                   LIB3166-015-P1-K1-E4
                   BLASTX
Method
NCBI GI
                   g4115377
BLAST score
                   381
                   9.0e-37
E value
                   107
Match length
                   73
% identity
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
                   224631
Seq. No.
                   LIB3166-015-P1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4337189
BLAST score
                   472
                   2.0e-47
E value
Match length
                   142
% identity
                   61
NCBI Description
                   (AC006403) putative calmodulin-binding protein [Arabidopsis
                   thaliana]
Seq. No.
                   224632
Seq. ID
                   LIB3166-015-P1-K1-E7
                   BLASTX
Method
NCBI GI
                   q4454457
BLAST score
                   339
                   8.0e-32
E value
Match length
                   71
% identity
NCBI Description
                   (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.
                   224633
```

g2739376

LIB3166-015-P1-K1-E8

BLASTX

262

```
E value
                  9.0e-23
Match length
                  68
% identity
                  72
NCBI Description (AC002505) putative permease [Arabidopsis thaliana]
                  224634
Seq. No.
Seq. ID
                  LIB3166-015-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  q4099914
BLAST score
                  301
E value
                  2.0e-27
Match length
                  96
% identity
                  62
                  (U91857) ethylene-responsive element binding protein
NCBI Description
                  homolog [Stylosanthes hamata]
Seq. No.
                  224635
Seq. ID
                  LIB3166-015-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  q22240
BLAST score
                  505
E value
                  2.0e-51
Match length
                  126
% identity
                  80
NCBI Description
                  (X07157) GADPH (383 AA) [Zea mays]
Seq. No.
                  224636
Seq. ID
                  LIB3166-015-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g2493318
                  240
BLAST score
                  3.0e-20
E value
                  90
Match length
                  51
% identity
                 BLUE COPPER PROTEIN PRECURSOR >gi 562779 emb CAA80963
NCBI Description
```

(Z25471) blue copper protein [Pisum sativum]

>gi\_1098264\_prf\_\_2115352A blue Cu protein [Pisum sativum]

Seq. No. 224637

Seq. ID LIB3166-015-P1-K1-F11

Method BLASTX
NCBI GI g2388689
BLAST score 246
E value 9.0e-22
Match length 103
% identity 60

NCBI Description (AF016633) GH1 protein [Glycine max]

Seq. No. 224638

Seq. ID LIB3166-015-P1-K1-F12

Method BLASTX
NCBI GI g2440044
BLAST score 450
E value 6.0e-52
Match length 131
% identity 80

NCBI Description (AJ001293) major intrinsic protein PIPB [Craterostigma

BLAST score

E value Match length 510 2.0e-53

124



## plantagineum]

Seq. No. 224639 Seq. ID LIB3166-015-P1-K1-F3 BLASTX Method NCBI GI g114661 BLAST score 602 1.0e-62 E value Match length 142 84 % identity ATP SYNTHASE A CHAIN PRECURSOR (SUBUNIT IV) NCBI Description >gi 67924 pir LWNT6 H+-transporting ATP synthase (EC 3.6.1.34) chain a - common tobacco chloroplast >gi 11813\_emb\_CAA77344\_ (Z00044) ATPase sunthase IV subunit [Nicotiana tabacum] >gi\_225273\_prf\_\_1211235H ATPase a [Nicotiana tabacum] 224640 Seq. No. Seq. ID LIB3166-015-P1-K1-F5 Method BLASTX NCBI GI g3342798 BLAST score 386 2.0e-37 E value 128 Match length 59 % identity NCBI Description (AF061240) glutamine cyclotransferase precursor [Carica papaya] 224641 Seq. No. Seq. ID LIB3166-015-P1-K1-F8 Method BLASTX NCBI GI g3142292 BLAST score 318 8.0e - 34E value Match length 106 % identity 67 (AC002411) Contains similarity to tetratricopeptide repeat NCBI Description protein gb U46571 from home sapiens. EST gb Z47802 and gb\_Z48402 come from this gene. [Arabidopsis Thaliana] Seq. No. 224642 LIB3166-015-P1-K1-G4 Seq. ID Method BLASTX NCBI GI q2384696 BLAST score 335 E value 2.0e-31 Match length 139 53 % identity NCBI Description (AF013216) acyl-CoA oxidase [Myxococcus xanthus] 224643 Seq. No. LIB3166-015-P1-K1-G5 Seq. ID Method BLASTX g4510363 NCBI GI



132

72

% identity

% identity (AC007017) putative DNA-binding protein [Arabidopsis NCBI Description thaliana] Seq. No. 224644 Seq. ID LIB3166-015-P1-K1-G8 Method BLASTX NCBI GI q1255951 BLAST score 619 1.0e-64 E value Match length 143 % identity 81 NCBI Description (X96932) PS60 [Nicotiana tabacum] Seq. No. 224645 Seq. ID LIB3166-015-P1-K1-H1 Method BLASTX NCBI GI q3063396 BLAST score 457 1.0e-45 E value Match length 116 77 % identity (AB012947) vcCyP [Vicia faba] NCBI Description Seq. No. 224646 Seq. ID LIB3166-015-P1-K1-H11 Method BLASTX NCBI GI q832876 BLAST score 461 E value 3.0e-46Match length 96 % identity 94 NCBI Description (L41345) ascorbate free radical reductase [Solanum lycopersicum] >qi 1097368 prf 2113407A ascorbate free radical reductase [Lycopersicon esculentum] Seq. No. 224647 LIB3166-015-P1-K1-H8 Seq. ID Method BLASTX NCBI GI q4539452 349 BLAST score E value 6.0e - 38Match length 122 62 % identity (AL049500) putative phosphoribosylanthranilate transferase NCBI Description [Arabidopsis thaliana] Seq. No. 224648 LIB3166-016-P1-K1-A1 Seq. ID Method BLASTX NCBI GI g1871185 536 BLAST score E value 6.0e-55 Match length

NCBI Description (U90439) seven in absentia isolog [Arabidopsis thaliana]

Method

NCBI GI

BLASTX

g629600



```
Seq. No.
                   224649
                   LIB3166-016-P1-K1-A10
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2738949
                   358
 BLAST score
                   3.0e - 34
 E value
                   80
 Match length
                   85
 % identity
                   (AF022213) cytosolic ascorbate peroxidase [Fragaria x
 NCBI Description
                   ananassa]
 Seq. No.
                   224650
                   LIB3166-016-P1-K1-A11
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g1076603
 BLAST score
                   164
                   1.0e-11
 E value
 Match length
                   71
                   55
 % identity
 NCBI Description vsf-1 protein - tomato
 Seq. No.
                   224651
 Seq. ID
                   LIB3166-016-P1-K1-A2
 Method
                   BLASTX
 NCBI GI
                   g3182981
 BLAST score
                   316
                   3.0e-29
 E value
 Match length
                   82
 % identity
                   76
 NCBI Description CELL ELONGATION PROTEIN DIMINUTO >gi 1695692 dbj BAA13096
                    (D86494) diminuto [Pisum sativum]
                   224652
 Seq. No.
                   LIB3166-016-P1-K1-A5
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g4220541
                  * 139
 BLAST score
 E value
                   1.0e-08
                   70
 Match length
 % identity
                   43
                   (AL035356) Rab geranylgeranyl transferase like protein
 NCBI Description
                    [Arabidopsis thaliana]
                   224653
 Seq. No.
                   LIB3166-016-P1-K1-A6
 Seq. ID
 Method
                   BLASTX
- NCBI GI
                   g2815246
 BLAST score
                   223
                   3.0e-18
 E value
 Match length
                   55
                   73
 % identity
 NCBI Description (X95709) class I type 2 metallothionein [Cicer arietinum]
 Seq. No.
                   224654
                   LIB3166-016-P1-K1-A7
 Seq. ID
```



BLAST score 409 E value 3.0e-40 Match length 95 % identity 74

NCBI Description 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) -

wild cabbage >gi\_562280\_emb\_CAA57724\_ (X82273)

1-aminocyclopropane-1-carboxylate synthase [Brassica

oleracea]

Seq. No. 224655

Seq. ID LIB3166-016-P1-K1-A8

Method BLASTX
NCBI GI g1707922
BLAST score 599
E value 2.0e-62
Match length 128

% identity 88

NCBI Description GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT

PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE

PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE

ADENYL TRANSFERASE) >gi\_1076255\_pir\_\_S51944

glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) large chain S1 precursor - beet >gi\_556624\_emb\_CAA55516\_ (X78900) glucose-1-phosphate adenylyltransferase [Beta vulgaris]

Seq. No. 224656

Seq. ID LIB3166-016-P1-K1-A9

Method BLASTX
NCBI GI g1707922
BLAST score 322
E value 1.0e-30
Match length 114
% identity 63

NCBI Description GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT

PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE

PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE

ADENYL TRANSFERASE) >gi\_1076255 pir S51944

glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) large chain S1 precursor - beet >gi\_556624 emb\_CAA55516\_ (X78900) glucose-1-phosphate adenylyltransferase [Beta vulgaris]

Seq. No. 224657

Seq. ID LIB3166-016-P1-K1-B10

Method BLASTX
NCBI GI g3043428
BLAST score 419
E value 3.0e-41
Match length 92
% identity 85

NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Seq. No. 224658

Seq. ID LIB3166-016-P1-K1-B11

Method BLASTX
NCBI GI g267120
BLAST score 266
E value 2.0e-23



Match length 101 % identity 57

NCBI Description THIOREDOXIN F-TYPE PRECURSOR (TRX-F) >gi 100070 pir S20929

thioredoxin f precursor - garden pea

>gi 20907 emb CAA45098 (X63537) thioredoxin F [Pisum

satīvum] >gi\_1388086 (U35830) thioredoxin f [Pisum sativum]

Seq. No. 224659

Seq. ID LIB3166-016-P1-K1-B2

Method BLASTX
NCBI GI g3297816
BLAST score 550
E value 1.0e-56
Match length 126
% identity 83

NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 224660

Seq. ID LIB3166-016-P1-K1-B5

Method BLASTX
NCBI GI g1706319
BLAST score 334
E value 2.0e-31
Match length 102
% identity 61

NCBI Description HISTIDINE DECARBOXYLASE (HDC) (TOM92)

>gi\_481829\_pir\_\_S39554 histidine decarboxylase (EC
4.1.1.22) - tomato >gi\_416534\_emb\_CAA50719\_ (X71900)
histidine decarboxylase [Lycopersicon esculentum]

Seq. No. 224661

Seq. ID LIB3166-016-P1-K1-B6

Method BLASTX
NCBI GI g113360
BLAST score 375
E value 5.0e-48
Match length 130
% identity 75

NCBI Description ALCOHOL DEHYDROGENASE 1 >gi\_100652\_pir\_\_JQ0474 alcohol

dehydrogenase (EC 1.1.1.1) 1 - rice >gi 20165 emb CAA34363

(X16296) alcohol dehydrogenase 1 [Oryza sativa]

Seq. No. 224662

Seq. ID LIB3166-016-P1-K1-C1

Method BLASTX
NCBI GI g2623309
BLAST score 159
E value 8.0e-11
Match length 107
% identity 37

NCBI Description (AC002409) similar to tgacg-specific DNA-binding protein

[Arabidopsis thaliana]

Seq. No. 224663

Seq. ID LIB3166-016-P1-K1-C10

Method BLASTX NCBI GI g3249105



```
BLAST score
                  318
                  5.0e-32
E value
Match length
                  117
% identity
                  67
NCBI Description
                  (AC003114) Contains similarity to protein phosphatase 2C
                  (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                  224664
Seq. ID
                  LIB3166-016-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  q479406
BLAST score
                  484
E value
                  2.0e-49
Match length
                  106
                  87
% identity
                  chlorophyll a/b-binding protein - garden pea
NCBI Description
                  >gi_20671_emb_CAA49149 (X69215) chlorophyll a/b-binding
                  protein [Pisum sativum]
Seq. No.
                  224665
Seq. ID
                  LIB3166-016-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  q1495804
BLAST score
                  22,0
                  3.0e-18
E value
Match length
                  90
                  53
% identity
NCBI Description (X96406) 13-lipoxygenase [Solanum tuberosum]
Seq. No.
                  224666
Seq. ID
                  LIB3166-016-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q488727
BLAST score
                  381
E value
                  7.0e-37
Match length
                  84
                  75
% identity
NCBI Description (X72676) 1-aminocyclopropane-1-carboxylate synthase
                  [Brassica juncea]
Seq. No.
                  224667
                  LIB3166-016-P1-K1-C4
Seq. ID
Method
                  BLASTX
                  g114682
NCBI GI
BLAST score
                  206
E value
                  3.0e-16
                  71
Match length
% identity
                  63
                  ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)
                  >gi_100471_pir__A35227 H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, mitochondrial - sweet
                  potato >gi 168270 (J05397) F-1-ATPase delta subunit
```

Seq. No. 224668

Seq. ID LIB3166-016-P1-K1-C6

precursor (EC 3.6.1.3) [Ipomoea batatas]



```
Method
                  BLASTX
NCBI GI
                  g2662341
BLAST score
                  483
                  2.0e-52
E value
Match length
                  116
                  88
% identity
NCBI Description
                  (D63580) EF-1 alpha [Oryza sativa]
                  >gi 2662345 dbj BAA23659 (D63582) EF-1 alpha [Oryza
                  satīva] >gi 2662347 dbj BAA23660 (D63583) EF-1 alpha
                   [Oryza sativa]
Seq. No.
                  224669
Seq. ID
                  LIB3166-016-P1-K1-D11
                  BLASTX
Method
NCBI GI
                  q4406777
BLAST score
                  185
E value
                  8.0e-14
Match length
                  85
% identity
                   47
                  (AC006532) putative zinc-finger protein [Arabidopsis
NCBI Description
                  thaliana]
                  224670
Seq. No.
Seq. ID
                  LIB3166-016-P1-K1-D3
                  BLASTX
Method
NCBI GI
                  q4508070
BLAST score
                  377
                  2.0e-36
E value
Match length
                  121
% identity
                  55
NCBI Description
                  (AC005882) 24349 [Arabidopsis thaliana]
Seq. No.
                  224671
                  LIB3166-016-P1-K1-D4
Seq. ID
Method
                  BLASTX
                  g289920
NCBI GI
                   395
BLAST score
                  2.0e-38
E value
Match length
                  84
% identity
                   89
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                   224672
Seq. No.
                  LIB3166-016-P1-K1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3402678
                   269
BLAST score
E value
                   7.0e-24
Match length
                   99
                   57
% identity
NCBI Description (AC004697) putative adenylate kinase [Arabidopsis thaliana]
```

Seq. No. 224673

Seq. ID LIB3166-016-P1-K1-E1

Method BLASTX NCBI GI g3885334



```
BLAST score 408
E value 5.0e-40
Match length 119
% identity 62
NCBI Description (AC005623) putative argonaute protein [Arabidopsis thaliana]
```

Seq. No. 224674 Seq. ID LIB3166-016-P1-K1-E12

Method BLASTX
NCBI GI g544184
BLAST score 305
E value 7.0e-28
Match length 73
% identity 71

NCBI Description 4-ALPHA-GLUCANOTRANSFERASE PRECURSOR (AMYLOMALTASE)

(DISPROPORTIONATING ENZYME) (D-ENZYME)

>gi\_322785\_pir\_\_A45049 4-alpha-glucanotransferase (EC
2.4.1.25) - potato >gi\_296692\_emb\_CAA48630\_ (X68664)
4-alpha-glucanotransferase [Solanum tuberosum]

Seq. No. 224675

Seq. ID LIB3166-016-P1-K1-E3

Method BLASTX
NCBI GI g1076634
BLAST score 225
E value 2.0e-18
Match length 69
% identity 61

NCBI Description protein-serine/threonine kinase NPK15 - common tobacco

>gi 505146 dbj BAA06538 (D31737) protein-serine/threonine

kinase [Nicotiana tabacum]

Seq. No. 224676

Seq. ID LIB3166-016-P1-K1-E5

Method BLASTX
NCBI GI g123684
BLAST score 425
E value 5.0e-42
Match length 93
% identity 84

NCBI Description HEAT SHOCK FACTOR PROTEIN HSF24 (HEAT SHOCK TRANSCRIPTION

FACTOR 24) (HSTF 24) (HEAT STRESS TRANSCRIPTION FACTOR) >gi\_100267\_pir\_\_S12361 heat shock transcription factor HSF24 - Peruvian tomato >gi\_19488\_emb\_CAA39034\_ (X55347) heat stress transcription factor [Lycopersicon peruvianum]

Seq. No. 224677

Seq. ID LIB3166-016-P1-K1-E6

Method BLASTX
NCBI GI g1174199
BLAST score 218
E value 9.0e-18
Match length 87
% identity 51

NCBI Description (U44760) S25-PR6 [Nicotiana tabacum]



```
Seq. No.
                  224678
Seq. ID
                  LIB3166-016-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  q3915031
BLAST score
                  573
                  2.0e-59
E value
Match length
                  110
% identity
                  98
NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
                  (STEAROYL-ACP DESATURASE) >gi 1217628 emb CAA65232
                   (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase
                   [Gossypium hirsutum]
Seq. No.
                  224679
Seq. ID
                  LIB3166-016-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  q585973
BLAST score
                  496
E value
                  3.0e-50
Match length
                  118
% identity
                  83
NCBI Description FRUCTOKINASE > gi 626018 pir S39997 fructokinase (EC
                  2.7.1.4) - potato >gi 297015 emb CAA78283 (Z12823)
                  fructokinase [Solanum tuberosum] >gi_1095321_prf__2108342A
                  fructokinase [Solanum tuberosum]
Seq. No.
                  224680
Seq. ID
                  LIB3166-016-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g1263291
BLAST score
                  544
E value
                  6.0e-56
Match length
                  114
% identity
                  89
NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]
Seq. No.
                  224681
Seq. ID
                  LIB3166-016-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g3860263
BLAST score
                  269
E value
                  1.0e-23
Match length
                  65
% identity
                  71
NCBI Description
                  (AC005824) putative cytochrome p450 protein [Arabidopsis
                  thaliana]
Seq. No.
                  224682
Seq. ID
                  LIB3166-016-P1-K1-F12
Method
                  BLASTX
```

NCBI GI g2827712 BLAST score 100 E value 5.0e-12 Match length 102 % identity 44

NCBI Description (AL021684) endoxyloglucan tranferase-like protein

[Arabidopsis thaliana]



```
Seq. No.
                  224683
Seq. ID
                  LIB3166-016-P1-K1-F9
                  BLASTX
Method
NCBI GI
                  q117290
BLAST score
                  382
E value
                  3.0e - 37
Match length
                  89
% identity
                  85
NCBI Description
                  CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)
                  (P36) (E30) >gi 100071 pir S23774 triose
                  phosphate/3-phosphoglycerate/phosphate translocator
                  precursor - garden pea >qi 20691 emb CAA38451 (X54639)
                  chloroplast import receptor p36 [Pisum sativum]
                  >gi 20853 emb CAA48210 (X68077) phosphate translocator
                  [Pisum sativum] >gi 228551 prf 1805409A phosphate
                  translocator [Pisum sativum]
Seq. No.
                  224684
                  LIB3166-016-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g584778
BLAST score
                  214
E value
                  3.0e-17
Match length
                  107
% identity
                  50
NCBI Description
                  PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 2 PRECURSOR
                  (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 2) (DAHP
                  SYNTHETASE 2) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE
                  SYNTHASE 2) >gi 542033 pir S40412
                  2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 2
                  precursor - tomato >qi 410488 emb CAA79856 (221793)
                  phospho-2-dehydro-3-deoxyheptonate aldolase [Lycopersicon
                  esculentum]
                  224685
Seq. No.
                  LIB3166-016-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539348
BLAST score
                  303
E value
                  1.0e-27
Match length
                  114
                  53
% identity
NCBI Description (AL035539) putative pollen allergen [Arabidopsis thaliana]
Seq. No.
                  224686
                  LIB3166-016-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2736186
BLAST score
                  476
```

E value 6.0e-48Match length 128 % identity 69

NCBI Description (AF024623) galactose kinase [Arabidopsis thaliana]

Seq. No. 224687

LIB3166-016-P1-K1-G9 Seq. ID

Method

NCBI GI

BLASTX

g4102600



```
Method
                   BLASTX
NCBI GI
                   g2833375
BLAST score
                   356
                   7.0e-34
E value
Match length
                   71
% identity
                   93
NCBI Description
                   DNA-DIRECTED RNA POLYMERASE II 8.2 KD POLYPEPTIDE (RPB10)
                   (RP10) (ABC10) >qi 533690 (U12133) RNA polymerase II
                   subunit RPB10 homolog; similar to yeast RNA polymerase II
                   subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica
                   napus]
Seq. No.
                   224688
                   LIB3166-016-P1-K1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4006899
BLAST score
                   467
                   7.0e-47
E value
Match length
                   128
% identity
NCBI Description
                  (Z99708) putative protein [Arabidopsis thaliana]
Seq. No.
                   224689
Seq. ID
                   LIB3166-016-P1-K1-H11
Method
                   BLASTX
NCBI GI
                   q3776005
BLAST score
                   337
E value
                   7.0e-40
Match length
                   104
% identity
                   84
NCBI Description
                  (AJ010466) RNA helicase [Arabidopsis thaliana]
Seq. No.
                   224690
Seq. ID
                   LIB3166-016-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   q3859659
BLAST score
                   246
                   2.0e-21
E value
Match length
                   65
% identity
                   78
NCBI Description
                   (AL031394) putative potassium transporter AtKT5p (AtKT5)
                   [Arabidopsis thaliana]
Seq. No.
                   224691
                   LIB3166-016-P1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4538905
                   437
BLAST score
                   2.0e-43
E value
Match length
                   98
                   82
% identity
NCBI Description
                  (AL049482) putative protein [Arabidopsis thaliana]
Seq. No.
                   224692
Seq. ID
                   LIB3166-016-P1-K1-H5
```

Seq. No.



```
BLAST score
                  594
E value
                  1.0e-61
Match length
                  132
% identity
                  83
                  (AF013467) ARF6 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  224693
                  LIB3166-016-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3695388
BLAST score
                  165
                  2.0e-11
E value
Match length
                   43
                   60
% identity
                  (AF096371) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   224694
Seq. ID
                  LIB3166-016-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  q2244846
BLAST score
                   326
                  2.0e-32
E value
Match length
                   95
% identity
                  77
                  (Z97337) ferredoxin [Arabidopsis thaliana]
NCBI Description
```

224695

LIB3166-017-P1-K1-A1 Seq. ID Method BLASTX NCBI GI g541816 BLAST score 415 E value 7.0e-41Match length 108 % identity 69

protein kinase - common ice plant >gi 457689\_emb\_CAA82990 NCBI Description (Z30329) protein kinase [Mesembryanthemum crystallinum]

224696 Seq. No.

Seq. ID LIB3166-017-P1-K1-A10

Method BLASTX NCBI GI q4337175 BLAST score 420 2.0e-41 E value Match length 118 % identity 67

(AC006416) ESTs gb T20589, gb T04648, gb AA597906, NCBI Description

gb\_T04111, gb\_R84180, gb\_R65428, gb\_T44439, gb\_T76570, gb\_R90004, gb\_T45020, gb\_T42457, gb\_T20921, gb\_AA042762 and gb\_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No. 224697

LIB3166-017-P1-K1-A11 Seq. ID

Method BLASTX NCBI GI g3822036 BLAST score 243 1.0e-20 E value 124 Match length



```
% identity
                  (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]
NCBI Description
Seq. No.
                  224698
                  LIB3166-017-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q478673
BLAST score
                  273
                  4.0e-24
E value
Match length
                  73
                  67
% identity
NCBI Description
                  proline-rich protein precursor - kidney bean
                  >gi_21046_emb_CAA42942_ (X60391) proline-rich protein
                  [Phaseolus vulgaris]
Seq. No.
                  224699
                  LIB3166-017-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1297359
BLAST score
                  484
E value
                  8.0e-49
Match length
                  130
                  71
% identity
                 (U53701) alcohol dehydrogenase 2d [Gossypium hirsutum]
NCBI Description
Seq. No.
                  224700
Seq. ID
                  LIB3166-017-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g2243118
BLAST score
                  382
                  7.0e-37
E value
                  91
Match length
                  75
% identity
NCBI Description (Y10984) glutathione synthetase [Brassica juncea]
                  224701
Seq. No.
                  LIB3166-017-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455199
BLAST score
                  225
                  9.0e-19
E value
                  95
Match length
                  59
% identity
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
                  224702
Seq. No.
                  LIB3166-017-P1-K1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1762914
BLAST score
                  174
                  2.0e-12
E value
                  48
Match length
                  69
% identity
NCBI Description
                  (U65973) alcohol dehydrogenase A [Washingtonia robusta]
```

Seq. No. 224703

Seq. ID LIB3166-017-P1-K1-B1



```
Method
                   BLASTX
NCBI GI
                   g2194124
BLAST score
                   531
                   2.0e-54
E value
Match length
                   134
% identity
                   75
                   (AC002062) Similar to Glycine metalloendoproteinase
NCBI Description
                   (gb U63725). [Arabidopsis thaliana]
                   224704
Seq. No.
Seq. ID
                  LIB3166-017-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g3927838
BLAST score
                   212
E value
                   6.0e-17
Match length
                   45
                   91
% identity
NCBI Description
                  (AC005727) unknown protein [Arabidopsis thaliana]
Seq. No.
                  224705
Seq. ID
                  LIB3166-017-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q2980782
BLAST score
                   142
E value
                   9.0e-09
                  95
Match length
                   41
% identity
NCBI Description
                  (AL022198) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  224706
                  LIB3166-017-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129771
                  465
BLAST score
E value
                  9.0e-47
Match length
                  100
% identity
                  82
NCBI Description
                  xyloglucan endotransglycosylase-related protein XTR-6 -
                  Arabidopsis thaliana >gi_1244758 (U43488) xyloglucan
                  endotransglycosylase-related protein [Arabidopsis thaliana]
                  >gi_4539299_emb_CAB39602.1_ (AL049480) xyloglucan endo-1,
                  4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana]
Seq. No.
                  224707
Seq. ID
                  LIB3166-017-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q2352492
BLAST score
                  538
E value
                  3.0e-55
Match length
                  125
% identity
NCBI Description
                  (AF005047) transport inhibitor response 1 [Arabidopsis
```

thaliana] >gi\_2352494 (AF005048) transport inhibitor

response 1 [Arabidopsis thaliana]

Seq. No. 224708

Seq. ID LIB3166-017-P1-K1-B9



```
Method
                   BLASTX
NCBI GI
                   g4512625
BLAST score
                   177
                   7.0e-13
E value
Match length
                  106
% identity
                   31
NCBI Description
                   (AC004793) ESTs gb T20423, gb AA712864, gb H76323 and
                  gb_Z25560 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  224709
Seq. ID
                  LIB3166-017-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g3881507
BLAST score
                  149
E value
                  1.0e-09
Match length
                  46
% identity
                  52
NCBI Description
                  (Z47357) cDNA EST yk375c3.5 comes from this gene; cDNA EST
                  yk375c3.3 comes from this gene [Caenorhabditis elegans]
Seq. No.
                  224710
Seq. ID
                  LIB3166-017-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g3123264
BLAST score
                  407
E value
                  7.0e-40
Match length
                  85
% identity
                  87
NCBI Description
                  60S RIBOSOMAL PROTEIN L27 >gi 2244857 emb CAB10279
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  224711
Seq. ID
                  LIB3166-017-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g4510373
BLAST score
                  249
E value
                  3.0e-21
Match length
                  102
% identity
                  53
                  (AC007017) putative harpin-induced protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  224712
Seq. ID
                  LIB3166-017-P1-K1-C3
                  BLASTX
                  g729273
                  656
                  5.0e-69
                  136
```

Method NCBI GI BLAST score E value Match length % identity 90

CYPRO4 PROTEIN >gi\_322804\_pir\_\_S28592 cypro4 protein -NCBI Description

cardoon >gi\_17959\_emb\_CAA49354 (X69672) cypro4 [Cynara

cardunculus]

Seq. No. 224713

Seq. ID LIB3166-017-P1-K1-C4

Method BLASTX



```
NCBI GI
                   q4455155
BLAST score
                   307
E value
                   4.0e-28
Match length
                   129
% identity
                   46
NCBI Description
                  (AL022023) EF-1 alpha - like protein (fragment)
                   [Arabidopsis thaliana]
Seq. No.
                   224714
Seq. ID
                  LIB3166-017-P1-K1-C5
Method
                  BLASTX
NCBI GI
                   g1679794
BLAST score
                   306
E value
                   6.0e-28
Match length
                   115
% identity
                   52
NCBI Description (U77627) Allele: hi2 [Danio rerio]
Seq. No.
                  224715
Seq. ID
                  LIB3166-017-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g4567279
BLAST score
                   336
E value
                   2.0e-31
Match length
                  87
% identity
                   69
NCBI Description
                  (AC006841) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                  224716
                  LIB3166-017-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1362009
BLAST score
                  463
E value
                  2.0e-46
Match length
                  130
% identity
                  52
NCBI Description ubiquitin-like protein 7 - Arabidopsis thaliana
```

Seq. No. 224717

LIB3166-017-P1-K1-D11 Seq. ID

Method BLASTX NCBI GI g3024127 BLAST score 613 E value 5.0e-64 Match length 123 93 % identity

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)

>gi 1655578\_emb\_CAA95857\_ (Z71272) S-adenosyl-L-methionine

synthetase 2 [Catharanthus roseus]

Seq. No. 224718

Seq. ID LIB3166-017-P1-K1-D12

Method BLASTX NCBI GI q4098128 BLAST score 373



69

% identity

NCBI Description

```
E value
                  6.0e-36
Match length
                  79
% identity
                  96
NCBI Description
                  (U73588) sucrose synthase [Gossypium hirsutum]
                  224719
Seq. No.
Seq. ID
                  LIB3166-017-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g125606
BLAST score
                  389
                  9.0e-38
E value
Match length
                  84
                  87
% identity
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >qi 100463 pir S12248
NCBI Description
                  pyruvate kinase (EC 2.7.1.40) - potato
                  >gi 22576 emb CAA37727 (X53688) pyruvate kinase [Solanum
                  tuberosum]
Seq. No.
                  224720
                  LIB3166-017-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2661840
BLAST score
                  373
                  7.0e-36
E value
                  98
Match length
% identity
                  69
NCBI Description
                  (Y15430) adenosine kinase [Physcomitrella patens]
Seq. No.
                  224721
                  LIB3166-017-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454032
BLAST score
                  140
                  1.0e-08
E value
                  72
Match length
                  42
% identity
NCBI Description
                  (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                  224722
                  LIB3166-017-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3953471
BLAST score
                  238
E value
                  5.0e-20
Match length
                  68
                  68
% identity
NCBI Description
                  (AC002328) F2202.16 [Arabidopsis thaliana]
Seq. No.
                  224723
Seq. ID
                  LIB3166-017-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g3834307
BLAST score
                  434
E value
                  5.0e-43
Match length
                  128
```

31943

(AC005679) Strong similarity to gene T10I14.120 gi 2832679



putative protein from Arabidopsis thaliana BAC gb\_AL021712. ESTs gb\_N65887 and gb\_N65627 come from this gene. [Arabidopsis thaliana]

Seq. No. 224724

Seq. ID LIB3166-017-P1-K1-E5

Method BLASTX
NCBI GI g1871192
BLAST score 162
E value 4.0e-11
Match length 73
% identity 48

NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis

thaliana]

Seq. No. 224725

Seq. ID LIB3166-017-P1-K1-E6

Method BLASTX
NCBI GI g2160166
BLAST score 493
E value 7.0e-50
Match length 140
% identity 67

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 224726

Seq. ID LIB3166-017-P1-K1-F10

Method BLASTX
NCBI GI g3367568
BLAST score 330
E value 3.0e-33
Match length 108
% identity 64

NCBI Description (AL031135) protein kinase - like protein [Arabidopsis

thaliana]

Seq. No. 224727

Seq. ID LIB3166-017-P1-K1-F12

Method BLASTX
NCBI GI g3281846
BLAST score 170
E value 5.0e-12
Match length 59
% identity 59

NCBI Description (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]

Seq. No. 224728

Seq. ID LIB3166-017-P1-K1-F2

Method BLASTX
NCBI GI g4539408
BLAST score 366
E value 5.0e-35
Match length 135
% identity 60

NCBI Description (AL049524) putative alpha NAC [Arabidopsis thaliana]

Seq. No. 224729



Seq. ID LIB3166-017-P1-K1-F3 Method BLASTX NCBI GI g3746069 BLAST score 144 5.0e-09 E value Match length 104 % identity 30 NCBI Description (AC005311) putative reverse transcriptase [Arabidopsis thaliana] 224730 Seq. No. Seq. ID LIB3166-017-P1-K1-F7 Method BLASTX NCBI GI g2494111 BLAST score 407 7.0e-40 E value Match length 105 % identity 74 (AC002376) Contains similarity to Glycine protein kinase 6 NCBI Description (gb M67449). [Arabidopsis thaliana] Seq. No. 224731 Seq. ID LIB3166-017-P1-K1-F8 Method BLASTX NCBI GI g2961107 BLAST score 186 E value 6.0e-14 Match length 84 % identity 45 (AF042383) TLS-associated protein with SR repeats [Mus NCBI Description musculus] >gi 2961149 (AF047448) TLS-associated protein TASR [Homo sapiens] 224732 Seq. No. LIB3166-017-P1-K1-F9 Seq. ID Method BLASTX NCBI GI g3747050 BLAST score 416 E value 6.0e-41Match length 106 76 % identity (AF093540) ribosomal protein L26 [Zea mays] NCBI Description Seq. No. 224733 LIB3166-017-P1-K1-G10 Seq. ID Method BLASTX NCBI GI g1805359 BLAST score 285 E value 1.0e-25 Match length 131 % identity 43 NCBI Description (AB000623) glucosyl transferase [Nicotiana tabacum] Seq. No. 224734 LIB3166-017-P1-K1-G11

Method BLASTX NCBI GI g1172441

Seq. ID Method



BLAST score 239
E value 3.0e-20
Match length 104
% identity 56.

NCBI Description POSSIBLE TRANSCRIPTION FACTOR POSF21 >gi\_99685\_pir\_\_S21883

DNA-binding protein POSF21 - Arabidopsis thaliana >gi\_16429\_emb\_CAA43366\_ (X61031) posF21 [Arabidopsis

thaliana]

Seq. No. 224735

Seq. ID LIB3166-017-P1-K1-G12

Method BLASTX
NCBI GI g2160692
BLAST score 225
E value 1.0e-18
Match length 82
% identity 55

NCBI Description (U73527) B' regulatory subunit of PP2A [Arabidopsis

thaliana]

Seq. No. 224736

Seq. ID LIB3166-017-P1-K1-G3

Method BLASTX
NCBI GI g1469930
BLAST score 379
E value 2.0e-36
Match length 113

% identity 73

NCBI Description (U48777) fiber-specific acyl carrier protein [Gossypium

hirsutum]

Seq. No. 224737

Seq. ID LIB3166-017-P1-K1-G7

Method BLASTX
NCBI GI g1709651
BLAST score 328
E value 1.0e-30
Match length 112
% identity 58

NCBI Description PLASTOCYANIN A PRECURSOR >gi\_2117431\_pir\_\_S58209

plastocyanin a precursor - black poplar

>gi\_929813\_emb\_CAA90564\_ (Z50185) plastocyanin a [Populus

nigra]

Seq. No. 224738

Seq. ID LIB3166-017-P1-K1-G8

Method BLASTX
NCBI GI 9445612
BLAST score 507
E value 1.0e-51
Match length 102
% identity 96

NCBI Description ribosomal protein S19 [Solanum tuberosum]

Seq. No. 224739

Seq. ID LIB3166-017-P1-K1-H1

Method BLASTX



```
NCBI GI
                   g120669
BLAST score
                   530
E value
                   3.0e-54
Match length
                   113
% identity
                   88
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi 66014 pir DEJMG glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi 19566 emb CAA42905 (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                   224740
Seq. ID
                  LIB3166-017-P1-K1-H11
Method
                  BLASTX
NCBI GI
                   g1086252
BLAST score
                   371
E value
                   1.0e-35
Match length
                  103
% identity
                   68
NCBI Description
                  sucrose cleavage protein - Potato >gi 707001 bbs 157931
                   (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum
                  tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa]
                   [Solanum tuberosum]
Seq. No.
                  224741
Seq. ID
                  LIB3166-017-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g1061040
BLAST score
                   488
E value
                  2.0e-49
Match length
                  96
                  92
% identity
NCBI Description
                   (X89867) sterol-C-methyltransferase [Arabidopsis thaliana]
                  >gi 1587694 prf 2207220A sterol C-methyltransferase
                  [Arabidopsis thaliana]
Seq. No.
                  224742
Seq. ID
                  LIB3166-017-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g3123271
BLAST score
                  487
E value
                  3.0e-49
Match length
                  100
                  88
% identity
                 40S RIBOSOMAL PROTEIN S6 >gi 2224751 emb CAA74381 (Y14052)
NCBI Description
                  ribosomal protein S6 [Arabidopsis thaliana]
Seq. No.
                  224743
Seq. ID
                  LIB3166-017-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g2842689
BLAST score
                  144
E value
                  4.0e-09
Match length
```

% identity 36 NCBI Description HYPOTHETICAL 50.4 KD PROTEIN C1F8.04C IN CHROMOSOME I >gi\_1638851\_emb\_CAB03598\_ (Z81312) unknown

Seq. ID Method



## [Schizosaccharomyces pombe]

```
Seq. No.
                  224744
Seq. ID
                  LIB3166-017-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q2213884
BLAST score
                  514
E value
                  2.0e-52
Match length
                  134
                  71
% identity
                  (AF004166) 2-isopropylmalate synthase [Lycopersicon
NCBI Description
                  pennellii]
                  224745
Seq. No.
                  LIB3166-017-P1-K1-H7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2286153
BLAST score
                  535
E value
                  6.0e-55
                  112
Match length
% identity
                  96
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
                  224746
Seq. No.
                  LIB3166-018-P1-K1-A10
Seq. ID
                  BLASTX
Method
                  q4539348
NCBI GI
BLAST score
                  274
E value
                  3.0e-24
Match length
                  104
                  52
% identity
NCBI Description (AL035539) putative pollen allergen [Arabidopsis thaliana]
Seq. No.
                  224747
                  LIB3166-018-P1-K1-A2
Seq. ID
Method
                  BLASTX
               , g1170312
NCBI GI
BLAST score
                  452
E value
                  4.0e-45
Match length
                  111
% identity
                  87
NCBI Description HOMEOBOX PROTEIN SBH1 >gi_629614_pir__S42543 hypothetical
                  protein - soybean >gi 485406 (L13663) SBH1 [Glycine max]
                  224748
Seq. No.
                  LIB3166-018-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2865427
BLAST score
                  214
                  2.0e-17
E value
                  95
Match length
% identity
                   48
NCBI Description (AF039372) polyprotein [Arabidopsis thaliana]
Seq. No.
                  224749
```

31948

LIB3166-018-P1-K1-A5

BLASTX



```
NCBI GI
                  g1220196
BLAST score
                  540
                  2.0e-55
E value
Match length
                  111
% identity
                  89
                  (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
NCBI Description
                  224750
Seq. No.
Seq. ID
                  LIB3166-018-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g2347199
BLAST score
                  261
                  7.0e-23
E value
                  109
Match length
                  51
% identity
                 (AC002338) protein kinase isolog [Arabidopsis thaliana]
NCBI Description
                  224751
Seq. No.
Seq. ID
                  LIB3166-018-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g2961384
BLAST score
                  238
                  5.0e-20
E value
Match length
                  127
% identity
                  36
                  (AL022141) aldehyde dehydrogenase like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  224752
Seq. ID
                  LIB3166-018-P1-K1-B1
                  BLASTX
Method
NCBI GI
                  q4580517
BLAST score
                  396
E value
                  3.0e-39
Match length
                  135
% identity
                  61
                  (AF036302) scarecrow-like 5 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  224753
Seq. ID
                  LIB3166-018-P1-K1-B10
Method
                  BLASTX
                  g2078350
NCBI GI
BLAST score
                  216
                  1.0e-17
E value
Match length
                  51
% identity
                  88
                  (U95923) transaldolase [Solanum tuberosum]
NCBI Description
                  224754
Seq. No.
                  LIB3166-018-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129758
BLAST score
                  292
                  1.0e-36
E value
                  82
Match length
                  78
% identity
```

NCBI Description ubiquitin conjugating enzyme E2 protein - Arabidopsis



thaliana >gi\_992704 (U33757) UBC7 [Arabidopsis thaliana]

Seq. No. 224755 Seq. ID LIB3166-018-P1-K1-B5 Method BLASTX NCBI GI q2160189 BLAST score 264 E value 4.0e-23 Match length 106 52 % identity (AC000132) Similar to A. thaliana receptor-like protein NCBI Description kinase (gb\_RLK5\_ARATH). ESTs gb\_ATTS0475,gb\_ATTS4362 come from this gene. [Arabidopsis thaliana] Seq. No. 224756 Seq. ID LIB3166-018-P1-K1-B8 Method BLASTX NCBI GI q3758833 BLAST score 216 E value 3.0e-23 Match length 124 % identity 53 NCBI Description (Y18225) MtN6 [Medicago truncatula] Seq. No. 224757 Seq. ID LIB3166-018-P1-K1-C1 Method BLASTX NCBI GI q4455208 BLAST score 487 E value 3.0e-49Match length 116 % identity 81 NCBI Description (AL035440) putative protein [Arabidopsis thaliana] Seq. No. 224758 LIB3166-018-P1-K1-C10 Seq. ID Method BLASTX NCBI GI g3885329 503 BLAST score E value 3.0e-5196 Match length 98 % identity NCBI Description (AC005623) alien-like protein [Arabidopsis thaliana] Seq. No. 224759 Seq. ID LIB3166-018-P1-K1-C11 Method BLASTX NCBI GI g2498982 BLAST score 221 E value 4.0e-18 Match length 78 % identity 51 NCBI Description TRANSCRIPTION INITIATION FACTOR TFIID 31 KD SUBUNIT (TAFII-31) (TAFII-32) (TAFII32) (NEURONAL CELL DEATH RELATED GENE IN NEURON -7) (DN-7) >gi\_1103900 (U40188)

induced upon programmed cell death in neuronally
differentiated PC12 cells [Rattus norvegicus]



71

NCBI Description

```
Seq. No.
                   224760
                   LIB3166-018-P1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4210948
BLAST score
                   545
                   6.0e-56
E value
                   104
Match length
% identity
                   98
NCBI Description
                  (AF085275) DnaJ protein [Hevea brasiliensis]
Seq. No.
                   224761
                   LIB3166-018-P1-K1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3402279
BLAST score
                   576
E value
                   1.0e-59
Match length
                   121
% identity
                   89
NCBI Description
                   (AJ000999) putative beta-subunit of K+ channels [Solanum
                   tuberosum]
Seq. No.
                   224762
                  LIB3166-018-P1-K1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4103324
BLAST score
                   583
E value
                   2.0e-60
Match length
                   127
% identity
                   87
NCBI Description
                   (AF022716) GDP-mannose pyrophosphorylase [Solanum
                   tuberosum]
                   224763
Seq. No.
Seq. ID
                  LIB3166-018-P1-K1-C7
Method
                  BLASTX
NCBI GI
                   g4218011
                   142
BLAST score
E value
                   8.0e-09
                   115
Match length
                   34
% identity
NCBI Description
                   (AC006135) putative protein kinase [Arabidopsis thaliana]
                   >gi_4309721_gb_AAD15491_ (AC006439) putative
                   serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.
                   224764
                  LIB3166-018-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3551983
BLAST score
                   402
E value
                  2.0e-39
Match length
                  117
% identity
```

(AF085073) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_3551985 (AF085074) alcohol dehydrogenase A [Gossypium hirsutum] >gi 3551987 (AF085075) alcohol dehydrogenase A [Gossypium hirsutum] >gi 3551989 (AF085076) alcohol



dehydrogenase A [Gossypium hirsutum] >gi\_4140602 (AF090150) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140612 (AF090155) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140614 (AF090156) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140616 (AF090157) alcohol dehydrogenase A [Gossypium hirsutum]

224765 Seq. No. LIB3166-018-P1-K1-C9 Seq. ID Method BLASTX NCBI GI g3033395 BLAST score 293 E value 2.0e-26 Match length 75 % identity 69 NCBI Description (AC004238) putative zinc-finger protein [Arabidopsis thaliana] 224766 Seq. No. Seq. ID LIB3166-018-P1-K1-D10 Method BLASTX NCBI GI g3122060 BLAST score 303 7.0e-28 E value 59 Match length 98 \*\*identity NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2598657 emb CAA10847 (AJ222579) elongation factor 1-alpha (EF1-a) [Vicia faba] Seq. No. 224767 Seq. ID LIB3166-018-P1-K1-D11 Method BLASTX NCBI GI g4558553 BLAST score 313 E value 7.0e-29 Match length 100 % identity 59 NCBI Description (AC007138) putative potassium channel [Arabidopsis thaliana] Seq. No. 224768 LIB3166-018-P1-K1-D12 Seq. ID Method BLASTX NCBI GI g3334320 BLAST score 452 E value 4.0e-45 Match length 98 % identity 94 NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553) ribosome-associated protein p40 [Glycine max]

Seq. No. 224769

Seq. ID LIB3166-018-P1-K1-D3

MethodBLASTXNCBI GIg4539335BLAST score306

Seq. ID Method

NCBI GI

E value

BLAST score



```
E value
                   6.0e-28
Match length
                  123
                  50
% identity
                  (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                  224770
Seq. No.
                  LIB3166-018-P1-K1-D4
Seq. ID
Method
                  BLASTX
                  q1943751
NCBI GI
BLAST score
                  595
                  7.0e-62
E value
                  131
Match length
                  85
% identity
                  (U93845) Arabidopsis thaliana ER-type calcium pump
NCBI Description
                  protein, complete sequence >gi 2078292 (U96455) ER-type
                  Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]
Seq. No.
                  224771
Seq. ID
                  LIB3166-018-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  q2980770
                  329
BLAST score
                  1.0e-30
E value
Match length
                  134
                  57
% identity
NCBI Description
                  (AL022198) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  224772
Seq. ID
                  LIB3166-018-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q118548
BLAST score
                   439
                  1.0e-43
E value
                  133
Match length
% identity
                  59
NCBI Description
                  NADP-SPECIFIC GLUTAMATE DEHYDROGENASE (NADP-GDH)
                  >gi_283447_pir__A42489 glutamate dehydrogenase (NADP+) (EC
                  1.4.1.4) - Giardia lamblia >gi 159109 (M84604)
                  NADP-dependent glutamate dehydrogenase [Giardia lamblia]
Seq. No.
                   224773
                  LIB3166-018-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82040
BLAST score
                   600
                  2.0e-62
E value
Match length
                  122
% identity
                  27
                  ubiquitin precursor - flax (fragment) >gi 168304 (M57895)
NCBI Description
                  ubiquitin [Linum usitatissimum]
                  224774
Seq. No.
```

31953

LIB3166-018-P1-K1-E10

BLASTX

388 1.0e-37

g2739365



```
Match length
                  81
                  83
% identity
NCBI Description
                  (AC002505) unknown protein [Arabidopsis thaliana]
Seq. No.
                  224775
                  LIB3166-018-P1-K1-E6
Seq. ID
Method
                  BLASTX
                  g2500354
NCBI GI
BLAST score
                  638
E value
                  7.0e-67
                  123
Match length
                  95
% identity
                  60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462
NCBI Description
                  (AB001891) QM family protein [Solanum melongena]
                  224776
Seq. No.
                  LIB3166-018-P1-K1-E8
Seq. ID
Method
                  BLASTX
                  g119137
NCBI GI
BLAST score
                  532
E value
                  1.0e-54
Match length
                  102
                  97
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi_82771_pir_S06300 translation elongation factor eEF-1
                  alpha chain, cytosolic (gene TEF2) - Rhizomucor
                  circinelloides f. lusitanicus >gi 2963 emb CAA35507
                  (X17476) EF-1-alpha [Rhizomucor racemosus]
                  224777
Seq. No.
                  LIB3166-018-P1-K1-F1
Seq. ID
Method
                  BLASTX
                  g4490732
NCBI GI
BLAST score
                  638
E value
                  7.0e-67
Match length
                  123
% identity
                  93
NCBI Description
                 (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
                  protein [Arabidopsis thaliana]
                  224778
Seq. No.
Seq. ID
                  LIB3166-018-P1-K1-F3
Method
                  BLASTX
                  g2852688
NCBI GI
BLAST score
                  219
                  7.0e-18
E value
Match length
                  95
% identity
                  45
NCBI Description (AF017753) resistance protein candidate [Lactuca sativa]
Seq. No.
                  224779
```

Seq. ID LIB3166-018-P1-K1-F5

Method BLASTX
NCBI GI g4432846
BLAST score 362
E value 2.0e-34
Match length 135



```
% identity
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                  224780
Seq. No.
                  LIB3166-018-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173257
BLAST score
                  172
                  2.0e-12
E value
                  61
Match length
                  56
% identity
                  40S RIBOSOMAL PROTEIN S4 >gi 1076674 pir S47642 ribosomal
NCBI Description
                  protein S4 - potato >gi 457803 emb CAA54095 (X76651)
                  ribosomal protein S4 [Solanum tuberosum]
Seq. No.
                  224781
                  LIB3166-018-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3775989
BLAST score
                  149
                  7.0e-10
E value
Match length
                  33
% identity
                  88
                  (AJ010458) RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  224782
                  LIB3166-018-P1-K1-G1
Seq. ID
Method
                  BLASTX
                  g4218535
NCBI GI
BLAST score
                  387
                  2.0e-37
E value
Match length
                  96
                   68
% identity
NCBI Description
                  (AJ010829) GRAB1 protein [Triticum sp.]
                  224783
Seq. No.
Seq. ID
                  LIB3166-018-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  a886116
BLAST score
                   496
E value
                   3.0e-50
Match length
                  123
% identity
                   71
                   (U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473
NCBI Description
                   (AF051338) xyloglucan endotransglycosylase related protein
                   [Arabidopsis thaliana]
Seq. No.
                   224784
Seq. ID
                  LIB3166-018-P1-K1-G12
Method
                  BLASTX
NCBI GI
                   g1220196
BLAST score
                   560
```

E value 9.0e-58 Match length 120 % identity 88

NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]



```
224785
Seq. No.
                  LIB3166-018-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4468994
BLAST score
                  334
E value
                  3.0e-31
                  115
Match length
                  55
% identity
                  (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  224786
Seq. ID
                  LIB3166-018-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q2136258
BLAST score
                  149
E value
                  1.0e-09
                  66
Match length
                   44
% identity
                  template activating factor-I, splice form alpha - human
NCBI Description
                  >gi_971272_dbj_BAA08139_ (D45198) template acyivating
                   factor-I alpha [Homo sapiens]
                   224787
Seq. No.
                  LIB3166-018-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539333
BLAST score
                   438
                   2.0e-43
E value
Match length
                  131
                   64
% identity
NCBI Description
                  (AL035539) putative amino acid transport protein
                   [Arabidopsis thaliana]
                   224788
Seq. No.
                  LIB3166-018-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4006829
BLAST score
                   250
E value
                   2.0e-21
Match length
                   135
% identity
                   39
NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   224789
                   LIB3166-018-P1-K1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2708743 -
BLAST score
                   145
E value
                   2.0e-15
Match length
                   127
                   39
% identity
NCBI Description
                   (AC003952) putative Tal-1-like reverse transcriptase
                   [Arabidopsis thaliana]
```

Seq. No. 224790

Seq. ID LIB3166-018-P1-K1-H12

Method BLASTX

E value

Match length

6.0e-33

104



```
g4262237
  NCBI GI
BLAST score
                     279
  E value
                     8.0e-25
  Match length
                     64
  % identity
                     75
  NCBI Description (AC006200) hypothetical protein [Arabidopsis thaliana]
  Seq. No.
                     224791
  Seq. ID
                    LIB3166-018-P1-K1-H2
  Method
                    BLASTX
  NCBI GI
                     g349379
  BLAST score
                     163
  E value
                     3.0e-11
  Match length
                     62
                     58
  % identity
  NCBI Description (L22847) HAHB-1 [Helianthus annuus]
                    224792
  Seq. No.
                    LIB3166-018-P1-K1-H3
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g1439609
  BLAST score
                     595
  E value
                    7.0e-62
  Match length
                    123
  % identity
                     61
  NCBI Description
                    (U62778) delta-tonoplast intrinsic protein [Gossypium
                    hirsutum]
  Seq. No.
                     224793
  Seq. ID
                    LIB3166-018-P1-K1-H4
  Method
                    BLASTX
  NCBI GI
                    g2370312
  BLAST score
                    298
  E value
                     4.0e-27
  Match length
                    108
  % identity
                    56
  NCBI Description
                    (AJ000995) DnaJ-like protein [Medicago sativa] >gi 3202020
                     (AF069507) DnaJ-like protein MsJ1 [Medicago sativa]
  Seq. No.
                    224794
  Seq. ID
                    LIB3166-018-P1-K1-H5
  Method
                    BLASTX
  NCBI GI
                    g1370589
  BLAST score
                    187
  E value
                    5.0e-14
  Match length
                    88
  % identity
                    51
  NCBI Description
                    (X98304) protein induced upon tuberization [Solanum
                    demissum]
  Seq. No.
                    224795
  Seq. ID
                    LIB3166-018-P1-K1-H7
  Method
                    BLASTX
  NCBI GI
                    g4539348
  BLAST score
                    347
```



% identity (AL035539) putative pollen allergen [Arabidopsis thaliana] NCBI Description 224796 Seq. No. Seq. ID LIB3166-018-P1-K1-H8 Method BLASTX NCBI GI g3193316 BLAST score 279 6.0e-25 E value 105 Match length 56 % identity (AF069299) contains similarity to nucleotide sugar NCBI Description epimerases [Arabidopsis thaliana] 224797 Seq. No. LIB3166-018-P1-K1-H9 Seq. ID Method BLASTX NCBI GI q4115337 BLAST score 426 2.0e-42 E value 88 Match length % identity 17 (L81141) ubiquitin [Pisum sativum] NCBI Description Seq. No. 224798 LIB3166-019-P1-K1-A10 Seq. ID Method BLASTX NCBI GI g2583108 BLAST score 360 3.0e - 34E value 140 Match length 60 % identity NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana] 224799 Seq. No. LIB3166-019-P1-K1-A3 Seq. ID Method BLASTX NCBI GI g82426 BLAST score 570 6.0e-59 E value Match length 117 46 % identity

NCBI Description ubiquitin precursor - barley (fragment)

>gi\_755763\_emb\_CAA27751\_ (X04133) ubiquitin polyprecursor

(171 aa) [Hordeum vulgare]

224800 Seq. No.

Seq. ID LIB3166-019-P1-K1-A8

Method BLASTX NCBI GI q3024126 BLAST score 490 E value 1.0e-49 Match length 98 % identity 95

S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi\_1655576\_emb\_CAA95856\_ (Z71271) S-adenosyl-L-methionine

Method

NCBI GI

BLASTX g1514977



## synthetase 1 [Catharanthus roseus]

```
Seq. No.
                  224801
Seq. ID
                  LIB3166-019-P1-K1-A9
Method
                  BLASTX
                  q2129820
NCBI GI
BLAST score
                  209
E value
                  7.0e-17
                  83
Match length
                  49
% identity
                  chitinase (EC 3.2.1.14) class II - peanut
NCBI Description
                  >gi 1237025 emb CAA57773 (X82329) chitinase (class II)
                   [Arachis hypogaea]
                  224802
Seq. No.
                  LIB3166-019-P1-K1-B1
Seq. ID
Method
                  BLASTX
                  q544382
NCBI GI
BLAST score
                  161
                  5.0e-11
E value
                  76
Match length
                   47
% identity
                  GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE
NCBI Description
                   (ISOMERIZING) (HEXOSEPHOSPHATE AMINOTRANSFERASE)
                   (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GFAT)
                  >gi 345855 pir A45055 glutamine--fructose-6-phosphate
                   transaminase (isomerizing) (EC 2.6.1.16) - human >gi_183082
                   (M90516) glutamine:fructose-6-phosphate amidotransferase
                   [Homo sapiens] >gi 4503981 ref NP 002047.1 pGFPTa_
                  glutamine-fructose-6-phosphate transaminase
Seq. No.
                  224803
                  LIB3166-019-P1-K1-B11
Sea. ID
                  BLASTX
Method
NCBI GI
                  g3789911
BLAST score
                   295
                   1.0e-26
E value
Match length
                   114
% identity
                   49
                   (AF081802) developmental protein DG1118 [Dictyostelium
NCBI Description
                   discoideum]
                   224804
Seq. No.
                  LIB3166-019-P1-K1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4406780
BLAST score
                   577
                   1.0e-59
E value
Match length
                   139
% identity
                   81
                   (AC006532) putative multispanning membrane protein
NCBI Description
                   [Arabidopsis thaliana]
                   224805
Seq. No.
                  LIB3166-019-P1-K1-B4
Seq. ID
```



BLAST score 534 E value 1.0e-54 Match length 125 % identity 56

NCBI Description (D84669) VM23 [Raphanus sativus]

Seq. No. 224806

Seq. ID LIB3166-019-P1-K1-B6

Method BLASTX
NCBI GI g421826
BLAST score 390
E value 8.0e-38
Match length 79
% identity 86

NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

>gi 298036 emb CAA50712 (X71878) CP29 [Arabidopsis

thaliana]

Seq. No. 224807

Seq. ID LIB3166-019-P1-K1-B7

Method BLASTX
NCBI GI g136636
BLAST score 359
E value 3.0e-34
Match length 72
% identity 92

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi\_1076424\_pir\_\_S43781 ubiquitin-conjugating enzyme UBC1 -

Arabidopsis thaliana >gi\_442594\_pdb\_1AAK\_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi\_2981894\_pdb\_2AAK\_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi\_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi\_431260 (L19351) ubiquitin conjugating enzyme

[Arabidopsis thaliana]

Seq. No. 224808

Seq. ID LIB3166-019-P1-K1-B8

Method BLASTX
NCBI GI g1263291
BLAST score 578
E value 7.0e-60
Match length 110
% identity 98

NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No. 224809

Seq. ID LIB3166-019-P1-K1-B9

Method BLASTX
NCBI GI g3550454
BLAST score 165
E value 7.0e-20
Match length 69
% identity 81

NCBI Description (AF085820) alcohol dehydrogenase A [Gossypium barbadense]

>gi\_3550458 (AF085821) alcohol dehydrogenase A [Gossypium barbadense] >gi 3551965 (AF085064) alcohol dehydrogenase A



[Gossypium hirsutum] >gi\_3551967 (AF085065) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_3551971 (AF085067) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_3551975 (AF085069) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_3551977 (AF085070) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140594 (AF090146) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140604 (AF090151) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140606 (AF090152) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140608 (AF090153) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140610 (AF090154) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140610 (AF090154) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. No. 224810 LIB3166-019-P1-K1-C1 Seq. ID Method BLASTX NCBI GI g417073 BLAST score 463 2.0e-46 E value Match length 120 % identity 78

NCBI Description GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT)

>gi\_484529\_pir\_\_JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi\_166412 (L01660) NADH-glutamate

synthase [Medicago sativa]

Seq. No. 224811

Seq. ID LIB3166-019-P1-K1-C10

Method BLASTX
NCBI GI g2576411
BLAST score 280
E value 6.0e-25
Match length 109
% identity 61

NCBI Description (AF012833) similar to dynamin-like protein encoded by GenBank Accession Number X99669 [Arabidopsis thaliana]

Seq. No. 224812

Seq. ID LIB3166-019-P1-K1-C3

Method BLASTX
NCBI GI g2129921
BLAST score 195
E value 6.0e-15
Match length 51
% identity 75

NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi\_758694

(U12573) putative [Catharanthus roseus]

Seq. No. 224813

Seq. ID LIB3166-019-P1-K1-C4

Method BLASTX
NCBI GI g3548810
BLAST score 200
E value 2.0e-15
Match length 113
% identity 42

NCBI Description (AC005313) putative chloroplast nucleoid DNA binding

NCBI Description



## protein [Arabidopsis thaliana]

```
Seq. No.
                   224814
                   LIB3166-019-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3924602
BLAST score
                   262
                   4.0e-23
E value
                   82
Match length
% identity
                   62
                   (AF069442) predicted OR23 protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                  224815
Seq. No.
Seq. ID
                  LIB3166-019-P1-K1-D1
Method
                  BLASTX
NCBI GI
                   q3046731
BLAST score
                   236
E value
                   1.0e-34
Match length
                   129
% identity
                   67
NCBI Description
                 (AJ005373) protein kinase [Craterostigma plantagineum]
Seq. No.
                  224816
                  LIB3166-019-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2499710
BLAST score
                   661
E value
                   1.0e-69
Match length
                  135
% identity
                   86
                 PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
NCBI Description
                   (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                  >gi 1438075 (L33686) phospholipase D [Ricinus communis]
                  224817
Seq. No.
Seq. ID
                  LIB3166-019-P1-K1-D11
Method
                  BLASTX
NCBI GI
                   q2288981
BLAST score
                  162
E value
                   3.0e-11
Match length
                  97
% identity
                  25
                  (AC002335) calcium binding protein isolog [Arabidopsis
NCBI Description
                  thaliana] >gi_3763938 (AC004450) putative calcium binding
                  protein [Arabidopsis thaliana]
Seq. No.
                  224818
                  LIB3166-019-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q556347
BLAST score
                  269
E value
                   6.0e-24
Match length
                  92
                   49
% identity
```

>gi 445608\_prf\_\_1909355A protein kinase [Pisum sativum]

(M92989) protein kinase [Pisum sativum]

% identity

70



```
224819
Seq. No.
Seq. ID
                  LIB3166-019-P1-K1-D2
                  BLASTX
Method
                  g2213592
NCBI GI
                  232
BLAST score
                  3.0e-19
E value
                  72
Match length
                  33
% identity
                  (AC000348) T7N9.12 [Arabidopsis thaliana]
NCBI Description
                  224820
Seq. No.
                  LIB3166-019-P1-K1-D4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2605621
BLAST score
                  369
E value
                  2.0e-46
Match length
                  122
% identity
                  78
NCBI Description (D88619) OSMYB3 [Oryza sativa]
                  224821
Seq. No.
Seq. ID
                  LIB3166-019-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g1709651
BLAST score
                  326
                  2.0e - 34
E value
Match length
                  113
% identity
                  69
                 PLASTOCYANIN A PRECURSOR >gi 2117431 pir S58209
NCBI Description
                  plastocyanin a precursor - black poplar
                  >gi 929813 emb CAA90564 (Z50185) plastocyanin a [Populus
                  nigra]
                  224822
Seq. No.
                  LIB3166-019-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4056469
                  597
BLAST score
                   4.0e-62
E value
                  118
Match length
                   98
% identity
                  (AC005990) Strong similarity to gb_M95166 ADP-ribosylation
NCBI Description
                   factor from Arabidopsis thaliana. ESTs gb_Z25826,
                  gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,
                   gb AA712956, gb T46403, gb T46050, gb AI100391 and
                   gb_Z25043 come from t
                   224823
Seq. No.
                  LIB3166-019-P1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                  g2160189
BLAST score
                  508
E value
                   1.0e-51
                  135
Match length
```

NCBI Description (AC000132) Similar to A. thaliana receptor-like protein



kinase (gb\_RLK5\_ARATH). ESTs gb\_ATTS0475,gb\_ATTS4362 come from this gene. [Arabidopsis thaliana]

Seq. No. 224824 LIB3166-019-P1-K1-E1 Seq. ID Method BLASTX NCBI GI q4371290 BLAST score 273 E value 5.0e-24 Match length 105 51 % identity NCBI Description (AC006260) unknown protein [Arabidopsis thaliana] Seq. No. 224825 Seq. ID LIB3166-019-P1-K1-E2

Method BLASTX
NCBI GI g1871192
BLAST score 224
E value 2.0e-18

Match length 91 % identity 48

NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis

thaliana]

Seq. No. 224826

Seq. ID LIB3166-019-P1-K1-E3

Method BLASTX
NCBI GI g4105794
BLAST score 209
E value 1.0e-16
Match length 67
% identity 52

NCBI Description (AF049928) PGP224 [Petunia x hybrida]

Seq. No. 224827

Seq. ID LIB3166-019-P1-K1-E4

Method BLASTX
NCBI GI g4371284
BLAST score 647
E value 6.0e-68
Match length 137
% identity 89

NCBI Description (AC006260) putative plasma membrane intrinsic protein 2B

[Arabidopsis thaliana]

Seq. No. 224828

Seq. ID LIB3166-019-P1-K1-E5

Method BLASTX
NCBI GI g1220196
BLAST score 615
E value 3.0e-64
Match length 115
% identity 99

NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No. 224829

Seq. ID LIB3166-019-P1-K1-E6



```
Method
                  BLASTX
NCBI GI
                  q3461833
BLAST score
                  466
E value
                  9.0e-47
Match length
                  120
% identity
                  (AC004138) putative expansin [Arabidopsis thaliana]
NCBI Description
                  224830
Seq. No.
                  LIB3166-019-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q547683
BLAST score
                  593
                  1.0e-61
E value
Match length
                  126
% identity
                  91
NCBI Description
                  HEAT SHOCK COGNATE PROTEIN 80 >gi 170456 (M96549) heat
                  shock cognate protein 80 [Solanum lycopersicum]
                  >gi_445601_prf 1909348A heat shock protein hsp80
                  [Lycopersicon esculentum]
Seq. No.
                  224831
                  LIB3166-019-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3953457
BLAST score
                  238
                  4.0e-20
E value
                  101
Match length
% identity
                  52
NCBI Description (AC002328) F20N2.2 [Arabidopsis thaliana]
                  224832
Seq. No.
Seq. ID
                  LIB3166-019-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g3877723
BLAST score
                  228
E value
                  8.0e-19
Match length
                  118
% identity
                  42
NCBI Description
                  (Z69646) similar to Na(+)/H(+) exchanger; cDNA EST
                  yk249c8.5 comes from this gene; cDNA EST yk255a8.5 comes
                  from this gene; cDNA EST EMBL: C12746 comes from this gene;
                  cDNA EST yk471c10.5 comes from this gene [Caenorhabditis
                  ele
                  224833
Seq. No.
                  LIB3166-019-P1-K1-F4
Seq. ID
Method
                  BLASTX
                  g4580523
NCBI GI
BLAST score
                  179
                  4.0e-13
E value
Match length
                  51
% identity
                  67
NCBI Description
                  (AF036305) scarecrow-like 8 [Arabidopsis thaliana]
```

224834

LIB3166-019-P1-K1-F5

Seq. No.

Seq. ID

% identity

57



```
Method
                  BLASTX
NCBI GI
                   g3451072
BLAST score
                   314
E value
                   3.0e-29
Match length
                   91
                   69
% identity
NCBI Description
                  (AL031326) putative protein [Arabidopsis thaliana]
                  224835
Seq. No.
                  LIB3166-019-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4008159
BLAST score
                   356
                  1.0e-39
E value
Match length
                  99
% identity
                  84
NCBI Description
                  (AB015601) DnaJ homolog [Salix gilgiana]
Seq. No.
                   224836
Seq. ID
                  LIB3166-019-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g1871577
BLAST score
                   324
                  4.0e-30
E value
Match length
                  111
% identity
                  55
NCBI Description
                  (Y11553) putative 21kD protein precursor [Medicago sativa]
Seq. No.
                  224837
                  LIB3166-019-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4220537
BLAST score
                  153
E value
                   4.0e-10
                  32
Match length
% identity
                  91
NCBI Description
                 (AL035356) PsRT17-1 like protein [Arabidopsis thaliana]
Seq. No.
                  224838
Seq. ID
                  LIB3166-019-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g3434967
BLAST score
                  212
E value
                  6.0e-17
Match length
                  77
% identity
                  55
                  (AB008103) ethylene responsive element binding factor 1
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  224839
Seq. ID
                  LIB3166-019-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g1709358
BLAST score
                  237
E value
                  1.0e-31
Match length
                  134
```



```
NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE
NCBI Description
                  PHOSPHOHYDROLASE) (NTPASE) >gi 629638 pir S48859
                  nucleoside triphosphatase - garden pea
                  >qi 2129890 pir S65147 nucleoside triphosphatase
                  precursor, chromatin-associated - garden pea
                  >qi 563612 emb CAA83655 (Z32743) nucleoside triphosphatase
                  [Pisum sativum] >gi 4519173 dbj BAA75506.1 (AB022319)
                  nucleoside triphosphatase (NTPase) [Pisum sativum]
Seq. No.
                  224840
                  LIB3166-019-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1220196
BLAST score
                  268
                  8.0e-24
E value
Match length
                  90
% identity
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.
                  224841
Seq. ID
                  LIB3166-019-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g2244732
BLAST score
                  207
                  2.0e-16
E value
                  65
Match length
                  71
% identity
NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
Seq. No.
                  224842
Seq. ID
                  LIB3166-019-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g2827699
BLAST score
                  212
E value
                  6.0e-17
Match length
                  67
% identity
                  60
                  (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
                  224843
Seq. No.
                  LIB3166-019-P1-K1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4545262
BLAST score
                  241
                  1.0e-20
E value
Match length
                  54
                  83
% identity
                  (AF118230) metallothionein-like protein [Gossypium
NCBI Description
                  hirsutum]
```

224844 Seq. No.

LIB3166-019-P1-K1-H3 Seq. ID

Method BLASTX NCBI GI g2129921 BLAST score 194 E value 8.0e-15 Match length 51

% identity

NCBI Description



```
% identity
NCBI Description
                   hypothetical protein 1 - Madagascar periwinkle >qi 758694
                   (U12573) putative [Catharanthus roseus]
                   224845
Seq. No.
                   LIB3166-019-P1-K1-H5
Seq. ID
Method
                   BLASTX
                   g4510395
NCBI GI
BLAST score
                   520
                   5.0e-53
E value
Match length
                   132
% identity
                   72
                   (AC006587) putative beta-galactosidase precursor
NCBI Description
                   [Arabidopsis thaliana]
                   224846
Seq. No.
                   LIB3166-019-P1-K1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2463569
BLAST score
                   352
                   2.0e-33
E value
Match length
                   75
% identity
                   87
                  (AB007503) squalene synthase [Glycine max]
NCBI Description
Seq. No.
                   224847
                   LIB3166-019-P1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1362093
BLAST score
                   181
E value
                   2.0e-13
Match length
                   41
% identity
                   85
NCBI Description
                  hypothetical protein (clone TPP15) - tomato (fragment)
                  >gi_924632 (U20595) unknown [Solanum lycopersicum]
Seq. No.
                   224848
Seq. ID
                   LIB3166-019-P1-K1-H9
Method
                  BLASTX
                   g485518
NCBI GI
BLAST score
                   381
E value
                   8.0e-37
                   104
Match length
                   75
% identity
NCBI Description
                  ubiquitin / ribosomal protein CEP52 - rice
                   >gi_303857 dbj BAA02154 (D12629) ubiquitin/ribosomal
                  polyprotein [Oryza sativa]
Seq. No.
                   224849
                  LIB3166-020-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1130682
BLAST score
                   434
E value
                   4.0e-43
Match length
                  111
```

(Z46959) acetohydroxyacid synthase [Gossypium hirsutum]



```
224850
Seq. No.
                  LIB3166-020-P1-K1-A2
Seq. ID
Method
                  BLASTX
                  g419760
NCBI GI
BLAST score
                  606
E value
                  4.0e-63
Match length
                  136
% identity
                  43
NCBI Description
                  P-glycoprotein atpgp1 - Arabidopsis thaliana
                  >gi_3849833_emb_CAA43646_ (X61370) P-glycoprotein
                   [Arabidopsis thaliana]
                  224851
Seq. No.
                  LIB3166-020-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3493172
BLAST score
                  668
E value
                  2.0e-70
Match length
                  137
% identity
                  51
NCBI Description
                 (U89609) fiber annexin [Gossypium hirsutum]
Seq. No.
                  224852
                  LIB3166-020-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2129771
BLAST score
                  469
E value
                  4.0e-47
Match length
                  114
% identity
                  76
                  xyloglucan endotransglycosylase-related protein XTR-6 -
NCBI Description
                  Arabidopsis thaliana >gi_1244758 (U43488) xyloglucan
                  endotransglycosylase-related protein [Arabidopsis thaliana]
                  >gi_4539299_emb_CAB39602.1_ (AL049480) xyloglucan endo-1,
                  4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana]
                  224853
                  LIB3166-020-P1-K1-B1
                  BLASTX
                  g2827143
                  614
```

3 t. f w.

```
Seq. No.
Seq. ID
Method
NCBI GI
BLAST score
E value
                   4.0e-64
Match length
                  135
% identity
NCBI Description
                  (AF027174) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
```

Seq. No. 224854 Seq. ID LIB3166-020-P1-K1-B12

Method BLASTX NCBI GI g2465008 BLAST score 359 E value 3.0e-34 Match length 135 % identity

(AJ001445) ripening-induced protein [Fragaria vesca] NCBI Description



```
Seq. No.
                   224855
                  LIB3166-020-P1-K1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2281633
BLAST score
                   317
E value
                   3.0e-29
Match length
                  130
% identity
                   53
                  (AF003097) AP2 domain containing protein RAP2.4
NCBI Description
                   [Arabidopsis thaliana]
                  224856
Seq. No.
                  LIB3166-020-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g128194
BLAST score
                  531
                  2.0e-54
E value
Match length
                  129
% identity
                  79
NCBI Description
                  NITRATE REDUCTASE (NR) >qi 81572 pir A41667 nitrate
                  reductase (NADH) (EC 1.6.6.1) - winter squash >gi 167499
                   (M33154) nitrate reductase [Cucurbita maxima]
Seq. No.
                  224857
                  LIB3166-020-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455364
BLAST score
                  315
                  5.0e-29
E value
Match length
                  102
                  60
% identity
NCBI Description
                  (AL035524) senescence-associated protein-like [Arabidopsis
                  thaliana]
                  224858
Seq. No.
Seq. ID
                  LIB3166-020-P1-K1-C11
Method
                  BLASTX
                  g3288883
NCBI GI
BLAST score
                  182
E value
                  2.0e-29
Match length
                  113
% identity
                   64
NCBI Description (AB015431) SAR DNA binding protein [Oryza sativa]
                  224859
Seq. No.
                  LIB3166-020-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2262178
BLAST score
                  149
E value
                  1.0e-09
Match length
                  34
% identity
                  74
```

Seq. No. 224860

NCBI Description

Seq. ID LIB3166-020-P1-K1-C9

(AC002329) putative Mlo-like protein [Arabidopsis thaliana]



Method BLASTX NCBI GI g2618723 BLAST score 209 E value 1.0e-16 Match length 89 55 % identity NCBI Description (U49073) IAA17 [Arabidopsis thaliana] >gi 2921756 (AF040631) IAA17/AXR3 protein [Arabidopsis thaliana] >gi 4389514 gb AAB70451 (AC000104) Identical to Arabidopsis gb AF040632 and gb U49073 IAA17/AXR3 gene. ESTs gb\_H36782 and gb\_F14074 come from this gene. [Arabidopsis thaliana] 224861 Seq. No. Seq. ID LIB3166-020-P1-K1-D1 BLASTX Method NCBI GI q3096922 BLAST score 260 E value 1.0e-22 84 Match length 64 % identity (AL023094) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 224862 LIB3166-020-P1-K1-D10 Seq. ID BLASTX Method NCBI GI q4572679 BLAST score 339 E value 2.0e-33 Match length 81 86 % identity (AC006954) RSZp22 splicing factor; contains RNA recognition NCBI Description motif [Arabidopsis thaliana] Seq. No. 224863 LIB3166-020-P1-K1-D11 Seq. ID Method BLASTX g3377843 NCBI GI BLAST score 290 E value 4.0e-26 Match length 120 53 % identity (AF076274) contains similarity to rat p47 protein NCBI Description (GB:AB002086) [Arabidopsis thaliana] 224864 Seq. No. LIB3166-020-P1-K1-D2 Seq. ID BLASTX Method NCBI GI g128194 BLAST score 523

E value 2.0e-53

Match length 128 79 % identity

NCBI Description NITRATE REDUCTASE (NR) >gi\_81572\_pir\_\_A41667 nitrate reductase (NADH) (EC 1.6.6.1) - winter squash >gi 167499

(M33154) nitrate reductase [Cucurbita maxima]



```
224865
Seq. No.
                  LIB3166-020-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3676071
BLAST score
                   402
E value
                   2.0e-39
                  108
Match length
                   69
% identity
                  (Y17969) ERG protein [Arabidopsis thaliana]
NCBI Description
                   224866
Seq. No.
                  LIB3166-020-P1-K1-D6
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3377843
BLAST score
                   198
E value
                   2.0e-19
                   122
Match length
% identity
                   48
                   (AF076274) contains similarity to rat p47 protein
NCBI Description
                   (GB:AB002086) [Arabidopsis thaliana]
Seq. No.
                  224867
                  LIB3166-020-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3252866
BLAST score
                   181
                   6.0e-16
E value
Match length
                   132
% identity
                   45
NCBI Description
                  (AF033535) putative zinc transporter [Arabidopsis thaliana]
Seq. No.
                  224868
                  LIB3166-020-P1-K1-E10
Seq. ID
Method
                  {\tt BLASTX}
NCBI GI
                   g2257598
BLAST score
                   539
E value
                   3.0e-55
                  135
Match length
                   79
% identity
NCBI Description (AB005551) phosphoglycerate kinase [Robinia pseudoacacia]
                   224869
Seq. No.
Seq. ID
                  LIB3166-020-P1-K1-E11
Method
                  BLASTX
                   g289920
NCBI GI
BLAST score
                   672
E value
                   6.0e-71
Match length
                   128
                   98
% identity
NCBI Description
                   (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
Seq. No.
                   224870
```

Seq. ID LIB3166-020-P1-K1-E3

Method BLASTX NCBI GI g4512670 BLAST score 148

% identity

NCBI Description

71



```
E value
                   2.0e-09
Match length
                   115
% identity
                   31
                  (AC006931) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   224871
Seq. ID
                   LIB3166-020-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g4539348
BLAST score
                   331
E value
                   7.0e-31
Match length
                   133
% identity
                   51
NCBI Description
                  (AL035539) putative pollen allergen [Arabidopsis thaliana]
Seq. No.
                   224872
Seq. ID
                   LIB3166-020-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   g2811028
BLAST score
                   278
E value
                   7.0e-25
Match length
                   88
% identity
                   66
NCBI Description
                  HYPOTHETICAL 47.9 KD PROTEIN M021B04.12 >gi 2191188
                   (AF007271) similar to S. cerevisiae SIK1P (PID:g984964)
                   [Arabidopsis thaliana]
                   224873
Seq. No.
                   LIB3166-020-P1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2981167
BLAST score
                   119
E value
                   3.0e-10
Match length
                   52
% identity
                   71
NCBI Description
                   (AF053076) late embryogenis abundant protein 5 [Nicotiana
                   tabacumi
Seq. No.
                   224874
Seq. ID
                   LIB3166-020-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   g3341687
BLAST score
                   207
E value
                   2.0e-16
Match length
                   69
% identity
NCBI Description (AC003672) putative ras protein [Arabidopsis thaliana]
Seq. No.
                   224875
Seq. ID
                   LIB3166-020-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   g1771160
BLAST score
                   457
E value
                   1.0e-45
Match length
                  131
```

(X98929) SBT1 [Lycopersicon esculentum]



>gi\_3687305\_emb\_CAA06999\_ (AJ006378) subtilisin-like
protease [Lycopersicon esculentum]

Seq. No. 224876

Seq. ID LIB3166-020-P1-K1-F1

Method BLASTX
NCBI GI g4190952
BLAST score 314
E value 6.0e-29
Match length 102
% identity 62

NCBI Description (AB022689) similar to hsr203J [Lycopersicon esculentum]

Seq. No. 224877

Seq. ID LIB3166-020-P1-K1-F12

Method BLASTX
NCBI GI g2065013
BLAST score 398
E value 9.0e-39
Match length 118
% identity 65

NCBI Description (Y11650) cyclic phosphodiesterase [Arabidopsis thaliana]

>gi\_2832621\_emb\_CAA16750\_ (AL021711) cyclic phosphodiesterase [Arabidopsis thaliana]

Seq. No. 224878

Seq. ID LIB3166-020-P1-K1-F2

Method BLASTX
NCBI GI g1706323
BLAST score 248
E value 3.0e-21
Match length 85
% identity 56

NCBI Description ORNITHINE DECARBOXYLASE (ODC) >gi\_2118242\_pir\_\_\$64704

ornithine decarboxylase (EC 4.1.1.17) - jimsonweed

 $\geq$ gi\_871008\_emb\_CAA61121\_ (X87847) ornithine decarboxylase

[Datura stramonium]

Seq. No. 224879

Seq. ID LIB3166-020-P1-K1-F4

Method BLASTX
NCBI GI g3036951
BLAST score 368
E value 2.0e-35
Match length 74
% identity 96

NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein

[Nicotiana sylvestris]

Seq. No. 224880

Seq. ID LIB3166-020-P1-K1-F6

Method BLASTX
NCBI GI 94406819
BLAST score 226
E value 1.0e-32
Match length 133
% identity 64



```
NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]
                   224881
Seq. No.
Seq. ID
                  LIB3166-020-P1-K1-F9
Method
                   BLASTX
NCBI GI
                  g3334115
BLAST score
                   670
                  1.0e-70
E value
Match length
                  136
% identity
                   63
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >qi 2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                  hirsutum]
                  224882
Seq. No.
Seq. ID
                  LIB3166-020-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q3600061
BLAST score
                  389
E value
                  1.0e-37
Match length
                  117
% identity
                   63
NCBI Description
                  (AF080120) contains similarity to DNA binding proteins
                   [Arabidopsis thaliana]
Seq. No.
                  224883
Seq. ID
                  LIB3166-020-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q3757523
BLAST score
                  202
                  9.0e-16
E value
Match length
                  81
% identity
                  57
NCBI Description (AC005167) putative transportin [Arabidopsis thaliana]
Seq. No.
                  224884
Seq. ID
                  LIB3166-020-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g2618721
BLAST score
                  292
E value
                  2.0e-26
Match length
                  96
                  65
% identity
NCBI Description (U49072) IAA16 [Arabidopsis thaliana]
Seq. No.
                  224885
Seq. ID
                  LIB3166-020-P1-K1-G3
```

Method BLASTX
NCBI GI g4567228
BLAST score 248
E value 2.0e-26
Match length 83
% identity 77

NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]

Seq. No. 224886



```
LIB3166-020-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1944216
BLAST score
                  479
E value
                  3.0e-48
Match length
                  105
% identity
                  86
NCBI Description
                  (D84246) alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.
                  224887
Seq. ID
                  LIB3166-020-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g3901012
BLAST score
                  184
                  4.0e-14
E value
Match length
                  72
% identity
                  53
NCBI Description
                  (AJ130885) xyloglucan endotransqlycosylase 1 [Fagus
                  sylvatica]
Seq. No.
                  224888
Seq. ID
                  LIB3166-020-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g3212871
BLAST score
                  240
E value
                  3.0e-20
Match length
                  54
% identity
                  78
                  (AC004005) putative translation initiation factor
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  224889
Seq. ID
                  LIB3166-020-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g172215
BLAST score
                  200
E value
                  1.0e-15
Match length
                  84
% identity
                  49
NCBI Description
                  (J03530) RNA polymerase A(I) large subunit [Saccharomyces
                  cerevisiael
Seq. No.
                  224890
Seq. ID
                  LIB3166-020-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q585053
BLAST score
                  208
E value
                  1.0e-16
Match length
                  122
% identity
NCBI Description MITOTIC CONTROL PROTEIN DIS3 >gi_283075_pir__A41944 mitotic
```

control protein dis3+ - fission yeast (Schizosaccharomyces

pombe) >gi\_173381 (M74094) mitotic control protein [Schizosaccharomyces pombe] >gi\_3650393\_emb\_CAA21102\_

(AL031743) mitotic control protein dis3.

[Schizosaccharomyces pombe]

Match length

% identity

134 57



```
224891
Seq. No.
                  LIB3166-020-P1-K1-H10
Seq. ID
Method
                  BLASTX
                  g4539414
NCBI GI
BLAST score
                  236
                  9.0e-20
E value
                  103
Match length
                  50
% identity
                  (AL049524) putative subtilisin-like protease [Arabidopsis
NCBI Description
                  thaliana]
                  224892
Seq. No.
                  LIB3166-020-P1-K1-H11
Seq. ID
                  BLASTX
Method
                  g132805
NCBI GI
BLAST score
                  114
                  5.0e-14
E value
                  95
Match length
                  52
% identity
                  60S RIBOSOMAL PROTEIN L17 (L23) (AMINO ACID
NCBI Description
                  STARVATION-INDUCED PROTEIN) (ASI) >gi 71282_pir__R5RT17
                  ribosomal protein L17 - rat >gi_57111_emb_CAA42765_
                   (X60212) ribosomal protein L22 [Rattus norvegicus]
                  >gi 57682 emb CAA41278 (X58389) ribosomal protein L17
                   [Rattus rattus]
Seq. No.
                  224893
                  LIB3166-020-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4210948
BLAST score
                  236
                  1.0e-24
E value
                  78
Match length
                   78
% identity
                  (AF085275) DnaJ protein [Hevea brasiliensis]
NCBI Description
Seq. No.
                   224894
                  LIB3166-020-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1439609
                   587
BLAST score
                   6.0e-61
E value
                  123
Match length
% identity
NCBI Description
                   (U62778) delta-tonoplast intrinsic protein [Gossypium
                   hirsutum]
Seq. No.
                   224895
Seq. ID
                  LIB3166-020-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   q4490297
BLAST score
                   401
E value
                   4.0e-39
```

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]



```
224896
Seq. No.
                  LIB3166-021-P1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2827548
                   309
BLAST score
E value
                  2.0e-28
Match length
                  120
                   52
% identity
                  (AL021635) cytochrome P450 - like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  224897
                  LIB3166-021-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q485514
BLAST score
                   197
                   3.0e-15
E value
Match length
                   44
                   86
% identity
                  ADR11-2 protein - soybean (fragment)
NCBI Description
                  >gi 296443 emb CAA49341 (X69640) auxin down regulated
                   [Glycine max]
                   224898
Seq. No.
                  LIB3166-021-P1-K1-A5
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3256035
BLAST score
                   231
                   3.0e-19
E value
Match length
                   124
% identity
                   44
NCBI Description
                  (Y14274) putative serine/threonine protein kinase [Sorghum
                  bicolor]
                   224899
Seq. No.
                  LIB3166-021-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1063415
BLAST score
                   603
                  7.0e-63
E value
                  120
Match length
                   93
% identity
NCBI Description (L40948) K+ channel protein [Arabidopsis thaliana]
                   224900
Seq. No.
                  LIB3166-021-P1-K1-A8
Seq. ID
Method
                  BLASTX
                  g2213599
NCBI GI
                  346
BLAST score
E value
                  9.0e-33
Match length
                  120
                   57
% identity
NCBI Description (AC000348) T7N9.19 [Arabidopsis thaliana]
```

Seq. No. 224901

Seq. ID LIB3166-021-P1-K1-A9

Method BLASTX



```
NCBI GI
                  q602076
BLAST score
                  527
                  5.0e-54
E value
Match length
                  107
% identity
                  23
                  (X77456) pentameric polyubiquitin [Nicotiana tabacum]
NCBI Description
Seq. No.
                  224902
                  LIB3166-021-P1-K1-B10
Seq. ID
Method
                  BLASTX
                  g3269289
NCBI GI
BLAST score
                  315
                  4.0e-29
E value
Match length
                  89
% identity
                  70
NCBI Description
                  (AL030978) putative protein [Arabidopsis thaliana]
Seq. No.
                  224903
                  LIB3166-021-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2829863
BLAST score
                   320
E value
                  1.0e-29
Match length
                  103
                  57
% identity
                  (AC002396) Putative peroxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  224904
Seq. ID
                  LIB3166-021-P1-K1-B3
Method
                  BLASTX
                  q4126399
NCBI GI
BLAST score
                   469
                   4.0e-47
E value
Match length
                  114
                   81
% identity
                  (AB011794) chalcone isomerase [Citrus sinensis]
NCBI Description
Seq. No.
                  224905
                  LIB3166-021-P1-K1-B4
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2407639
BLAST score
                   231
E value
                   3.0e-19
                  126
Match length
                   38
% identity
                 (AF018263) protein phosphatase 5; PP5 [Xenopus laevis]
NCBI Description
                   224906
Seq. No.
                  LIB3166-021-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3242702
BLAST score
                   510
```

Method BLASTX
NCBI GI g3242702
BLAST score 510
E value 6.0e-52
Match length 117
% identity 78

NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]



224907

Seq. No.

LIB3166-021-P1-K1-B6 Seq. ID Method BLASTX q4559331 NCBI GI 400 \_ BLAST score 4.0e-39 E value 83 Match length 83 % identity (AC007087) unknown protein [Arabidopsis thaliana] NCBI Description 224908 Seq. No. LIB3166-021-P1-K1-B7 Seq. ID BLASTX Method g2736186 NCBI GI BLAST score 454 E value 2.0e-45 122 Match length % identity 70 (AF024623) galactose kinase [Arabidopsis thaliana] NCBI Description 224909 Seq. No. LIB3166-021-P1-K1-B9 Seq. ID Method BLASTX g2980770 NCBI GI BLAST score 615 3.0e-64E value Match length 126 % identity 90 (AL022198) putative protein kinase [Arabidopsis thaliana] NCBI Description 224910 Seq. No. LIB3166-021-P1-K1-C3 Seq. ID Method BLASTX NCBI GI g2947063 181 BLAST score 2.0e-13 E value Match length 77 % identity 44 (AC002521) putative Ser/Thr protein kinase [Arabidopsis NCBI Description thaliana] 224911 Seq. No. LIB3166-021-P1-K1-C5 Seq. ID BLASTX Method NCBI GI g2459431 BLAST score 387 2.0e-37 E value Match length 110 73 % identity NCBI Description (AC002332) unknown protein [Arabidopsis thaliana] 224912 Seq. No. Seq. ID LIB3166-021-P1-K1-C6 BLASTX Method NCBI GI q3434969 BLAST score 342 E value 3.0e-32



```
Match length
                  80
% identity
                  81
                  (AB008104) ethylene responsive element binding factor 2
NCBI Description
                   [Arabidopsis thaliana]
                  224913
Seq. No.
                  LIB3166-021-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3860274
BLAST score
                  209
                  1.0e-16
E value
Match length
                  53
% identity
                  72
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4314397 gb AAD15607 (AC006232) putative zinc finger
                  protein [Arabidopsis thaliana]
                  224914
Seq. No.
                  LIB3166-021-P1-K1-D1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1777443
BLAST score
                   242
                   1.0e-20
E value
Match length
                  106
                   53
% identity
                   (U28422) CCA1 [Arabidopsis thaliana] >gi_3510263 (AC005310)
NCBI Description
                   DNA-binding protein CCA1 [Arabidopsis thaliana] >gi_4090569
                   (U79156) CCA1 [Arabidopsis thaliana]
                   224915
Seq. No.
                  LIB3166-021-P1-K1-D10
Seq. ID
                   BLASTX
Method
                   g4263821
NCBI GI
                   321
BLAST score
                   8.0e-30
E value
                   116
Match length
                   63
% identity
                  (AC006067) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   224916
Seq. No.
                   LIB3166-021-P1-K1-D2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2281645
                   228
BLAST score
                   6.0e-19
E value
                   70
Match length
                   61
% identity
                   (AF003103) AP2 domain containing protein RAP2.10
NCBI Description
                   [Arabidopsis thaliana] >gi_2632063_emb_CAA05630_ (AJ002598)
                   TINY-like protein [Arabidopsis thaliana]
```

Seq. ID LIB3166-021-P1-K1-D3

224917

Method BLASTX NCBI GI g730645 BLAST score 430 1.0e-42 E value

Seq. No.



Match length 111 % identity 79 NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi 629556 pir S43412 ribosomal protein S15 - Arabidopsis thaliana >gi 313152 emb CAA80679 (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi\_313188\_emb\_CAA80681\_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi\_1903366 gb AAB70449 (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb\_R29788,gb\_ATTS0365 come from this gene. [Arabidopsis thaliana] Seq. No. 224918 Seq. ID LIB3166-021-P1-K1-D9 Method BLASTX NCBI GI q116343 BLAST score 248 E value 3.0e-21 Match length 122 41 % identity NCBI Description BASIC ENDOCHITINASE PRECURSOR 224919 Seq. No. LIB3166-021-P1-K1-E10 Seq. ID Method BLASTX NCBI GI g2618721 BLAST score 292 E value 2.0e-26 57 Match length 89 % identity NCBI Description (U49072) IAA16 [Arabidopsis thaliana] Seq. No. 224920 LIB3166-021-P1-K1-E11 Seq. ID Method BLASTX NCBI GI q3080423 BLAST score 193 E value 8.0e-15 Match length 85 % identity 51 NCBI Description (AL022604) putative protein [Arabidopsis thaliana] Seq. No. 224921 Seq. ID LIB3166-021-P1-K1-E12 Method BLASTX NCBI GI q3434967 BLAST score 197

E value 3.0e-15 Match length 70 % identity 57

NCBI Description (AB008103) ethylene responsive element binding factor 1

[Arabidopsis thaliana]

Seq. No. 224922

Seq. ID LIB3166-021-P1-K1-E2

Method BLASTX NCBI GI g3335337 BLAST score 147



E value 2.0e-09 Match length 34 % identity 85

NCBI Description (AC004512) Simil

(AC004512) Similar to acyl carrier protein, mitochondrial precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD subunit (MYACP-1), gb\_L23574 from A. thaliana. ESTs gb\_Z30712, gb\_Z30713, gb\_Z26204, gb\_N37975 and gb\_N96330

come from this gene

Seq. No. 224923

Seq. ID LIB3166-021-P1-K1-E3

Method BLASTX
NCBI GI g2507300
BLAST score 467
E value 2.0e-47
Match length 123
% identity 79

NCBI Description ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD

SUBUNIT) (A1 40 KD SUBUNIT) (RF-C 40 KD SUBUNIT) (RFC40) >gi\_1590811 (M87338) replication factor C, 40-kDa subunit [Homo sapiens] >gi\_2914760 (AF045555) replication factor C subunit 2 [Homo sapiens] >gi\_4506487\_ref\_NP\_002905.1\_pRFC2\_

replication factor C (activator 1) 2 (40kD)

Seq. No. 224924

Seq. ID LIB3166-021-P1-K1-E6

Method BLASTX
NCBI GI g729470
BLAST score 415
E value 8.0e-41
Match length 104
% identity 76

NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR

(NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)

>gi\_542089\_pir\_\_JQ2272 formate dehydrogenase (EC 1.2.1.2)
precursor, mitochondrial - potato >gi\_297798\_emb\_CAA79702\_
(Z21493) mitochondrial formate dehydrogenase precursor

[Solanum tuberosum]

Seq. No. 224925

Seq. ID LIB3166-021-P1-K1-E7

Method BLASTX
NCBI GI 94375833
BLAST score 430
E value 1.0e-42
Match length 119
% identity 66

NCBI Description (AL021713) receptor serine/threonine kinase-like protein

[Arabidopsis thaliana]

Seq. No. 224926

Seq. ID LIB3166-021-P1-K1-E9

Method BLASTX
NCBI GI g3434973
BLAST score 196
E value 3.0e-15
Match length 73



% identity (AB008106) ethylene responsive element binding factor 4NCBI Description [Arabidopsis thaliana] 224927 Seq. No. LIB3166-021-P1-K1-F10 Seq. ID BLASTX Method g1170745 NCBI GI 595 BLAST score 6.0e-62 E value 116 Match length 100 % identity LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA14-A >gi\_167326 NCBI Description (M88321) Group 4 late embryogenesis-abundant protein [Gossypium hirsutum]  $>gi_167328$  (M88322) Group 4 late embryogenesis-abundant protein [Gossypium hirsutum] 224928 Seq. No. LIB3166-021-P1-K1-F5 Seq. ID BLASTX Method NCBI GI g2660676 BLAST score 534 9.0e-55 E value Match length 125 78 % identity (AC002342) Dreg-2 like protein [Arabidopsis thaliana] NCBI Description Seq. No. 224929 LIB3166-021-P1-K1-F7 Seq. ID BLASTX Method q464621 NCBI GI 339 BLAST score 6.0e-32E value Match length 118 58 % identity 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi\_280374\_pir\_\_S28586 NCBI Description ribosomal protein ML16 - common ice plant >gi 19539\_emb\_CAA49175\_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum] 224930 Seq. No. LIB3166-021-P1-K1-F8 Seq. ID BLASTX Method g4454042 NCBI GI 381 BLAST score 7.0e-37 E value 86 Match length 79 % identity NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

224931 Seq. No.

LIB3166-021-P1-K1-F9 Seq. ID

BLASTX Method NCBI GI g1129145 465 BLAST score 1.0e-46 E value 122 Match length



```
% identity
                  (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]
NCBI Description
                  224932
Seq. No.
                  LIB3166-021-P1-K1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                  a2507421
BLAST score
                  247
                  1.0e-21
E value
                  58
Match length
                  81
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277
NCBI Description
                  (U81042) translation initiation factor [Arabidopsis
                  thaliana] >gi_4490709 emb_CAB38843.1 (AL035680)
                  translation initiation factor [Arabidopsis thaliana]
Seq. No.
                  224933
                  LIB3166-021-P1-K1-G11
Seq. ID
Method
                  BLASTX
                  q2352492
NCBI GI
BLAST score
                  290
                   4.0e-26
E value
                  121
Match length
% identity
                   49
                   (AF005047) transport inhibitor response 1 [Arabidopsis
NCBI Description
                   thaliana] >gi_2352494 (AF005048) transport inhibitor
                   response 1 [Arabidopsis thaliana]
Seq. No.
                   224934
                  LIB3166-021-P1-K1-G12
Seq. ID
Method
                   BLASTX
                   q466160
NCBI GI
                   198
BLAST score
                   1.0e-15
E value
                   63
Match length
                   60
% identity
                  HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III
NCBI Description
                   >gi 630771 pir__S44903 ZK652.3 protein - Caenorhabditis
                   elegans >gi_289769 (L14429) putative [Caenorhabditis
                   elegans]
                   224935
Seq. No.
                   LIB3166-021-P1-K1-G2
Seq. ID
                   BLASTX
Method
                   g2498291
NCBI GI
                   243
BLAST score
                   1.0e-20
E value
Match length
                   120
                   45
% identity
                   DIHYDRODIPICOLINATE REDUCTASE >gi 1651716 dbj_BAA16644_
NCBI Description
                   (D90899) dihydrodipicolinate reductase [Synechocystis sp.]
                   224936
Seq. No.
                   LIB3166-021-P1-K1-G4
Seq. ID
```

BLASTX Method q3335378 NCBI GI BLAST score 439

Seq. No.

Seq. ID Method

224941

BLASTX

LIB3166-021-P1-K1-G9



```
1.0e-43
E value
Match length
                  90
                   88
% identity
                   (AC003028) Myb-related transcription activator [Arabidopsis
NCBI Description
                  thaliana]
                  224937
Seq. No.
                  LIB3166-021-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q462195
BLAST score
                  412
                  2.0e-40
E value
                  86
Match length
                   93
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                   >gi 100682_pir__S21636 GOS2 protein - rice
                   >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                   >gi_3789950 (AF094774) translation initiation factor [Oryza
                   sativa]
Seq. No.
                   224938
                  LIB3166-021-P1-K1-G6
Seq. ID
                   BLASTX
Method
                   g466160
NCBI GI
                   366
BLAST score
                   5.0e-35
E value
Match length
                   84
                   85
% identity
                  HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III
NCBI Description
                   >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis
                   elegans >gi 289769 (L14429) putative [Caenorhabditis
                   elegans]
                   224939
Seq. No.
                   LIB3166-021-P1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3080371
                   233
BLAST score
                   2.0e-19
E value
Match length
                   62
% identity
                   63
                   (AL022580) putative pectinacetylesterase protein
NCBI Description
                   [Arabidopsis thaliana]
                   224940
Seq. No.
                   LIB3166-021-P1-K1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4220481
BLAST score
                   186
E value
                   5.0e-14
                   71
Match length
% identity
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
```

E value

Match length

% identity

1.0e-29

114

54



```
NCBI GI
                  g3335375
BLAST score
                  428
                  2.0e-42
E value
Match length
                  83
                  93
% identity
                  (AC003028) putative amidase [Arabidopsis thaliana]
NCBI Description
                  224942
Seq. No.
                  LIB3166-021-P1-K1-H1
Seq. ID
                  BLASTX
Method
                  g480669
NCBI GI
BLAST score
                  454
                  2.0e-45
E value
Match length
                  107
                  80
% identity
NCBI Description
                  NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Jerusalem
                  artichoke (fragment) >gi_1359894_emb_CAA81210_ (Z26251)
                  NADPH-ferrihemoprotein reductase [Helianthus tuberosus]
                  224943
Seq. No.
                  LIB3166-021-P1-K1-H3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2245005
BLAST score
                  190
                  2.0e-14
E value
Match length
                  76
% identity
                  58
                  (Z97341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  224944
Seq. No.
                  LIB3166-021-P1-K1-H4
Seq. ID
Method
                  BLASTX
                  g4490702
NCBI GI
BLAST score
                  290
                  4.0e-26
E value
Match length
                  127
% identity
                  57
                  (AL035680) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  224945
Seq. No.
                  LIB3166-021-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100200
BLAST score
                  362
                  1.0e-34
E value
Match length
                  100
% identity
                  71
NCBI Description
                  chlorophyll a/b-binding protein type I precursor - tomato
                  224946
Seq. No.
Seq. ID
                  LIB3166-021-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q2213583
BLAST score
                  320
```

Seq. No.



(AC000348) T7N9.3 [Arabidopsis thaliana] NCBI Description 224947 Seq. No. LIB3166-021-P1-K1-H7 Seq. ID BLASTX Method g2980788 NCBI GI 189 BLAST score 2.0e-14 E value 124 Match length 39 % identity (AL022197) putative protein [Arabidopsis thaliana] NCBI Description 224948 Seq. No. LIB3166-021-P1-K1-H8 Seq. ID BLASTX Method NCBI GI q2462925 BLAST score 428 1.0e-42 E value 92 Match length 87 % identity (AJ000053) GTP cyclohydrolase II / NCBI Description 3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis thaliana] 224949 Seq. No. LIB3166-022-P1-K1-A10 Seq. ID Method BLASTX g1800147 NCBI GI 351 BLAST score 3.0e - 33E value 84 Match length 77 % identity NCBI Description (U83655) membrane associated protein [Arabidopsis thaliana] 224950 Seq. No. LIB3166-022-P1-K1-A11 Seq. ID Method BLASTX q4371290 NCBI GI 282 BLAST score 3.0e-25 E value 91 Match length % identity 59 NCBI Description (AC006260) unknown protein [Arabidopsis thaliana] 224951 Seq. No. LIB3166-022-P1-K1-A12 Seq. ID Method BLASTX NCBI GI g2642153 BLAST score 168 E value 7.0e-12 Match length 90 38 % identity NCBI Description (AC003000) unknown protein [Arabidopsis thaliana] >gi 2795810 (AC003674) unknown protein [Arabidopsis thaliana]



```
LIB3166-022-P1-K1-A2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1363484
BLAST score
                  263
                  5.0e-23
E value
Match length
                  121
                  52
% identity
                  IAA13 protein - Arabidopsis thaliana >gi_972929 (U18415)
NCBI Description
                  IAA13 [Arabidopsis thaliana] >gi_2459414 (AC002332) auxin
                  inducible protein, IAA13 [Arabidopsis thaliana]
                  224953
Seq. No.
                  LIB3166-022-P1-K1-A5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1206005
BLAST score
                  295
                  1.0e-26
E value
Match length
                  65
% identity
                  89
                  (U42400) putative MADS-box family transcription factor
NCBI Description
                   [Pinus radiata]
Seq. No.
                  224954
                  LIB3166-022-P1-K1-A7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g99737
BLAST score
                  566
                   2.0e-58
E value
Match length
                  128
% identity
                   84
                  NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -
NCBI Description
                   Arabidopsis thaliana >gi_16189_emb_CAA46815_ (X66017)
                  NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]
                   224955
Seq. No.
                  LIB3166-022-P1-K1-B1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2811029
                   587
BLAST score
                   6.0e-61
E value
                   129
Match length
                   84
% identity
                  ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT)
NCBI Description
                   (ACETYLORNITHINE TRANSAMINASE) (AOTA)
                   >gi 1944511 emb CAA69936_ (Y08680) acetylornithine
                   aminotransferase [Alnus glutinosa]
                   224956
Seq. No.
                   LIB3166-022-P1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1345919
                   307
BLAST score
E value
                   1.0e-28
Match length
                   66
                   92
% identity
```

NCBI Description APOCYTOCHROME F PRECURSOR >gi\_984315 (U26948) cytochrome f

precursor [Glycine max]



```
224957
 Seq. No.
                    LIB3166-022-P1-K1-B4
 Seq. ID
 Method
                    BLASTX
                    q1363483
 NCBI GI
 BLAST score
                    243
                    1.0e-20
 E value
 Match length
                    63
                    76
 % identity
                    IAA12 protein - Arabidopsis thaliana >gi_972927 (U18414)
 NCBI Description
                    IAA12 [Arabidopsis thaliana] >gi_2494122 (AC002376) Match
                    to Arabidopsis IAA12 (gb_U18414). [Arabidopsis thaliana]
                    224958
 Seq. No.
                    LIB3166-022-P1-K1-B5
 Seq. ID
 Method
                    BLASTX
                    q3834323
 NCBI GI
 BLAST score
                    149
                    1.0e-09
 E value
 Match length
                    50
                    58
 % identity
                   (AC005679) F9K20.25 [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    224959
                    LIB3166-022-P1-K1-B7
 Seq. ID
                    BLASTX
 Method
                    q2997755
 NCBI GI
 BLAST score
                    173
 E value
                    2.0e-12
                    98
 Match length
                    38
 % identity
                    (AF054823) TFIIH transcription/DNA repair factor p52
 NCBI Description
                    subunit [Mus musculus]
                    224960
  Seq. No.
                    LIB3166-022-P1-K1-B8
  Seq. ID
                    BLASTX
 Method
. NCBI GI
                    g1439609
                    559
 BLAST score
                    1.0e-57
 E value
                    115
 Match length
                    53
  % identity
                    (U62778) delta-tonoplast intrinsic protein [Gossypium
 NCBI Description
                    hirsutum]
                    224961
  Seq. No.
                    LIB3166-022-P1-K1-B9
  Seq. ID
                    BLASTX
 Method
                    g1351974
  NCBI GI
  BLAST score
                    502
                     5.0e-51
  E value
                    97
 Match length
                    100
  % identity
  NCBI Description ADP-RIBOSYLATION FACTOR >gi_1076788_pir__S49325
```

(X80042) ADP-ribosylation factor [Zea mays]

ADP-ribosylation factor - maize >gi\_1076789\_pir\_\_S53486 ADP-ribosylation factor - maize >gi\_556686\_emb\_CAA56351\_



Seq. No.

224962

```
Seq. ID
                  LIB3166-022-P1-K1-C12
Method
                  BLASTX
                  g4468979
NCBI GI
BLAST score
                  345
                   1.0e-32
E value
Match length
                  79
                  81
% identity
                  (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  224963
                  LIB3166-022-P1-K1-C3
Seq. ID
Method
                  BLASTX
                   g1220196
NCBI GI
BLAST score
                   410
                   4.0e-54
E value
Match length
                   107
% identity
                   99
                  (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
NCBI Description
                   224964
Seq. No.
Seq. ID
                   LIB3166-022-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   g3107905
BLAST score
                   440
                   9.0e-44
E value
Match length
                   117
% identity
                   12
                  (D85101) leaf protein [Ipomoea nil]
NCBI Description
                   224965
Seq. No.
                   LIB3166-022-P1-K1-C7
Seq. ID
Method
                   BLASTX
                   g4512122
NCBI GI
                   219
BLAST score
                   7.0e-18
E value
Match length
                   120
% identity
                   47
                  (AF131219) chorismate mutase 3 [Arabidopsis thaliana]
NCBI Description
                   224966
Seq. No.
                   LIB3166-022-P1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4249382
                   437
BLAST score
                   2.0e-43
E value
                   126
Match length
                   67
% identity
                  (AC005966) Strong similarity to gi_3337350 F13P17.3
NCBI Description
                   putative permease from Arabidopsis thaliana BAC
                   gb AC004481. [Arabidopsis thaliana]
                   224967
Seq. No.
                   LIB3166-022-P1-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g584778
```



BLAST score 221 5.0e-18 E value 115 Match length 45 % identity PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 2 PRECURSOR NCBI Description (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 2) (DAHP SYNTHETASE 2) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE 2) >gi\_542033\_pir\_\_S40412 2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 2 precursor - tomato >gi\_410488\_emb\_CAA79856\_ (Z21793) phospho-2-dehydro-3-deoxyheptonate aldolase [Lycopersicon esculentum] 224968 Seq. No. LIB3166-022-P1-K1-D10 Seq. ID BLASTX Method NCBI GI q2618731 584 BLAST score E value 1.0e-60 124 Match length 88 % identity (U49077) IAA21 [Arabidopsis thaliana] NCBI Description 224969 Seq. No. LIB3166-022-P1-K1-D12 Seq. ID BLASTX Method q68200 NCBI GI 470 BLAST score 3.0e-47E value Match length 118 81 % identity fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, NCBI Description chloroplast - spinach >gi\_22633\_emb\_CAA47293\_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea] 224970 Seq. No. LIB3166-022-P1-K1-D4 Seq. ID BLASTX Method NCBI GI q3434967 BLAST score 344 2.0e-32 E value 123 Match length 62 % identity (AB008103) ethylene responsive element binding factor 1 NCBI Description [Arabidopsis thaliana] 224971 Seq. No. LIB3166-022-P1-K1-D5 Seq. ID BLASTX Method g421867 NCBI GI 203 BLAST score 1.0e-18 E value

Match length 115 % identity 45

NCBI Description ubiquitin / ribosomal protein CEP52 - turnip >gi\_347064 (L21898) ubiquitin/ribosomal protein [Brassica rapa] >gi 395079\_emb\_CAA80863\_ (Z24738) ubiquitin/ribosomal



## protein [Brassica rapa] 224972 Seq. No. LIB3166-022-P1-K1-D8 Seq. ID BLASTX Method g3885884 NCBI GI 580 BLAST score 4.0e-60 E value 117 Match length 91 % identity (AF093630) 60S ribosomal protein L21 [Oryza sativa] NCBI Description 224973 Seq. No. LIB3166-022-P1-K1-E1 Seq. ID Method BLASTX NCBI GI g553107 286 BLAST score 1.0e-25 E value 105 Match length 57 % identity (L04967) triosephosphate isomerase [Oryza sativa] NCBI Description 224974 Seq. No. LIB3166-022-P1-K1-E11 Seq. ID BLASTX Method q3059095 NCBI GI 471 BLAST score 2.0e-47 E value 97 Match length 92 \* % identity (AJ001091) magnesium chelatase subunit [Glycine max] NCBI Description 224975 Seq. No. LIB3166-022-P1-K1-E3 Seq. ID BLASTX Method q3334261 NCBI GI BLAST score 232

2.0e-19 E value 54 Match length

74 % identity

NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi 1655851 (U61973)

metallothionein-like protein [Malus domestica]

224976 Seq. No.

LIB3166-022-P1-K1-E6 Seq. ID

BLASTX Method NCBI GI q3608412 BLAST score 324 E value 4.0e-30 122 Match length % identity

(AF079355) protein phosphatase-2c [Mesembryanthemum NCBI Description

crystallinum]

224977 Seq. No.

LIB3166-022-P1-K1-E8 Seq. ID

Method BLASTX



```
g2244781
NCBI GI
BLAST score
                  242
                  2.0e-20
E value
Match length
                   126
                   31
% identity
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   224978
                  LIB3166-022-P1-K1-F10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1403522
BLAST score
                   263
E value
                   5.0e-23
                   88
Match length
                   59
% identity
                  (X57187) chitinase [Phaseolus vulgaris]
NCBI Description
                   224979
Seq. No.
                   LIB3166-022-P1-K1-F11
Seq. ID
                   BLASTX
Method
                   q1161575
NCBI GI
                   161
BLAST score
                   5.0e-11
E value
                   84
Match length
                   50
% identity
                  (X94947) homeobox [Lycopersicon esculentum]
NCBI Description
                   224980
Seq. No.
Seq. ID
                   LIB3166-022-P1-K1-F12
Method
                   BLASTX
                   g2914709
NCBI GI
                   339
BLAST score
                   7.0e-32
E value
                   87
Match length
                   75
% identity
                   (AC003974) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   224981
Seq. No.
                   LIB3166-022-P1-K1-F2
Seq. ID
                   BLASTX
Method
                   g2160161
NCBI GI
                   189
 BLAST score
                   3.0e-14
 E value
                   120
Match length
                   4
 % identity
                   (AC000132) F21M12.7 gene product [Arabidopsis thaliana]
 NCBI Description
                    224982
 Seq. No.
                   LIB3166-022-P1-K1-F9
 Seq. ID
                   BLASTX
 Method
                    g2462825
 NCBI GI
                    405
 BLAST score
                    1.0e-39
 E value
 Match length
                    90
                    86
 % identity
                   (AF000657) contains Procite 'RNP1' putative RNA-binding
 NCBI Description
```

31994

region [Arabidopsis thaliana]



```
224983
Seq. No.
                  LIB3166-022-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539383
BLAST score
                  195
                   5.0e-15
E value
Match length
                  86
                   43
% identity
                   (AL035526) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                   224984
Seq. No.
                   LIB3166-022-P1-K1-G11
Seq. ID
                   BLASTX
Method
NCBI GI `
                   g541951
BLAST score
                   320
                   1.0e-29
E value
Match length
                   107
                   60
% identity
                   SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26
NCBI Description
                   [Glycine max]
                   224985
Seq. No.
                   LIB3166-022-P1-K1-G2
Seq. ID
                   BLASTX
Method
                   q3935170
NCBI GI
BLAST score
                   192
E value
                   1.0e-14
Match length
                   132
                   47
% identity
                  (AC004557) F17L21.13 [Arabidopsis thaliana]
NCBI Description
                   224986
Seq. No.
                   LIB3166-022-P1-K1-G3
Seq. ID
                   BLASTX
Method
                   g1255954
NCBI GI
                   453
BLAST score
E value
                   3.0e-45
                   105
Match length
                   77
% identity
NCBI Description (Z70677) thioredoxin [Ricinus communis]
                   224987
Seq. No.
                   LIB3166-022-P1-K1-G4
Seq. ID
                   BLASTX
Method
                   g3451411
NCBI GI
                   504
BLAST score
                   3.0e-51
E value
                   140
Match length
% identity
                   69
NCBI Description (Z98761) seryl-tRNA synthetase [Helianthus annuus]
                   224988
Seq. No.
                   LIB3166-022-P1-K1-G6
Seq. ID
```

31995

BLASTX

g2443878

Method

NCBI GI

NCBI Description



```
177
BLAST score
                  8.0e-13
E value
Match length
                  128
                  38
% identity
                  (AC002294) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  224989
Seq. No.
                  LIB3166-022-P1-K1-G7
Seq. ID
                  BLASTX
Method
                  g2146739
NCBI GI
                  373
BLAST score
                  7.0e-36
E value
                  112
Match length
% identity
                  65
                  hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521
NCBI Description
                   (U28214) hexokinase 1 [Arabidopsis thaliana]
                  224990
Seq. No.
                  LIB3166-022-P1-K1-G8
Seq. ID
                  BLASTX
Method
                  g3582333
NCBI GI
                  199
BLAST score
                   2.0e-15
E value
                   92
Match length
                   47
% identity
                  (AC005496) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   224991
                  LIB3166-022-P1-K1-G9
Seq. ID
                   BLASTX
Method
                   g2829863
NCBI GI
                   306
BLAST score
                   5.0e-28
E value
                   101
Match length
                   56
% identity
                  (AC002396) Putative peroxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   224992
                   LIB3166-022-P1-K1-H1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4544443
BLAST score
                   159
E value
                   8.0e-11
                   34
Match length
                   91
% identity
                  (AC006592) putative mitochondrial uncoupling protein
NCBI Description
                   [Arabidopsis thaliana]
                   224993
Seq. No.
Seq. ID
                   LIB3166-022-P1-K1-H10
Method
                   BLASTX
NCBI GI
                   g4210948
BLAST score
                   522
                   2.0e-53
E value
Match length
                   99
                   99
% identity
```

% identity

Seq. No.

NCBI Description

53

224999



```
224994
Seq. No.
Seq. ID
                  LIB3166-022-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q1842140
BLAST score
                  164
E value
                  2.0e-11
                  103
Match length
% identity
                  31
                   (AB001024) similar to Saccharomyces cerevisiae ORM1 gene:
NCBI Description
                  EMBL Accession Number Y08687 [Schizosaccharomyces pombe]
                  224995
Seq. No.
                  LIB3166-022-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3892054
BLAST score
                  498
E value
                  2.0e-50
Match length
                  121
                   69
% identity
                   (AC002330) putative glycosyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                  224996
Seq. No.
                  LIB3166-022-P1-K1-H4
Seq. ID
Method
                  BLASTX
                  g4006890
NCBI GI
BLAST score
                   563
E value
                   4.0e-58
Match length
                  124
                   84
% identity
                  (Z99708) ubiquitin--protein ligase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   224997
Seq. No.
                  LIB3166-022-P1-K1-H5
Seq. ID
Method
                   BLASTX
                   g3482967
NCBI GI
BLAST score
                   168
                   9.0e-12
E value
Match length
                   46
                   70
% identity
                  (AL031369) Protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                   thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585)
                   protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.
                   224998
Seq. ID
                   LIB3166-022-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   g1107526
BLAST score
                   345
                   1.0e-32
E value
Match length
                   128
```

31997

(X87931) SIEP1L protein [Beta vulgaris]



```
Seq. ID
                   LIB3166-023-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   q2129739
BLAST score
                   299
                   3.0e-27
E value
Match length
                   65
                   91
% identity
                   shaggy-like kinase etha - Arabidopsis thaliana
NCBI Description
                   >gi 1161512 emb CAA64409 (X94939) shaggy-like kinase etha
                   [Arabidopsis thaliana] >gi_1627516_emb_CAA70144_ (Y08947)
                   shaggy-like kinase etha [Arabidopsis thaliana]
                   225000
Seq. No.
                   LIB3166-023-P1-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2829911
BLAST score
                   435
E value
                   4.0e-43
                   110
Match length
 % identity
                   45
                   (AC002291) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   225001
                   LIB3166-023-P1-K1-A7
 Seq. ID
Method
                   BLASTX
                   g2980760
NCBI GI
BLAST score
                   246
 E value
                   6.0e-21
Match length
                   76
                   62
% identity
                   (AL022198) putative protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   225002
                   LIB3166-023-P1-K1-B10
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q2662310
 BLAST score
                   412
 E value
                   2.0e-40
                   110
 Match length
                   70
 % identity
                   (AB009307) bpwl [Hordeum vulgare]
 NCBI Description
                   225003
 Seq. No.
                   LIB3166-023-P1-K1-B3
 Seq. ID
 Method
                   BLASTX
                   g3249084
 NCBI GI
 BLAST score
                   435
 E value
                    4.0e-43
 Match length
                   127
 % identity
                   22
                   (AC004473) Similar to red-1 (related to thioredoxin) gene
 NCBI Description
                   gb X92750 from Mus musculus. ESTs gb AA712687 and
                   gb Z37223 come from this gene [Arabidopsis thaliana]
 Seq. No.
                    225004
```

Seq. ID LIB3166-023-P1-K1-B4

Method BLASTX

Seq. ID Method

NCBI GI

BLASTX g100454



```
NCBI GI
                  q2865623
                  434
BLAST score
                  5.0e-43
E value
Match length
                  105
                  80
% identity
                   (AF045286)
NCBI Description
                  GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase
                   [Arabidopsis thaliana]
                  225005
Seq. No.
                  LIB3166-023-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3493172
BLAST score
                   278
E value
                   9.0e-25
Match length
                  70
% identity
                   80
                  (U89609) fiber annexin [Gossypium hirsutum]
NCBI Description
Seq. No.
                   225006
                  LIB3166-023-P1-K1-B7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3355474
BLAST score
                   109
                   1.0e-12
E value
Match length
                   51
                   58
% identity
NCBI Description
                  (AC004218) unknown protein [Arabidopsis thaliana]
Seq. No.
                   225007
                   LIB3166-023-P1-K1-B9
Seq. ID
Method
                   BLASTX
                   g3249084
NCBI GI
BLAST score
                   235
                   7.0e-20
E value
                   97
Match length
                   20
% identity
NCBI Description
                  (AC004473) Similar to red-1 (related to thioredoxin) gene
                   gb X92750 from Mus musculus. ESTs gb_AA712687 and
                   gb Z37223 come from this gene [Arabidopsis thaliana]
                   225008
Seq. No.
                   LIB3166-023-P1-K1-C1
Seq. ID
                   BLASTX
Method
                   g3785972
NCBI GI
                   130
BLAST score
                   2.0e-18
E value
Match length
                   83
                   75
% identity
                   (AC005560) putative auxin transport protein [Arabidopsis
NCBI Description
                   thaliana] >gi_4262249_gb_AAD14542_ (AC006200) putative
                   auxin transport protein [Arabidopsis thaliana]
                   225009
Seq. No.
                   LIB3166-023-P1-K1-C3
```



```
BLAST score
                  395
E value
                  2.0e-38
Match length
                  88
% identity
                  86
                  photosystem II oxygen-evolving complex protein 1 - potato
NCBI Description
                  >gi_809113_emb_CAA35601_ (X17578) 33kDa precursor protein
                  of oxygen-evolving complex [Solanum tuberosum]
                  225010
Seq. No.
Seq. ID
                  LIB3166-023-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  q3150402
BLAST score
                  189
E value
                  3.0e-14
Match length
                  90
                  56
% identity
                 (AC004165) putative malonyl-CoA:Acyl carrier protein
NCBI Description
                  transacylase [Arabidopsis thaliana]
Seq. No.
                  225011
                  LIB3166-023-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q445613
BLAST score
                  305
                  7.0e-28
E value
Match length
                  113
                  58
% identity
NCBI Description ribosomal protein L7 [Solanum tuberosum]
Seq. No.
                  225012
Seq. ID
                  LIB3166-023-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g3377509
BLAST score
                  348
                  6.0e-33
E value
                  88
Match length
% identity
NCBI Description (AF056027) auxin transport protein REH1 [Oryza sativa]
                  225013
Seq. No.
Seq. ID
                  LIB3166-023-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g571519
BLAST score
                  146
E value
                  2.0e-09
Match length
                  62
% identity
NCBI Description
                  (U16852) polyubiquitin [Gracilaria verrucosa]
                  >gi 1095488 prf 2109223A poly-ubiquitin [Gracilaria
                  verrucosa]
Seq. No.
                  225014
```

Seq. ID LIB3166-023-P1-K1-C9

Method BLASTX
NCBI GI g2244811
BLAST score 164
E value 2.0e-11



```
Match length 77 % identity 53
```

NCBI Description (Z97336) unnamed protein product [Arabidopsis thaliana]

Seq. No. 225015

Seq. ID LIB3166-023-P1-K1-D1

Method BLASTX
NCBI GI g544134
BLAST score 157
E value 1.0e-10
Match length 49
% identity 61

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR >gi\_99720\_pir\_S22863 hypothetical protein - Arabidopsis

thaliana >gi 421844 pir A46260 RecA functional analog

DRT100 - Arabidopsis thaliana (fragment)

Seq. No. 225016

Seq. ID LIB3166-023-P1-K1-D11

Method BLASTX
NCBI GI g1169476
BLAST score 268
E value 9.0e-25
Match length 123
% identity 67

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE

ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)

vitronectin-like adhesion protein [Nicotiana tabacum]

Seq. No. 225017

Seq. ID LIB3166-023-P1-K1-D12

Method BLASTX
NCBI GI g1531758
BLAST score 259
E value 2.0e-22
Match length 55
% identity 84

NCBI Description (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028)

unknown protein [Arabidopsis thaliana]

Seq. No. 225018

Seq. ID LIB3166-023-P1-K1-D6

Method BLASTX
NCBI GI g3928150
BLAST score 236
E value 1.0e-40
Match length 125
% identity 72

NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]

Seq. No. 225019

Seq. ID LIB3166-023-P1-K1-D7

Method BLASTX
NCBI GI g4379369
BLAST score 179
E value 2.0e-13
Match length 77

% identity

NCBI Description

46



```
% identity
NCBI Description (X90560) Calmodulin [Cloning vector pBluescript]
 Seq. No.
                   225020
Seq. ID
                   LIB3166-023-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   g3643598
BLAST score
                   532
E value
                   2.0e-54
Match length
                   126
                   72
% identity
                  (AC005395) putative poly(A) polymerase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   225021
Seq. ID
                   LIB3166-023-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   g3885338
BLAST score
                   215
E value
                   2.0e-17
Match length
                   109
% identity
                   36
NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]
Seq. No.
                   225022
Seq. ID
                   LIB3166-023-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   g1076621
BLAST score
                   487
E value
                   3.0e-49
Match length
                   110
% identity
                   78
NCBI Description cytochrome b5 - common tobacco >gi_296386_emb_CAA50575
                   (X71441) cytochrome b5 [Nicotiana tabacum]
Seq. No.
                   225023
                   LIB3166-023-P1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   a4490705
BLAST score
                   471
E value
                   2.0e-47
Match length
                   108
% identity
                   86
                  (AL035680) ribosomal protein L14-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   225024
Seq. ID
                  LIB3166-023-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  q1458245
BLAST score
                  270
E value
                  8.0e-24
Match length
                  128
```

32002

(U64834) coded for by C. elegans cDNA cm17a1; coded for by

C. elegans cDNA cm7g1; coded for by C. elegans cDNA CEMSE26F; similar to methyltransferases [Caenorhabditis



## elegans]

```
      Seq. No.
      225025

      Seq. ID
      LIB3166-023-P1-K1-E6

      Method
      BLASTX
```

Method BLASTX
NCBI GI 94508068
BLAST score 155
E value 3.0e-10
Match length 38
% identity 68

NCBI Description (AC005882) 3063 [Arabidopsis thaliana]

Seq. No. 225026

Seq. ID LIB3166-023-P1-K1-E7

Method BLASTX
NCBI GI g2335098
BLAST score 245
E value 7.0e-21
Match length 108
% identity 44

NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]

Seq. No. 225027

Seq. ID LIB3166-023-P1-K1-E8

Method BLASTX
NCBI GI g2245106
BLAST score 180
E value 2.0e-24
Match length 87

% identity 58

NCBI Description (Z97343) thioesterase homolog [Arabidopsis thaliana]

Seq. No. 225028

Seq. ID LIB3166-023-P1-K1-F5

Method BLASTX
NCBI GI g2827549
BLAST score 431
E value 1.0e-42
Match length 88
% identity 88

NCBI Description (AL021635) glycoprotein endopeptidase - like protein

[Arabidopsis thaliana]

Seq. No. 225029

Seq. ID LIB3166-023-P1-K1-G1

Method BLASTX
NCBI GI g3832512
BLAST score 146
E value 2.0e-20
Match length 64
% identity 84

NCBI Description (AF097922) granule-bound glycogen (starch) synthase

[Astragalus membranaceus]

Seq. No. 225030

Seq. ID LIB3166-023-P1-K1-G10

Method BLASTX



```
NCBI GI
                   q4455177
BLAST score
                   434
E value
                   5.0e-43
Match length
                   120
% identity
                   70
NCBI Description (AL035521) putative protein [Arabidopsis thaliana]
Seq. No.
                   225031
Seq. ID
                   LIB3166-023-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g2459419
BLAST score
                   216
E value
                   2.0e-17
Match length
                   126
% identity
                   46
NCBI Description (AC002332) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   225032
Seq. ID
                   LIB3166-023-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   g3451075
BLAST score
                   536
E value
                   4.0e-58
Match length
                   128
% identity
                   86
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]
Seq. No.
                   225033
Seq. ID
                  LIB3166-023-P1-K1-H1
Method
                  BLASTX
NCBI GI
                   g4580523
BLAST score
                  279
E value
                  7.0e-25
Match length
                  126
% identity
                   39
NCBI Description (AF036305) scarecrow-like 8 [Arabidopsis thaliana]
Seq. No.
                  225034
Seq. ID
                  LIB3166-023-P1-K1-H10
Method
                  BLASTX
                  g417154
                  668
                  2.0e-70
                  130
                  98
NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
```

NCBI GI BLAST score E value Match length % identity

protein 82 - rice (strain Taichung Native One)

>gi\_20256\_emb\_CAA77978\_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 225035

Seq. ID LIB3166-023-P1-K1-H11

Method BLASTX NCBI GI g3402678 BLAST score 191 E value 2.0e-14 Match length 53



% identity NCBI Description (AC004697) putative adenylate kinase [Arabidopsis thaliana] 225036 Seq. No. LIB3166-023-P1-K1-H12 Seq. ID Method BLASTX NCBI GI g2833389 BLAST score 350 E value 2.0e-33 Match length 86 % identity 41 NCBI Description SOLUBLE GLYCOGEN (STARCH) SYNTHASE PRECURSOR (SS III) >gi\_1200154\_emb\_CAA65065\_ (X95759) glycogen (starch) synthase [Solanum tuberosum] Seq. No. 225037 Seq. ID LIB3166-023-P1-K1-H4 Method BLASTX NCBI GI g1353352 BLAST score 272 E value 5.0e-32 Match length 115 % identity 57 NCBI Description (U31975) alanine aminotransferase [Chlamydomonas reinhardtii] Seq. No. 225038 Seq. ID LIB3166-023-P1-K1-H5 Method BLASTX NCBI GI g2982458 BLAST score 272 5.0e-24 E value Match length 81 % identity 67 NCBI Description (AL022223) putative protein [Arabidopsis thaliana] Seq. No. 225039 Seq. ID LIB3166-023-P1-K1-H6 Method BLASTX NCBI GI q1171579 BLAST score 173 E value 3.0e-15 Match length 83 % identity 60 NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum] Seq. No. 225040 Seq. ID LIB3166-023-P1-K1-H7 Method BLASTX NCBI GI g3046821 BLAST score 311 E value 1.0e-28 56 Match length % identity

Seq. No. 225041

NCBI Description (AB004785) homeobox gene [Nicotiana tabacum]

Seq. No.



```
Seq. ID
                   LIB3166-023-P1-K1-H8
Method
                   BLASTX
                   g136251
NCBI GI
BLAST score
                   172
E value
                   2.0e-12
                   63
Match length
                   60
% identity
NCBI Description
                   TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR
                   >gi_99767_pir__A31393 tryptophan synthase (EC 4.2.1.20)
                   beta chain - Arabidopsis thaliana >gi_166892 (M23872)
                   tryptophan synthase beta subunit [Arabidopsis thaliana]
Seq. No.
                   225042
Seq. ID
                   LIB3166-023-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   g3434967
BLAST score
                   225
E value
                   1.0e-18
Match length
                   77
% identity
                   58
NCBI Description
                  (AB008103) ethylene responsive element binding factor 1
                   [Arabidopsis thaliana]
Seq. No.
                   225043
Seg. ID
                   LIB3166-024-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g2147165
BLAST score
                   477
E value
                   5.0e-48
Match length
                   113
% identity
                   52
NCBI Description
                  calmodulin - Bidens pilosa >gi 939860 emb CAA61980
                   (X89890) Calmodulin [Bidens pilosa]
Seq. No.
                   225044
Seq. ID
                   LIB3166-024-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   q2880043
BLAST score
                   159
E value
                   8.0e-11
Match length
                   62
% identity
                   (AC002340) putative 3-hydroxyisobutyryl-coenzyme A
NCBI Description
                  hydrolase [Arabidopsis thaliana]
Seq. No.
                   225045
Seq. ID
                  LIB3166-024-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g3513745
BLAST score
                  193
E value
                   6.0e-19
Match length
                  112
% identity
                   44
NCBI Description
                  (AF080118) contains similarity to reverse trancriptase
                   (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
```

```
Seq. ID
                    LIB3166-024-P1-K1-A6
 Method
                    BLASTX
 N€BI GI
                    q3269293
 BLAST score
                    249
 E value
                    2.0e-21
 Match length
                    88
 % identity
 NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
Seq. No.
                    225047
 Seq. ID
                    LIB3166-024-P1-K1-A8
 Method
                    BLASTX
 NCBI GI
                    q1815759
 BLAST score
                    194
 E value
                    7.0e-15
 Match length
                    105
 % identity
                    40
 NCBI Description (U85499) pollen-specific protein [Phalaris coerulescens]
 Seq. No.
                    225048
 Seq. ID
                    LIB3166-024-P1-K1-B1
 Method
                    BLASTX
 NCBI GI
                    q3600032
 BLAST score
                    174
 E value
                    1.0e-12
 Match length
                    38
 % identity
                    87
                    (AF080119) contains similarity to tropomyosin (Pfam:
 NCBI Description
                    Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam:
                    ATP-synt B.hmm, score: 10.89) [Arabidopsis thaliana]
                    225049
 Seq. No.
 Seq. ID
                    LIB3166-024-P1-K1-B10
 Method
                    BLASTX
 NCBI GI
                    g2879867
 BLAST score
                    396
 E value
                    1.0e-38
 Match length
                    110
 % identity
                    68
 NCBI Description
                   (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces
                    pombe]
 Seq. No.
                    225050
 Seq. ID
                    LIB3166-024-P1-K1-B11
 Method
```

Method BLASTX
NCBI GI g4455199
BLAST score 435
E value 3.0e-43
Match length 116
% identity 74

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 225051

Seq. ID LIB3166-024-P1-K1-B12

Method BLASTX
NCBI GI g3063396
BLAST score 542



E value 1.0e-55 Match length 126 % identity 81

NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 225052

Seq. ID LIB3166-024-P1-K1-B2

Method BLASTX
NCBI GI g2959767
BLAST score 423
E value 1.0e-41
Match length 108
% identity 77

NCBI Description (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi\_3738292

(AC005309) glutathione-conjugate transporter AtMRP4

[Arabidopsis thaliana]

Seq. No. 225053

Seq. ID LIB3166-024-P1-K1-B3

Method BLASTX
NCBI GI g586004
BLAST score 530
E value 3.0e-54
Match length 109
% identity 89

NCBI Description SUPEROXIDE DISMUTASE [CU-ZN] >gi\_421962\_pir\_\_S34267

superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato
>gi\_542090\_pir\_\_S40404 superoxide dismutase (EC 1.15.1.1)
(Cu-Zn) - sweet potato >gi\_311971\_emb\_CAA51654\_ (X73139)

superoxide dismutase [Ipomoea batatas]

Seq. No. 225054

Seq. ID LIB3166-024-P1-K1-B4

Method BLASTX
NCBI GI g3776005
BLAST score 213
E value 4.0e-17
Match length 42
% identity 98

NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No. 225055

Seq. ID LIB3166-024-P1-K1-B5

Method BLASTX
NCBI GI g4567253
BLAST score 230
E value 4.0e-19
Match length 118
% identity 47

NCBI Description (AC007070) putative serpin protein [Arabidopsis thaliana]

Seq. No. 225056

Seq. ID LIB3166-024-P1-K1-B7

Method BLASTX
NCBI GI g3355475
BLAST score 298
E value 4.0e-27



```
Match length
                   66
% identity
                  92
                  (AC004218) ribosomal protein L23a [Arabidopsis thaliana]
NCBI Description
                  225057
Seq. No.
                  LIB3166-024-P1-K1-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2078561
BLAST score
                  186
                  7.0e-21
E value
Match length
                  106
% identity
                   67
                  (U96661) naringenin-chalcone synthase [Chrysosplenium
NCBI Description
                  americanum]
                  225058
Seq. No.
                  LIB3166-024-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2618721
BLAST score
                  139
                  1.0e-08
E value
Match length
                   45
                   62
% identity
                  (U49072) IAA16 [Arabidopsis thaliana]
NCBI Description
                  225059
Seq. No.
                  LIB3166-024-P1-K1-C12
Seq. ID
Method
                  BLASTX
                   g4262226
NCBI GI
BLAST score
                   155
E value
                   3.0e-10
Match length
                   31
% identity
                   87
                  (AC006200) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   225060
Seq. No.
Seq. ID
                  LIB3166-024-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   q4210948
                   565
BLAST score
E value
                   2.0e-58
Match length
                   109
% identity
                   96
                  (AF085275) DnaJ protein [Hevea brasiliensis]
NCBI Description
                   225061
Seq. No.
Seq. ID
                   LIB3166-024-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   q3757527
BLAST score
                   178
                   5.0e-13
E value
Match length
                   43
```

% identity

(AC005167) putative ribosomal protein L27 [Arabidopsis NCBI Description

thaliana]

Seq. No. 225062

Method

NCBI GI

BLASTX

g2245082



```
LIB3166-024-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3355468
BLAST score
                   261
E value
                   3.0e-23
                   63
Match length
                   87
% identity
                   (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                  thaliana]
                   225063
Seq. No.
                  LIB3166-024-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2194142
BLAST score
                   500
                  8.0e-51
E value
                  109
Match length
                   84
% identity
                  (AC002062) ESTs qb N38288, qb T43486, qb AA395242 come from
NCBI Description
                  this gene. [Arabidopsis thaliana]
Seq. No.
                   225064
                  LIB3166-024-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2289003
BLAST score
                   241
E value
                   2.0e-20
                  55
Match length
                   82
% identity
                  (AC002335) membrane transporter D1 isolog [Arabidopsis
NCBI Description
                  thaliana]
                   225065
Seq. No.
                  LIB3166-024-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3582342
                   221
BLAST score
E value
                   5.0e-18
                  125
Match length
% identity
                   41
                   (AC005496) putative flavonol 3-o-glucosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   225066
Seq. No.
                  LIB3166-024-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3033386
BLAST score
                   165
E value
                   2.0e-11
Match length
                   72
                   46
% identity
NCBI Description
                  (AC004238) RING3-like protein [Arabidopsis thaliana]
Seq. No.
                   225067
Seq. ID
                  LIB3166-024-P1-K1-D5
```



BLAST score 518 7.0e-53 E value Match length 115 84 % identity

NCBI Description (Z97343) SCARECROW homolog [Arabidopsis thaliana]

225068 Seq. No.

LIB3166-024-P1-K1-E1 Seq. ID

Method BLASTX NCBI GI g3947735 BLAST score 280 6.0e-25 E value Match length 107 % identity 51

NCBI Description (AJ009720) NL27 [Solanum tuberosum]

Seq. No.

LIB3166-024-P1-K1-E10 Seq. ID

225069

Method BLASTX NCBI GI g2289002 BLAST score 350 E value 3.0e-33 110 Match length

% identity 65

NCBI Description (AC002335) unknown protein [Arabidopsis thaliana]

225070 Seq. No.

LIB3166-024-P1-K1-E12 Seq. ID

Method BLASTX g1346524 NCBI GI BLAST score 601 1.0e-62 E value 126 Match length 90 % identity

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE

ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi\_497900 (M73430) S-adenosyl methionine synthetase [Populus

deltoides]

225071 Seq. No.

LIB3166-024-P1-K1-E4 Seq. ID

Method BLASTX NCBI GI g2342685 BLAST score 424 E value 7.0e-42Match length 127 % identity 65

NCBI Description (AC000106) Contains similarity to Rhodococcus amidase

(gb\_D16207). ESTs gb\_T20504,gb\_H36650,gb\_N97423,gb\_H36595

come from this gene. [Arabidopsis thaliana]

225072 Seq. No.

LIB3166-024-P1-K1-E6 Seq. ID

Method BLASTX NCBI GI g1871192 BLAST score 156 E value 2.0e-10



Match length 116 % identity 41

NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis

thaliana]

Seq. No. 225073

Seq. ID LIB3166-024-P1-K1-E7

Method BLASTX
NCBI GI g3135013
BLAST score 154
E value 3.0e-10
Match length 103
% identity 40

NCBI Description (AJ005963) 100 kDa protein [Ajellomyces capsulatus]

Seq. No. 225074

Seq. ID LIB3166-024-P1-K1-E9

Method BLASTX
NCBI GI g3334322
BLAST score 451
E value 5.0e-45
Match length 109
% identity 81

NCBI Description GTP-BINDING PROTEIN SAR1B >gi 2108347 (U55036) small

GTP-binding protein Bsarlb [Brassica rapa]

Seq. No. 225075

Seq. ID LIB3166-024-P1-K1-F12

Method BLASTX
NCBI GI g886116
BLAST score 428
E value 2.0e-42
Match length 119
% identity 66

NCBI Description (U27609) TCH4 protein [Arabidopsis thaliana] >gi 2952473

(AF051338) xyloglucan endotransglycosylase related protein

[Arabidopsis thaliana]

Seq. No. 225076

Seq. ID LIB3166-024-P1-K1-F4

Method BLASTX
NCBI GI g1351408
BLAST score 419
E value 3.0e-41
Match length 96
% identity 81

NCBI Description VACUOLAR PROCESSING ENZYME PRECURSOR (VPE)

>gi\_1076563\_pir\_\_S51117 cystein proteinase - sweet orange >gi\_633185\_emb\_CAA87720\_ (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi\_1588548\_prf\_\_2208463A

vascular processing protease [Citrus sinensis]

Seq. No. 225077

Seq. ID LIB3166-024-P1-K1-F5

Method BLASTX NCBI GI g1518540 BLAST score 574



```
2.0e-59
E value
                  133
Match length
                  86
% identity
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                  225078
Seq. No.
                  LIB3166-024-P1-K1-F7
Seq. ID
                  BLASTX
Method
                  g4567279
NCBI GI
BLAST score
                  409
                  4.0e-40
E value
                  112
Match length
                  71
% identity
                  (AC006841) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                  225079
Seq. No.
                  LIB3166-024-P1-K1-F9
Seq. ID
                  BLASTX
Method
                  g2342682
NCBI GI
                  448
BLAST score
E value
                  1.0e-44
                  114
Match length
                  75
% identity
                  (AC000106) Contains similarity to Rattus AMP-activated
NCBI Description
                  protein kinase (gb_X95577). [Arabidopsis thaliana]
Seq. No.
                  225080
                  LIB3166-024-P1-K1-G11
Seq. ID
                  BLASTX
Method
                   q4580460
NCBI GI
BLAST score
                   293
                   1.0e-26
E value
                  88
Match length
                   69
% identity
                  (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
NCBI Description
                   thaliana]
                   225081
Seq. No.
                   LIB3166-024-P1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1486472
BLAST score
                   405
                   1.0e-39
E value
Match length
                   92
% identity
                   86
NCBI Description (X99853) oxoglutarate malate translocator [Solanum
                   tuberosum]
                   225082
Seq. No.
                   LIB3166-024-P1-K1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2864622
```

NCBI GI g2864622 BLAST score 228 E value 7.0e-19 Match length 100 % identity 49



```
NCBI Description (AL021811) putative protein [Arabidopsis thaliana]
                  225083
Seq. No.
                  LIB3166-024-P1-K1-G5
Seq. ID
                  BLASTX
Method
                  g4539370
NCBI GI
                  337
BLAST score
                  1.0e-31
E value
                  86
Match length
                  73
% identity
                  (AL049525) UDP-galactose 4-epimerase-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  225084
Seq. No.
                  LIB3166-024-P1-K1-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3142303
                  522
BLAST score
                  2.0e-53
E value
                  127
Match length
                  83
% identity
                  (AC002411) Strong similarity to MRP-like ABC transporter
NCBI Description
                  gb U92650 from A. thaliana and canalicular multi-drug
                  resistance protein gb_L49379 from Rattus norvegicus.
                   [Arabidopsis thaliana]
                  225085
Seq. No.
                  LIB3166-024-P1-K1-G8
Seq. ID
                  BLASTX
Method
                  g3650030
NCBI GI
                  217
BLAST score
                  1.0e-17
E value
                  74
Match length
                   53
% identity
                  (AC005396) unknown protein [Arabidopsis thaliana]
NCBI Description
                   225086
Seq. No.
                  LIB3166-024-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                   q464981
                   354
BLAST score
E value
                   1.0e-33
Match length
                   65
                   98
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762)
                  ubiquitin carrier protein [Lycopersicon esculentum]
Seq. No.
                   225087
                   LIB3166-024-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4099914
BLAST score
                   279
E value
                   7.0e-25
                   79
Match length
% identity
```

NCBI Description (U91857) ethylene-responsive element binding protein

Match length

% identity

71

54



## homolog [Stylosanthes hamata]

```
225088
Seq. No.
                  LIB3166-024-P1-K1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3660471
                  590
BLAST score
                  2.0e-61
E value
Match length
                  124
                  91
% identity
                  (AJ001809) succinate dehydrogenase flavoprotein alpha
NCBI Description
                  subunit [Arabidopsis thaliana]
                  225089
Seq. No.
                  LIB3166-024-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q125887
BLAST score
                  196
                  4.0e-15
E value
                  101
Match length
                  45
% identity
                  ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
NCBI Description
                  >gi_82092_pir__S04765 LAT52 protein precursor - tomato
                  >gi 295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon
                  esculentum]
                  225090
Seq. No.
Seq. ID
                  LIB3166-024-P1-K1-H2
Method
                  BLASTX
                  g2702270
NCBI GI
BLAST score
                  302
E value
                  1.0e-27
                  85
Match length
                  66
% identity
NCBI Description (AC003033) unknown protein [Arabidopsis thaliana]
Seq. No.
                  225091
                  LIB3166-024-P1-K1-H3
Seq. ID
Method
                  BLASTX
                  g1173256
NCBI GI
                   572
BLAST score
E value
                   3.0e-59
Match length
                  129
                  88
% identity
                  40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal
NCBI Description
                   protein S4 - upland cotton >gi_488739_emb_CAA55882_
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
                   225092
Seq. No.
                  LIB3166-024-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3894190
BLAST score
                  208
E value
                   2.0e-16
```

```
NCBI Description (AC005662) putative RNA polymerase [Arabidopsis thaliana]
                  225093
Seq. No.
                  LIB3166-024-P1-K1-H7
Seq. ID
Method
                  BLASTX
                  g1353193
NCBI GI
BLAST score
                  157
                  1.0e-10
E value
Match length
                  71
                  49
% identity
NCBI Description
                  O-METHYLTRANSFERASE ZRP4 (OMT) >gi 542186 pir JQ2268
                  O-methyltransferase (EC 2.1.1.-) - maize >gi 404070
                  (L14063) O-methyltransferase [Zea mays]
                  225094
Seq. No.
                  LIB3166-024-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2529342
BLAST score
                  587
E value
                  5.0e-61
Match length
                  112
% identity
                  94
NCBI Description
                 (L76554) transketolase [Spinacia oleracea]
                  225095
Seq. No.
Seq. ID
                  LIB3166-024-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g4115914
BLAST score
                  319
E value
                  2.0e-29
Match length
                  117
                  52
% identity
NCBI Description
                  (AF118222) contains similarity to Iron/Ascorbate family of
                  oxidoreductases (Pfam: PF00671, Score=297.8, E=1.3e-85,
                  N=1) [Arabidopsis thaliana] >gi_4539410_emb_CAB40043.1
                  (AL049524) putative Fe(II)/ascorbate oxidase [Arabidopsis
```

thaliana]

Seq. No. 225096 Seq. ID LIB3166-025-P1-K1-A11 Method BLASTX

NCBI GI g3789911 BLAST score 266 E value 2.0e-23 Match length 117 % identity 43

NCBI Description (AF081802) developmental protein DG1118 [Dictyostelium

discoideum]

225097 Seq. No.

LIB3166-025-P1-K1-A2 Seq. ID

Method BLASTX NCBI GI a289920 BLAST score 507 E value 1.0e-51 Match length 104 % identity 90



```
(L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  225098
Seq. No.
                  LIB3166-025-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3273243
BLAST score
                  582
                  2.0e-60
E value
                  127
Match length
                  23
% identity
NCBI Description
                  (AB004660) NLS receptor [Oryza sativa]
                  >gi 3273245 dbj BAA31166 (AB004814) NLS receptor [Oryza
                  sativa]
Seq. No.
                  225099
                  LIB3166-025-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2660670
BLAST score
                  370
E value
                  1.0e-35
Match length
                  103
                  74
% identity
                  (AC002342) putative Cu2+-transporting ATPase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  225100
                  LIB3166-025-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827559
BLAST score
                  162
E value
                  3.0e-11
Match length
                  42
                  71
% identity
NCBI Description
                  (AL021635) predicted protein [Arabidopsis thaliana]
                  >gi_3292808_emb_CAA19798_ (AL031018) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                   225101
Seq. ID
                  LIB3166-025-P1-K1-A7
Method
                  BLASTX
NCBI GI
                   q4454026
BLAST score
                  166
E value
                   1.0e-11
Match length
                  53
% identity
                   62
NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]
Seq. No.
                  225102
Seq. ID
                  LIB3166-025-P1-K1-A8
Method
                  BLASTX
```

Method BLASTX
NCBI GI g4335739
BLAST score 173
E value 2.0e-12
Match length 71
% identity 48

NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]

E value

Match length

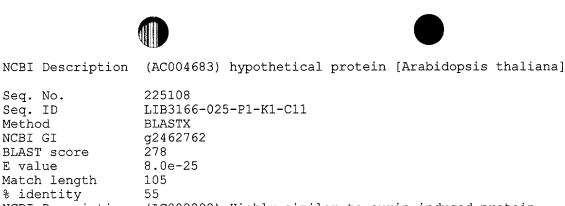
% identity

2.0e-29

127



```
Seq. No.
                  225103
                  LIB3166-025-P1-K1-A9
Seq. ID
                  BLASTX
Method
                  g3552003
NCBI GI
BLAST score
                  666
                  3.0e-70
E value
                  129
Match length
                  97
% identity
                  (AF085083) alcohol dehydrogenase A [Gossypium hirsutum]
NCBI Description
                  >gi_3552005 (AF085084) alcohol dehydrogenase A [Gossypium
                  hirsutum] >gi 3552007 (AF085085) alcohol dehydrogenase A
                  [Gossypium hirsutum] >gi_4140632 (AF090165) alcohol
                  dehydrogenase A [Gossypium hirsutum] >gi_4140634 (AF090166)
                  alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140636
                  (AF090167) alcohol dehydrogenase A [Gossypium hirsutum]
                  >gi 4140638 (AF090168) alcohol dehydrogenase A [Gossypium
                  hirsutum]
                  225104
Seq. No.
                  LIB3166-025-P1-K1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2462745
                  288
BLAST score
                  4.0e-26
E value
Match length
                  85
                  60
% identity
                 (AC002292) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  225105
Seq. No.
                  LIB3166-025-P1-K1-B2
Seq. ID
Method
                  BLASTX
                  g1843527
NCBI GI
BLAST score
                  444
                  3.0e-44
E value
Match length
                  118
% identity
                  76
NCBI Description (U73747) annexin [Gossypium hirsutum]
                  225106
Seq. No.
                  LIB3166-025-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4469023
                  229
BLAST score
                  6.0e-19
E value
Match length
                  66
% identity
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
                  225107
Seq. No.
Seq. ID
                  LIB3166-025-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g3395429
BLAST score
                  318
```



NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

225109 Seq. No. Seq. ID LIB3166-025-P1-K1-C12 Method BLASTX q4510407

NCBI GI BLAST score 142 8.0e-09 E value Match length 122 35 % identity

NCBI Description (AC006587) unknown protein [Arabidopsis thaliana]

225110 Seq. No.

LIB3166-025-P1-K1-C3 Seq. ID

BLASTX Method NCBI GI g2144271 BLAST score 597 4.0e-62 E value 127 Match length 91 % identity

trans-cinnamate 4-monooxygenase (EC 1.14.13.11) C - Populus NCBI Description kitakamiensis (fragment) >gi 1777372\_dbj\_BAA11578 (D82814)

cinnamic acid 4-hydroxylase [Populus kitakamiensis]

Seq. No. 225111

Seq. ID LIB3166-025-P1-K1-C5

Method BLASTX g1220196 NCBI GI BLAST score 537 E value 4.0e-55 115 Match length % identity 87

NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

225112 Seq. No.

Seq. ID LIB3166-025-P1-K1-C6

Method BLASTX NCBI GI q3805845 BLAST score 463 E value 2.0e-46 Match length 118 % identity 73

NCBI Description (AL031986) putative protein [Arabidopsis thaliana]

Seq. No. 225113

Seq. ID LIB3166-025-P1-K1-C7



```
Method
                   BLASTX
                   g131392
NCBI GI
BLAST score
                   331
                   6.0e - 31
E value
Match length
                   104
                   68
% identity
NCBI Description
                   OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD
                   SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II)
                   >gi 81479 pir S00005 photosystem II oxygen-evolving
                   complex protein 2 precursor - spinach
                   >gi_21265_emb_CAA29055_ (X05511) 23 kDa OEC protein
[Spinacia oleracea] >gi_225596_prf__1307179A luminal
                   protein 23kD [Spinacia oleracea]
Seq. No.
                   225114
Seq. ID
                   LIB3166-025-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   g4097579
BLAST score
                   441
E value
                   7.0e-44
Match length
                   92
% identity
                   89
NCBI Description
                  (U64922) NTGP1 [Nicotiana tabacum]
Seq. No.
                   225115
Seq. ID
                   LIB3166-025-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   q3738293
BLAST score
                   410
                   3.0e-40
E value
Match length
                   95
                   78
% identity
                   (AC005309) putative CCAAT-binding transcription factor
NCBI Description
                   subunit A (CBF-A) [Arabidopsis thaliana]
                   225116
Seq. No.
                   LIB3166-025-P1-K1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g509163
BLAST score
                   336
E value
                   2.0e-35
Match length
                   102
                   69
% identity
NCBI Description (X69193) cyprosin [Cynara cardunculus]
                   225117
Seq. No.
                   LIB3166-025-P1-K1-D5
Seq. ID
                   BLASTX
Method
                   g3080401
NCBI GI
BLAST score
                   438
E value
                   2.0e-43
Match length
                   112
```

% identity 77
NCBI Description (AL022603) putative protein [Arabidopsis thaliana]
>gi\_4455265\_emb\_CAB36801.1\_ (AL035527) putative protein



225118 Seq. No. Seq. ID LIB3166-025-P1-K1-D6 Method BLASTX NCBI GI q4510376 371 BLAST score E value 1.0e-35 Match length 83

% identity NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

225119 Seq. No.

Seq. ID LIB3166-025-P1-K1-D7

78

BLASTX Method NCBI GI g3763916 BLAST score 200 E value 1.0e-15 Match length 103 % identity 45

(AC004450) unknown protein [Arabidopsis thaliana] NCBI Description

>gi 4531439 gb AAD22124.1 AC006224 6 (AC006224) unknown

protein [Arabidopsis thaliana]

225120 Seq. No.

LIB3166-025-P1-K1-E1 Seq. ID

Method BLASTX NCBI GI g3367523 BLAST score 340 E value 4.0e-32 Match length 88 74 % identity

NCBI Description (AC004392) ESTs gb AA728658 and gb N95943 come from this

gene. [Arabidopsis thaliana]

225121 Seq. No.

Seq. ID LIB3166-025-P1-K1-E10

Method BLASTX NCBI GI g118564 BLAST score 531 E value 2.0e-54 Match length 125 % identity 82

NCBI Description GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE

REDUCTASE) (HPR) (GDH) >gi\_65955\_pir\_\_DEKVG glycerate dehydrogenase (EC 1.1.1.29) - cucumber

>gi\_18264\_emb\_CAA41434\_ (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >gi\_18275\_emb\_CAA32764\_ (X14609) NAPH-dependent

hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

Seq. No. 225122

Seq. ID LIB3166-025-P1-K1-E3

Method BLASTX NCBI GI g1352821 BLAST score, 537 · E value 4.0e-55 Match length 107 95 % identity



NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091)

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 225123

LIB3166-025-P1-K1-E4 Seq. ID

Method BLASTX NCBI GI g3421096 BLAST score 516 1.0e-52 E value Match length 114 89 % identity

(AF043528) 20S proteasome subunit PAG1 [Arabidopsis NCBI Description

thaliana] >gi 3885332 (AC005623) proteasome component

[Arabidopsis thaliana]

225124 Seq. No.

LIB3166-025-P1-K1-E5 Seq. ID

Method BLASTX g4567319 NCBI GI BLAST score 558 1.0e-57 E value Match length 124 87 % identity

NCBI Description (AC005956) putative copper amine oxidase [Arabidopsis

thaliana]

225125 Seq. No.

Seq. ID LIB3166-025-P1-K1-E8

Method BLASTX NCBI GI q1706318 BLAST score 268 E value 1.0e-23 Match length 106

% identity 55

NCBI Description GLUTAMATE DECARBOXYLASE (GAD) (ERT D1)

>gi\_1362098\_pir\_\_S56177 probable glutamate decarboxylase tomato >gi\_995555\_emb\_CAA56812\_ (X80840) homology to
pyroxidal-5'-phosphate-dependant glutamate decarboxylases;

putative start codon [Lycopersicon esculentum]

Seq. No. 225126

LIB3166-025-P1-K1-F10 Seq. ID

Method BLASTX NCBI GI g1220196 BLAST score 538 E value 3.0e-55 Match length 114

NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

225127 Seq. No.

% identity

Seq. ID LIB3166-025-P1-K1-F11

89

BLASTX Method NCBI GI g2894306 BLAST score 471 2.0e-47 E value 122 Match length 80 % identity (AJ223329) ubiquitin extension protein [Nicotiana tabacum] NCBI Description 225128 Seq. No. LIB3166-025-P1-K1-F3 Seq. ID Method BLASTX NCBI GI g477280 BLAST score 230 4.0e-19 E value 57 Match length 70 % identity NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) 55K protein precursor - potato >gi 410633 bbs 136740 cytochrome c reductase-processing peptidase subunit I, MPP subunit I, P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 534 aa] 225129 Seq. No. LIB3166-025-P1-K1-F5 Seq. ID Method BLASTX NCBI GI g118564 215 BLAST score E value 1.0e-23 Match length 82 78 % identity NCBI Description GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE REDUCTASE) (HPR) (GDH) >gi\_65955\_pir\_\_DEKVG glycerate dehydrogenase (EC 1.1.1.29) - cucumber >gi 18264 emb CAA41434 (X58542) NADH-dependent hydroxypyruvate reductase [Cucumis sativus] >gi\_18275\_emb\_CAA32764\_ (X14609) NAPH-dependent hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

Seq. No. 225130

Seq. ID LIB3166-025-P1-K1-F6

Method BLASTX
NCBI GI g2286153
BLAST score 614
E value 4.0e-64
Match length 126
% identity 95

NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No. 225131

Seq. ID LIB3166-025-P1-K1-F9

Method BLASTX
NCBI GI g1143427
BLAST score 548
E value 2.0e-56
Match length 127
% identity 88

NCBI Description (X73961) heat shock protein 70 [Cucumis sativus]

Seq. No. 225132

% identity

62



```
LIB3166-025-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  a3367522
BLAST score
                  323
                  5.0e-30
E value
Match length
                  105
% identity
                  61
NCBI Description
                  (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  225133
Seq. ID
                  LIB3166-025-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q82519
BLAST score
                  215
                  2.0e-17
E value
Match length
                  68
                  69
% identity
                  hypothetical 15K protein (trnH-trnV intergenic region) -
NCBI Description
                  rice chloroplast >gi_12029_emb_CAA33937_ (X15901) ORF137
                  [Oryza sativa] >gi_12073_emb_CAA33925_ (X15901) ORF137
                  [Oryza sativa] >gi_226651_prf__1603356CB ORF 137 [Oryza
                  sativa]
Seq. No.
                  225134
Seq. ID
                  LIB3166-025-P1-K1-G5
Method
                  BLASTX
                  g2435511
NCBI GI
BLAST score
                  172
E value
                  2.0e-12
Match length
                  59
% identity
                  58
NCBI Description (AF024504) contains similarity to prolyl 4-hydroxylase
                  alpha subunit [Arabidopsis thaliana]
Seq. No.
                  225135
Seq. ID
                  LIB3166-025-P1-K1-G6
                  BLASTX
Method
NCBI GI
                  q1173137
BLAST score
                  498
E value
                  1.0e-50
Match length
                  98
                  94
% identity
                 DNA-DIRECTED RNA POLYMERASE II 19 KD POLYPEPTIDE (RNA
NCBI Description
                  POLYMERASE II SUBUNIT 5) >gi_322700_pir__B44457 RNA
                  polymerase II fifth largest subunit - Glycine max=soybeans
                  >gi 170052 (M90504) RNA polymerase II [Glycine max]
Seq. No.
                  225136
Seq. ID
                  LIB3166-025-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g3935147
BLAST score
                  373
E value
                  7.0e-36
Match length
                  117
```

NCBI Description (AC005106) T25N20.11 [Arabidopsis thaliana]

NCBI Description

225142

Seq. No.



```
225137
Seq. No.
                  LIB3166-025-P1-K1-H10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3128228
BLAST score
                   146
                   3.0e-09
E value
Match length
                   32
                   84
% identity
                  (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                   thaliana] >gi_3337376 (AC004481) putative ribosomal protein
                   L18A [Arabidopsis thaliana]
                   225138
Seq. No.
                  LIB3166-025-P1-K1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4544443
BLAST score
                   166
                   1.0e-11
E value
                   34
Match length
                   94
% identity
NCBI Description
                  (AC006592) putative mitochondrial uncoupling protein
                   [Arabidopsis thaliana]
Seq. No.
                   225139
                  LIB3166-025-P1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3004560
BLAST score
                   433
                   6.0e-43
E value
Match length
                   97
% identity
                   81
NCBI Description
                  (AC003673) putative ATP binding protein [Arabidopsis
                   thaliana]
Seq. No.
                   225140
Seq. ID
                   LIB3166-026-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   q2462762
BLAST score
                   325
E value
                   3.0e - 30
Match length
                   120
% identity
                   57
NCBI Description
                  (AC002292) Highly similar to auxin-induced protein
                   (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                   225141
                   LIB3166-026-P1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2213624
BLAST score
                   378
E value
                   2.0e-36
Match length
                   126
% identity
                   60
```

32025

(AC000103) F21J9.16 [Arabidopsis thaliana]



```
LIB3166-026-P1-K1-A11
Seq. ID
                  BLASTX
Method
                  g2463569
NCBI GI
BLAST score
                  318
E value
                  2.0e-29
                  68
Match length
                  85
% identity
NCBI Description
                  (AB007503) squalene synthase [Glycine max]
                  225143
Seq. No.
                  LIB3166-026-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076626
BLAST score
                  452
                  3.0e-45
E value
Match length
                  120
                  72
% identity
NCBI Description
                  glycine rich protein - common tobacco
                  >gi_790473_emb_CAA58702_ (X83731) soluble, glycine rich
                  protein [Nicotiana tabacum]
                  225144
Seq. No.
                  LIB3166-026-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4056432
                  560
BLAST score
E value
                  8.0e-58
Match length
                  124
                  81
% identity
NCBI Description
                  (AC005990) Similar to gi_2245014 glucosyltransferase
                  homolog from Arabidopsis thaliana chromosome 4 contig
                  gb Z97341. ESTs gb T20778 and gb AA586281 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  225145
Seq. ID
                  LIB3166-026-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  q3955021
BLAST score
                  214
E value
                   4.0e-31
Match length
                  106
% identity
                  72
NCBI Description
                  (AJ010811) HB2 homeodomain protein [Populus tremula x
                  Populus tremuloides]
                  225146
Seq. No.
Seq. ID
                  LIB3166-026-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  q2980801
BLAST score
                  154
E value
                   4.0e-18
Match length
                  83
% identity
                  59
```

thaliana] >gi\_3660550\_dbj\_BAA33435\_ (AB013816) DREB1B [Arabidopsis thaliana] >gi\_3738226\_dbj\_BAA33792\_ (AB007788) DREB1B [Arabidopsis thaliana]

NCBI Description

(AL022197) transcriptional activator CBF1 [Arabidopsis

Seq. No.

Seq. ID



```
225147
Seq. No.
                  LIB3166-026-P1-K1-B11
Seq. ID
Method
                  BLASTX
                  q3183640
NCBI GI
                  542
BLAST score
E value
                  1.0e-55
                  107
Match length
                  97
% identity
                  (AJ005869) transmembrane channel protein [Cicer arietinum]
NCBI Description
Seq. No.
                  225148
                  LIB3166-026-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q886116
BLAST score
                   495
                   3.0e-50
E value
Match length
                  129
                   69
% identity
                   (U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473
NCBI Description
                   (AF051338) xyloglucan endotransglycosylase related protein
                   [Arabidopsis thaliana]
                   225149
Seq. No.
                   LIB3166-026-P1-K1-B6
Seq. ID
Method
                   BLASTX
                   q1946359
NCBI GI
BLAST score
                   149
                   1.0e-09
E value
                   31
Match length
% identity
                   87
NCBI Description
                  (U93215) unknown protein [Arabidopsis thaliana]
                   225150
Seq. No.
                   LIB3166-026-P1-K1-B8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2760830
BLAST score
                   399
                   6.0e-39
E value
                   122
Match length
                   60
% identity
NCBI Description
                   (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
                   thaliana]
                   225151
Seq. No.
                   LIB3166-026-P1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4490732
BLAST score
                   631
                   4.0e-66
E value
Match length
                   124
% identity
                   (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
NCBI Description
                   protein [Arabidopsis thaliana]
```

LIB3166-026-P1-K1-C3

225152



Method BLASTX NCBI GI g2815246 BLAST score 215 2.0e-17 E value Match length 53 72 % identity (X95709) class I type 2 metallothionein [Cicer arietinum] NCBI Description 225153 Seq. No. LIB3166-026-P1-K1-C5 Seq. ID Method BLASTX NCBI GI q4309744 BLAST score 209 E value 1.0e-16 Match length 115 37 % identity (AC006439) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 225154 LIB3166-026-P1-K1-C6 Seq. ID Method BLASTX NCBI GI g2129583 283 BLAST score 2.0e-25 E value 78 Match length 73 % identity NCBI Description ferritin - Arabidopsis thaliana >gi 1246401 emb CAA63932\_ (X94248) ferritin [Arabidopsis thaliana] 225155 Seq. No. LIB3166-026-P1-K1-C7 Seq. ID Method BLASTX NCBI GI g2829862 BLAST score 255 4.0e-22 E value 95 Match length % identity 53 (AC002396) Similar to glucosyltransferases [Arabidopsis NCBI Description thaliana] 225156 Seq. No. Seq. ID LIB3166-026-P1-K1-D10 Method BLASTX NCBI GI q2496731 228 BLAST score 3.0e-39 E value Match length 123 % identity 72 NCBI Description HYPOTHETICAL 30.2 KD PROTEIN Y40V >gi 2182566 (AE000089)

Y4oV [Rhizobium sp. NGR234]

Seq. No. 225157

Seq. ID LIB3166-026-P1-K1-D12

Method BLASTX
NCBI GI g439493
BLAST score 188
E value 3.0e-14



Match length 74 % identity 61

NCBI Description (D26086) zinc-finger protein [Petunia x hybrida]

Seq. No.

225158

Seq. ID Method LIB3166-026-P1-K1-D2 BLASTX

NCBI GI BLAST score E value Match length g2306917 387 2.0e-37

Match length 96 % identity 81

NCBI Description (AF003728) plasma membrane intrinsic protein [Arabidopsis

thaliana]

Seq. No.

225159

Seq. ID

LIB3166-026-P1-K1-D4

Method BLASTX
NCBI GI g232202
BLAST score 350
E value 3.0e-33
Match length 91
% identity 73

NCBI Description GLUTATHIONE S-TRANSFERASE PARB (CLASS-PHI)

>gi\_285295\_pir\_\_A41789 glutathione transferase (EC
2.5.1.18) - common tobacco >gi\_218294\_dbj\_BAA01394\_
(D10524) glutathione S-transferase [Nicotiana tabacum]

Seq. No. 225160

Seq. ID LIB3166-026-P1-K1-D7

Method BLASTX
NCBI GI g3355468
BLAST score 509
E value 8.0e-52
Match length 123
% identity 86

NCBI Description (AC004218) putative ribosomal protein L35 [Arabidopsis

thaliana]

Seq. No. 225161

Seq. ID LIB3166-026-P1-K1-D8

Method BLASTX
NCBI GI g1666234
BLAST score 540
E value 2.0e-55
Match length 103
% identity 99

NCBI Description (U76193) actin [Pisum sativum] >gi 1724143 (U81049) actin

[Pisum sativum]

Seq. No. 225162

Seq. ID LIB3166-026-P1-K1-E10

Method BLASTX
NCBI GI g4544409
BLAST score 416
E value 7.0e-41
Match length 114



% identity (AC006955) putative transcription factor [Arabidopsis NCBI Description thaliana] 225163 Seq. No. LIB3166-026-P1-K1-F10 Seq. ID Method BLASTX NCBI GI g1762428 BLAST score 417 5.0e-41 E value Match length 123 % identity 14 (U59467) aromatic rich glycoprotein JP630 [Arabidopsis NCBI Description thaliana] Seq. No. 225164 LIB3166-026-P1-K1-F3 Seq. ID Method BLASTX NCBI GI q2583117 BLAST score 161 5.0e-11 E value 54 Match length % identity 61 (AC002387) hypothetical protein [Arabidopsis thaliana] NCBI Description 225165 Seq. No. LIB3166-026-P1-K1-F6 Seq. ID Method BLASTX g2529668 NCBI GI 538 BLAST score E value 3.0e-55Match length 124 83 % identity NCBI Description (AC002535) putative photolyase/blue-light receptor [Arabidopsis thaliana] >gi\_3319288 (AF053366) photolyase/blue light photoreceptor PHR2 [Arabidopsis ٠. thaliana] 225166 Seq. No. LIB3166-026-P1-K1-G1 Seq. ID Method BLASTX NCBI GI q4204302 BLAST score 150 1.0e-09 E value Match length 41 % identity NCBI Description (AC003027) Hypothetical protein [Arabidopsis thaliana] Seq. No. 225167 Seq. ID LIB3166-026-P1-K1-G10 Method BLASTX

Method BLASTX
NCBI GI g3236259
BLAST score 378
E value 2.0e-36
Match length 112
% identity 63

NCBI Description (AC004684) putative alcohol dehydrogenase [Arabidopsis

E value

Match length

% identity

2.0e-58

114

98



## thaliana]

225168 Seq. No. Seq. ID LIB3166-026-P1-K1-G11 Method BLASTX NCBI GI g3360289 BLAST score 491 E value 9.0e-50 Match length 120 % identity 72 NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays] 225169 Seq. No. LIB3166-026-P1-K1-G12 Seq. ID Method BLASTX g2677828 NCBI GI BLAST score 311 E value 1.0e-28 Match length 100 % identity 57 NCBI Description (U93166) cysteine protease [Prunus armeniaca] 225170 Seq. No. Seq. ID LIB3166-026-P1-K1-G3 Method BLASTX NCBI GI q4098129 BLAST score 659 E value 2.0e-69 Match length 128 96 % identity NCBI Description (U73588) sucrose synthase [Gossypium hirsutum] Seq. No. 225171 LIB3166-026-P1-K1-G6 Seq. ID Method BLASTX NCBI GI q1172664 BLAST score 167 E value 9.0e-12 Match length 37 % identity 89 NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi\_419791\_pir\_\_S31165 photosystem I chain III precursor -Flaveria trinervia >gi\_298482 bbs\_127083 photosystem I reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi 168173 (M83119) photosystem I subunit III [Flaveria trinervia] Seq. No. 225172 Seq. ID LIB3166-026-P1-K1-G8 Method BLASTX NCBI GI q417103 BLAST score 565



NCBI Description HISTONE H3.2, MINOR >gi 282871 pir S24346 histone H3.3-like protein - Arabidopsis thaliana >gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563 (U09458) histone H3.2 [Medicago sativa] >gi 488567 ( $\overline{\text{U0}}$ 09460) histone H3.2 [Medicago sativa] >gi 488569 (U09461) histone H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2 [Medicago sativa]  $>gi_4885\overline{7}7$  (U09465) histone H3.2

[Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445\_ (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi 2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AFO93633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 225173 LIB3166-026-P1-K1-G9 Seq. ID Method BLASTX NCBI GI g4220534 163 BLAST score 2.0e-11 E value 60

Match length 58 % identity

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

225174 Seq. No.

LIB3166-026-P1-K1-H1 Seq. ID

Method BLASTX NCBI GI q4220534 274 BLAST score E value 3.0e-24Match length 122 % identity

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 225175

LIB3166-026-P1-K1-H12 Seq. ID

Method BLASTX NCBI GI g728949 BLAST score 139 E value 1.0e-08 Match length 49 % identity

NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi 99665 pir S25555 blue

copper protein - Arabidopsis thaliana >gi\_2147156\_pir\_\_I39698 blue copper-binding protein -Arabidopsis thaliana >gi 16203 emb CAA78771 (Z15058) blue

copper-binding protein [unidentified bacterium]

>gi 739987 prf 2004275A blue copper-binding protein

[Arabidopsis thaliana]

Seq. No. 225176

BLAST score

E value

157

4.0e-12



```
LIB3166-026-P1-K1-H3
Seq. ID
Method
                  BLASTX
                  g2244898
NCBI GI
                   190
BLAST score
                   2.0e-14
E value
Match length
                   55
                   69
% identity
                  (Z97338) strong similarity to protein phosphatase 2A
NCBI Description
                  regulatory chain, 74K [Arabidopsis thaliana]
                   225177
Seq. No.
                  LIB3166-026-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2459435
BLAST score
                   184
                   1.0e-13
E value
                   83
Match length
                   52
% identity
                  (AC002332) putative serine carboxypeptidase [Arabidopsis
NCBI Description
                  thaliana]
                   225178
Seq. No.
                  LIB3166-026-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3643603
                   516
BLAST score
E value
                   1.0e-52
                   123
Match length
                   77
% identity
NCBI Description
                  (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
                   225179
                  LIB3166-026-P1-K1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3885338
BLAST score
                   204
E value
                   2.0e-16
Match length
                   68
                   50
% identity
                  (AC005623) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   225180
Seq. ID
                   LIB3166-027-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   q3860323
BLAST score
                   322
E value
                   3.0e-30
Match length
                   69
% identity
NCBI Description
                  (AJ012688) hypothetical protein [Cicer arietinum]
Seq. No.
                   225181
Seq. ID
                   LIB3166-027-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   g1263291
```



```
Match length
                   85
                   49
% identity
NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]
Seq. No.
                  225182
                  LIB3166-027-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3928519
BLAST score
                  160
                   5.0e-11
E value
Match length
                   60
% identity
                   50
NCBI Description (AB011670) wpk4 protein kinase [Triticum aestivum]
                   225183
Seq. No.
                  LIB3166-027-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1513180
BLAST score
                   146
E value
                   2.0e-09
                   61
Match length
% identity
                   46
NCBI Description (U65511) stellacyanin [Cucumis sativus]
Seq. No.
                   225184
Seq. ID
                  LIB3166-027-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g2281631
BLAST score
                   280
                   6.0e-25
E value
Match length
                   128
                   54
% identity
NCBI Description
                  (AF003096) AP2 domain containing protein RAP2.3
                   [Arabidopsis thaliana]
Seq. No.
                   225185
Seq. ID
                   LIB3166-027-P1-K1-B1
Method
                  BLASTX
NCBI GI
                   q4567245
BLAST score
                   260
E value
                   1.0e-22
Match length
                   125
                   51
% identity
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
Seq. No.
                   225186
                  LIB3166-027-P1-K1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4164408
BLAST score
                   347
E value
                   6.0e - 33
Match length
                  89
                   73
% identity
NCBI Description (AJ132228) amino acid carrier [Ricinus communis]
```

Seq. No. 225187

Seq. ID LIB3166-027-P1-K1-B3

Match length

% identity

94

64



```
Method
                  BLASTX
NCBI GI
                  g3549679
BLAST score
                  159
E value
                  7.0e-11
Match length
                  41
                  83
% identity
NCBI Description (AL031394) putative protein [Arabidopsis thaliana]
                  225188
Seq. No.
                  LIB3166-027-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1326338
BLAST score
                  168
                  8.0e-12
E value
                  73
Match length
                  49
% identity
NCBI Description (U58746) R05G6.4 gene product [Caenorhabditis elegans]
                  225189
Seq. No.
Seq. ID
                  LIB3166-027-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g3135693
BLAST score
                  170
E value
                  4.0e-12
Match length
                  52
% identity
                  60
NCBI Description (AF064201) glutathione S-transferase [Gossypium hirsutum]
Seq. No.
                  225190
                  LIB3166-027-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2443836
BLAST score
                  180
E value
                  3.0e-13
Match length
                  51
% identity
                  57
NCBI Description (AF020793) tonoplast intrinsic protein homolog MSMCP1
                  [Medicago sativa]
                  225191
Seq. No.
Seq. ID
                  LIB3166-027-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2341034
BLAST score
                  406
E value
                  7.0e-40
Match length
                  83
% identity
                  96
NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]
Seq. No.
                  225192
                  LIB3166-027-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3264767
BLAST score
                  308
E value
                  2.0e-28
```



```
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
  Seq. No.
                     225193
  Seq. ID
                     LIB3166-027-P1-K1-C12
  Method
                     BLASTX
                     g4406771
  NCBI GI
  BLAST score
                     205
  E value
                     3.0e-16
  Match length
                     79
  % identity
                     54
  NCBI Description (AC006836) hypothetical protein [Arabidopsis thaliana]
  Seq. No.
                     225194
                     LIB3166-027-P1-K1-C2
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     q2351580
  BLAST score
                     347
  E value
                     5.0e-44
  Match length
                     120
                     73
  % identity
  NCBI Description
                    (U82433) thymidine diphospho-glucose 4-6-dehydratase
                     homolog [Prunus armeniaca]
                     225195
  Seq. No.
  Seq. ID
                     LIB3166-027-P1-K1-C4
  Method
                     BLASTX
                     g4158232
  NCBI GI
  BLAST score
                     535
  E value
                     7.0e-55
  Match length
                     110
  % identity
                     92
  NCBI Description
                     (Y18626) reversibly glycosylated polypeptide [Triticum
                     aestivum]
  Seq. No.
                     225196
  Seq. ID
                     LIB3166-027-P1-K1-C5
Method
                     BLASTX
  NCBI GI
                     q4235430
  BLAST score
                     470
  E value
                     3.0e-47
  Match length
                     100
  % identity
                     87
  NCBI Description (AF098458) latex-abundant protein [Hevea brasiliensis]
  Seq. No.
                     225197
  Seq. ID
                     LIB3166-027-P1-K1-C6
  Method
                     BLASTX
  NCBI GI
                     g1352821
  BLAST score
                     506
  E value
                     2.0e-51
  Match length
                     97
  % identity
                     98
  NCBI Description
                     RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                     (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                     precursor - upland cotton >gi 450505 emb CAA38026 (X54091)
```

ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No.

Seq. ID Method

NCBI GI

42

225203

BLASTX

g728949

```
225198
 Seq. No.
 Seq. ID
                   LIB3166-027-P1-K1-D10
 Method
                   BLASTX
 NCBI GI
                   q4220527
 BLAST score
                   168
                   6.0e-12
 E value
Match length
                   51
 % identity
                   59
                   (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                   225199
                   LIB3166-027-P1-K1-D11
 Seq. ID
Method
                   BLASTX
 NCBI GI
                   a2827528
 BLAST score
                   424
 E value
                   6.0e-42
Match length
                   103
 % identity
                   78
NCBI Description
                   (AL021633) predicted protein [Arabidopsis thaliana]
                   225200
 Seq. No.
                   LIB3166-027-P1-K1-D2
 Seq. ID
Method
                   BLASTX
 NCBI GI
                   g4455180
 BLAST score
                   276
 E value
                   1.0e-24
"Match length
                   105
 % identity
                   58
 NCBI Description
                   (AL035521) putative protein [Arabidopsis thaliana]
 Seq. No.
                   225201
                   LIB3166-027-P1-K1-E1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q1708924
 BLAST score
                   318
 E value
                    2.0e-29
 Match length
                   86
 % identity
                   71
 NCBI Description
                   MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT
                   MALIC ENZYME) (NADP-ME) >gi_515759 (L34836) malate
                   dehydrogenase (NADP+) [Vitis vinifera]
 Seq. No.
                    225202
 Seq. ID
                   LIB3166-027-P1-K1-E11
 Method
                   BLASTX
 NCBI GI
                   g1001253
 BLAST score
                   124
 E value
                   2.0e-09
 Match length
                   110
```

32037

NCBI Description (D64003) hypothetical protein [Synechocystis sp.]

LIB3166-027-P1-K1-E2



```
BLAST score
                  237
                  5.0e-20
E value
Match length
                  112
                  44
% identity
NCBI Description
                  BLUE COPPER PROTEIN PRECURSOR >gi 99665 pir S25555 blue
                  copper protein - Arabidopsis thaliana
                  >gi_2147156_pir__I39698 blue copper-binding protein -
                  Arabidopsis thaliana >gi_16203_emb_CAA78771_ (Z15058) blue
                  copper-binding protein [unidentified bacterium]
                  >gi_739987_prf__2004275A blue copper-binding protein
                   [Arabidopsis thaliana]
                  225204
Seq. No.
Seq. ID
                  LIB3166-027-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g3158476
BLAST score
                  511
                  4.0e-52
E value
                  116
Match length
% identity
                  84
                  (AF067185) aquaporin 2 [Samanea saman]
NCBI Description
                  225205
Seq. No.
                  LIB3166-027-P1-K1-E4
Seq. ID
Method .
                  BLASTX
NCBI GI
                  g2662343
                  577
BLAST score
E value
                  8.0e-60
                  110
Match length
                  100
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  225206
Seq. No.
                  LIB3166-027-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2369714
BLAST score
                  639
E value
                  4.0e-67
                  122
Match length
% identity
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.
                  225207
                  LIB3166-027-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3434973
BLAST score
                  237
E value
                  4.0e-20
Match length
                  60
                  75
% identity
                  (AB008106) ethylene responsive element binding factor 4
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 225208

Seq. ID LIB3166-027-P1-K1-F11

Method BLASTX NCBI GI g4539423



BLAST score 465 E value 8.0e-47 Match length 107 % identity 81

 ${\tt NCBI \ Description \ (ALO49171) \ pyrophosphate-dependent \ phosphofructo-1-kinase}$ 

[Arabidopsis thaliana]

Seq. No. 225209

Seq. ID LIB3166-027-P1-K1-F5

Method BLASTX
NCBI GI g3912923
BLAST score 152
E value 6.0e-10
Match length 69
% identity 61

NCBI Description (AF001308) hypothetical protein [Arabidopsis thaliana]

Seq. No. 225210

Seq. ID LIB3166-027-P1-K1-F6

Method BLASTX
NCBI GI g125887
BLAST score 182
E value 2.0e-13
Match length 95
% identity 44

NCBI Description ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR

>gi\_82092\_pir\_\_S04765 LAT52 protein precursor - tomato
>gi\_295812\_emb\_CAA33854\_ (X15855) LAT52 [Lycopersicon

esculentum]

Seq. No. 225211

Seq. ID LIB3166-027-P1-K1-G6

Method BLASTX
NCBI GI g3747044
BLAST score 175
E value 1.0e-12
Match length 75
% identity 47

NCBI Description (AF093537) blue copper protein [Zea mays]

Seq. No. 225212

Seq. ID LIB3166-027-P1-K1-G9

Method BLASTX
NCBI GI g3334245
BLAST score 325
E value 2.0e-30
Match length 74
% identity 84

NCBI Description LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)

(ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi\_2909424\_emb\_CAA12028\_ (AJ224520) Glyoxalase I [Cicer

arietinum]

Seq. No. 225213

Seq. ID LIB3166-027-P1-K1-H1

Method BLASTX

E value

Match length

1.0e-40

84



```
NCBI GI
                   q3702368
BLAST score
                   267
E value
                   2.0e-23
Match length
                  86
% identity
                   63
NCBI Description (AJ001855) alpha subunit of F-actin capping protein
                   [Arabidopsis thaliana]
                  225214
Seq. No.
Seq. ID
                  LIB3166-027-P1-K1-H10
Method
                  BLASTX
                  g4388826
NCBI GI
BLAST score
                  238
E value
                  3.0e-20
Match length
                  91
% identity
                  49
NCBI Description (AC006528) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  225215
                  LIB3166-027-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g456568
BLAST score
                  282
E value
                  2.0e-40
Match length
                  90
                  93
% identity
NCBI Description (L29077) ubiquitin conjugating enzyme [Pisum sativum]
Seq. No.
                  225216
Seq. ID
                  LIB3166-027-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g1703380
BLAST score
                  313
E value
                  8.0e-29
Match length
                  87
% identity
                  71
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760)
                  ADP-ribosylation factor [Oryza sativa]
Seq. No.
                  225217
Seq. ID
                  LIB3166-027-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q4090259
BLAST score
                  345
E value
                  2.0e-41
Match length
                  91
% identity
                  78
NCBI Description
                  (AJ131733) ubiquitin-conjugating enzyme E2 [Pseudotsuga
                  menziesii]
Seq. No.
                  225218
Seq. ID
                  LIB3166-028-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g543813
BLAST score
                  413
```

NCBI Description

55



```
% identity
NCBI Description FLORAL HOMEOTIC PROTEIN APETALA1 (AGL7 PROTEIN)
                  >gi 16162 emb CAA78909 (Z16421) AP1 [Arabidopsis thaliana]
Seq. No.
                  225219
Seq. ID
                  LIB3166-028-P1-K1-A12
Method
                  BLASTX
                  g602586
NCBI GI
BLAST score
                  181
E value
                  1.0e-13
Match length
                  99
% identity
                  47
NCBI Description (X83229) 1-amniocyclopropane-1-carboxylate oxidase
                   [Nicotiana tabacum]
Seq. No.
                  225220
                  LIB3166-028-P1-K1-A6
Seq. ID
Method
                  BLASTX
                  g4218535
NCBI GI
BLAST score
                  244
E value
                  5.0e-28
Match length
                  85
% identity
                  66
NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]
Seq. No.
                  225221
Seq. ID
                  LIB3166-028-P1-K1-A9
Method
                  BLASTX
                  g1076746
NCBI GI
BLAST score
                  418
E value
                  2.0e-41
Match length
                  82
                  99
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                  >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                  [Oryza sativa]
Seq. No.
                  225222
Seq. ID
                  LIB3166-028-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  q3250691
BLAST score
                  191
E value
                  1.0e-14
Match length
                  89
% identity
                  47
NCBI Description (AL024486) putative chitinase [Arabidopsis thaliana]
Seq. No.
                  225223
Seq. ID
                  LIB3166-028-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q3551999
BLAST score
                  272
E value
                  4.0e-24
Match length
                  110
```

32041

(AF085081) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_3552001 (AF085082) alcohol dehydrogenase A [Gossypium

NCBI Description



hirsutum] >gi\_4140628 (AF090163) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140630 (AF090164) alcohol dehydrogenase A [Gossypium hirsutum]

225224 Seq. No. Seq. ID LIB3166-028-P1-K1-B2 Method BLASTX NCBI GI g2244955 BLAST score 271 E value 6.0e-24 Match length 114 % identity 44 NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana] Seq. No. 225225 Seq. ID LIB3166-028-P1-K1-B3 Method BLASTX NCBI GI g2809243 BLAST score 210 E value 5.0e-17 Match length 75 % identity NCBI Description (AC002560) F21B7.12 [Arabidopsis thaliana] Seq. No. 225226 Seq. ID LIB3166-028-P1-K1-B4 Method BLASTX NCBI GI g1399380 BLAST score 510 E value 6.0e-52 Match length 102 % identity 90 NCBI Description (U43683) S-adenosyl-L-methionine:delta24-sterol-Cmethyltransferase [Glycine max]. 225227 Seq. No. Seq. ID LIB3166-028-P1-K1-B6 Method BLASTX NCBI GI q3785990 BLAST score 228 E value 6.0e-19 91 Match length % identity NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana] >gi\_4220487 (AC006069) hypothetical protein [Arabidopsis thaliana] 225228 Seq. No. Seq. ID LIB3166-028-P1-K1-B9 Method BLASTX NCBI GI g3193316 BLAST score 184 E value 3.0e-14Match length 48

32042

epimerases [Arabidopsis thaliana]

(AF069299) contains similarity to nucleotide sugar

85

```
225229
Seq. No.
Seq. ID
                  LIB3166-028-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g3461820
BLAST score
                  178
                  5.0e-13
E value
                  93
Match length
% identity
                  46
NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.
                  225230
                  LIB3166-028-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  a585564
BLAST score
                  561
                  6.0e-58
E value
                  122
Match length
                  87
% identity
NCBI Description
                  FERREDOXIN--NITRITE REDUCTASE PRECURSOR
                  >gi_81443_pir__S20495 ferredoxin--nitrite reductase (EC
                  1.7.7.1) precursor - European white birch
                  >gi_17927_emb_CAA42690_ (X60093) ferredoxin--nitrite
                  reductase [Betula pendula]
Seq. No.
                  225231
                  LIB3166-028-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760320
                  146
BLAST score
E value
                  3.0e-09
Match length
                  87
                  43
% identity
NCBI Description (AC002130) F1N21.4 [Arabidopsis thaliana]
Seq. No.
                  225232
Seq. ID
                  LIB3166-028-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g1498053
BLAST score
                  417
E value
                  5.0e-41
Match length
                  104
% identity
                  82
NCBI Description (U64436) ribosomal protein S8 [Zea mays]
Seq. No.
                  225233
Seq. ID
                  LIB3166-028-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g2500115
                  555
BLAST score
E value
                  3.0e-57
Match length
                  124
```

>gi\_529375\_dbj\_BAA07108\_ (D37870) Glutathione Reductase

NCBI Description GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE)

precursor [Spinacia oleracea]



```
Seq. No.
                   225234
Seq. ID
                  LIB3166-028-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g126896
BLAST score
                  450
                  6.0e-45
E value
                  112
Match length
                  79
% identity
                  MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi_319831_pir__DEPUMW malate dehydrogenase (EC 1.1.1.37)
                  precursor, mitochondrial - watermelon
                  >gi 18297 emb CAA35239 (X17362) precursor protein (AA -27
                  to 320) [Citrullus lanatus]
                  225235
Seq. No.
Seq. ID
                  LIB3166-028-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g1871192
BLAST score
                  282
E value
                  3.0e-25
Match length
                  116
% identity
                  56
                  (U90439) Cys3His zinc finger protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  225236
Seq. No.
Seq. ID
                  LIB3166-028-P1-K1-C9
Method
                  BLASTX
                  g2791834
NCBI GI
BLAST score
                  400
                  4.0e-39
E value
Match length
                  93
                  85
% identity
NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta]
                  225237
Seq. No.
Seq. ID
                  LIB3166-028-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g1762945
BLAST score
                  230
E value
                   4.0e-19
Match length
                  58
                  72
% identity
                  (U66269) ORF; able to induce HR-like lesions [Nicotiana
NCBI Description
                  tabacum]
Seq. No.
                  225238
Seq. ID
                  LIB3166-028-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g3212877
BLAST score
                  382
E value
                   6.0e-37
```

Seq. No. 225239

86

Match length

NCBI Description

% identity

(AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. ID

Method



LIB3166-028-P1-K1-D3 Seq. ID Method BLASTX NCBI GI q529707 BLAST score 253 E value 7.0e-22 Match length 110 % identity NCBI Description (U13070) No definition line found [Caenorhabditis elegans] Seq. No. 225240 Seq. ID LIB3166-028-P1-K1-D4 Method BLASTX NCBI GI q1707032 BLAST score 232 E value 2.0e-19 Match length 116 % identity 42 (U80445) coded for by C. elegans cDNA yk13g5.3; coded for NCBI Description by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8 Seq. No. 225241 Seq. ID LIB3166-028-P1-K1-D5 Method BLASTX NCBI GI g3617741 BLAST score 547 E value 2.0e-56 Match length 115 % identity 90 NCBI Description (AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis thaliana] Seq. No. 225242 Seq. ID LIB3166-028-P1-K1-D6 Method BLASTX NCBI GI q3297816 BLAST score 241 E value 2.0e-20 Match length 63 75 % identity NCBI Description (AL031032) putative protein [Arabidopsis thaliana] Seq. No. 225243 Seq. ID LIB3166-028-P1-K1-D9 Method BLASTX NCBI GI g2245066 BLAST score 329 E value 9.0e - 31Match length 118 % identity 54 NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana] Seq. No. 225244

32045

LIB3166-028-P1-K1-E1

BLASTX



```
NCBI GI
                   g1922242
BLAST score
                   186
E value
                   5.0e-14
Match length
                   99
                   44
% identity
NCBI Description (Y10084) hypothetical protein [Arabidopsis thaliana]
                   225245
Seq. No.
Seq. ID
                   LIB3166-028-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   q4220481
BLAST score
                   142
                   8.0e-09
E value
Match length
                   59
% identity
                   56
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
                   225246
Seq. No.
                   LIB3166-028-P1-K1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4101568
BLAST score
                   317
E value
                   2.0e-29
Match length
                   102
% identity
                   60
NCBI Description (AF004816) unknown [Triticum aestivum]
                   225247
Seq. No.
                   LIB3166-028-P1-K1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1621268
BLAST score
                   292
E value
                   2.0e-26
Match length
                   63
% identity
                   89
NCBI Description (Z81012) unknown [Ricinus communis]
Seq. No.
                   225248
                   LIB3166-028-P1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g462013
BLAST score
                   575
E value
                   1.0e-59
Match length
                   125
                   90
% identity
NCBI Description
                   ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
                   >gi_542022_pir__S39558 HSP90 homolog - Madagascar
periwinkle >gi_348696 (L14594) heat shock protein 90
                    [Catharanthus roseus]
Seq. No.
                   225249
```

Seq. ID LIB3166-028-P1-K1-E7

Method BLASTX
NCBI GI g1345698
BLAST score 527
E value 5.0e-54
Match length 105



% identity NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR (CAB-151) (LHCP) >gi\_99601\_pir\_\_S20917 chlorophyll a/b-binding protein - upland cotton >gi\_452314\_emb\_CAA38025 (X54090) chlorophyll ab binding protein [Gossypium hirsutum] Seq. No. 225250 Seq. ID LIB3166-028-P1-K1-F12 Method BLASTX NCBI GI q267073 BLAST score 404 E value 1.0e-39 Match length 78 % identity

NCBI Description TUBULIN BETA-2/BETA-3 CHAIN >gi\_320184\_pir\_\_JQ1587 tubulin beta chain - Arabidopsis thaliana >gi\_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi 166900 (M84701)

beta-3 tubulin [Arabidopsis thaliana]

Seq. No. 225251 Seq. ID LIB3166-028-P1-K1-F2 Method BLASTX NCBI GI q2980801 314

BLAST score E value 5.0e-29 Match length 90 % identity 69

NCBI Description (AL022197) transcriptional activator CBF1 [Arabidopsis

thaliana] >gi\_3660550\_dbj\_BAA33435\_ (AB013816) DREB1B [Arabidopsis thaliana] >gi\_3738226\_dbj\_BAA33792\_ (AB007788)

DREB1B [Arabidopsis thaliana]

225252 Seq. No.

Seq. ID LIB3166-028-P1-K1-F3

Method BLASTX NCBI GI q4454484 BLAST score 284 E value 2.0e-25 Match length 97 % identity

NCBI Description (AC006234) putative diacylglycerol kinase [Arabidopsis

thaliana]

Seq. No. 225253

Seq. ID LIB3166-028-P1-K1-F7

Method BLASTX NCBI GI g2317906 BLAST score 344 2.0e-32 E value Match length 67 % identity 99

NCBI Description (U89959) ARA-5 [Arabidopsis thaliana]

Seq. No. 225254

Seq. ID LIB3166-028-P1-K1-F8

Method BLASTX



NCBI GI g2352492 BLAST score 268 E value 1.0e-23 Match length 61 % identity 75

NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi\_2352494 (AF005048) transport inhibitor

response 1 [Arabidopsis thaliana]

Seq. No. 225255

Seq. ID LIB3166-028-P1-K1-F9

Method BLASTX
NCBI GI g232202
BLAST score 352
E value 2.0e-33
Match length 91
% identity 73

NCBI Description GLUTATHIONE S-TRANSFERASE PARB (CLASS-PHI)

>gi\_285295\_pir\_\_A41789 glutathione transferase (EC
2.5.1.18) - common tobacco >gi\_218294\_dbj\_BAA01394\_
(D10524) glutathione S-transferase [Nicotiana tabacum]

Seq. No. 225256

Seq. ID LIB3166-028-P1-K1-G1

Method BLASTX
NCBI GI g1723536
BLAST score 362
E value 1.0e-34
Match length 117
% identity 58

NCBI Description PROBABLE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 BETA

SUBUNIT (EIF-3 BETA) >gi\_1256531\_emb\_CAA94637\_ (Z70691) eukaryotic translation initiation factor 3 beta subunit

[Schizosaccharomyces pombe]

Seq. No. 225257

Seq. ID LIB3166-028-P1-K1-G10

Method BLASTX
NCBI GI 93402684
BLAST score 418
E value 3.0e-41
Match length 111
% identity 75

NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]

Seq. No. 225258

Seq. ID LIB3166-028-P1-K1-G11

Method BLASTX
NCBI GI 94006891
BLAST score 155
E value 3.0e-10
Match length 38
% identity 76

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 225259

Seq. ID LIB3166-028-P1-K1-G2



```
Method
                  BLASTX
                  g3080418
NCBI GI
                  213
BLAST score
                  4.0e-17
E value
Match length
                  57
                  56
% identity
                  (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
                  225260
Seq. No.
                  LIB3166-028-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3158474
BLAST score
                  286
                  1.0e-25
E value
                  73
Match length
% identity
                  79
NCBI Description (AF067184) aquaporin 1 [Samanea saman]
                  225261
Seq. No.
                  LIB3166-028-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760830
                  603
BLAST score
                  7.0e-63
E valùe
Match length
                  122
% identity
                  93
                  (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                  thaliana]
                  225262
Seq. No.
                  LIB3166-028-P1-K1-G9
Seq. ID
Method
                  BLASTX
                  q3158474
NCBI GI
BLAST score
                  181
                   2.0e-13
E value
Match length
                  70
% identity
NCBI Description (AF067184) aquaporin 1 [Samanea saman]
                   225263
Seq. No.
                  LIB3166-028-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g115764
BLAST score
                   262
E value
                   7.0e-23
Match length
                   93
% identity
                   59
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE I PRECURSOR
                   (CAB-6A) (LIGHT-HARVESTING COMPLEX I 26 KD PROTEIN)
                   >qi 170494 (J03558) chlorophyll a/b binding protein
                   precursor [Lycopersicon esculentum]
```

Seq. No. 225264

Seq. ID LIB3166-028-P1-K1-H11

Method BLASTX
NCBI GI g2459445
BLAST score 279



```
7.0e-25
E value
Match length
                  72
                  36
% identity
                   (AC002332) putative ribonucleoprotein [Arabidopsis
NCBI Description
                  thaliana]
                  225265
Seq. No.
                  LIB3166-028-P1-K1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2459445
BLAST score
                  259
                  1.0e-22
E value
Match length
                  70
                   37
% identity
                  (AC002332) putative ribonucleoprotein [Arabidopsis
NCBI Description
                  thaliana]
                  225266
Seq. No.
                  LIB3166-028-P1-K1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3212877
BLAST score
                   380
                   1.0e-36
E value
                  85
Match length
                   81
% identity
NCBI Description (AC004005) Lea-like protein [Arabidopsis thaliana]
Seq. No.
                   225267
                  LIB3166-028-P1-K1-H5
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2760322
BLAST score
                   449
E value
                   8.0e-45
Match length
                   123
                   65
% identity
NCBI Description (AC002130) F1N21.7 [Arabidopsis thaliana]
                   225268
Seq. No.
                   LIB3166-028-P1-K1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2459445
BLAST score
                   292
E value
                   2.0e-26
Match length
                   76
% identity
                   (AC002332) putative ribonucleoprotein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   225269
                   LIB3166-028-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  *q1737222
BLAST score
                   216
E value
                   5.0e-18
Match length
                   56
                   75
% identity
```

32050

NCBI Description (U79958) BP-80 vacuolar sorting receptor [Pisum sativum]

```
Seq. No.
                   225270
                   LIB3166-029-P1-K1-A12
Seq. ID
Method
                   BLASTX
                   g729668
NCBI GI
BLAST score
                   246
E value
                   4.0e-21
Match length
                   61
                   79
% identity
NCBI Description
                  HISTONE H1 >gi_2147479_pir__S65059 histone H1,
                   drought-inducible - Lycopersicon pennellii >gi 436823
                   (U01890) Solanum pennellii histone H1 [Solanum pennellii]
Seq. No.
                   225271
                  LIB3166-029-P1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                  g3377841
BLAST score
                   273
E value
                   1.0e-24
Match length
                   59
                   90
% identity
                  (AF075598) contains similarity to phosphofructokinases
NCBI Description
                   (Pfam; PFK.hmm, score; 36.60) [Arabidopsis thaliana]
Seq. No.
                   225272
                  LIB3166-029-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1531756
BLAST score
                   182
                   2.0e-13
E value
Match length
                   38
% identity
                   84
NCBI Description (X82413) proline-rich-like protein [Asparagus officinalis]
Seq. No.
                   225273
Seq. ID
                  LIB3166-029-P1-K1-B1
Method
                  BLASTX
NCBI GI
                   g2145358
BLAST score
                   313
E value
                   6.0e-29
Match length
                   108
% identity
                   56
                  (Y10922) HD-Zip protein [Arabidopsis thaliana]
NCBI Description
                   225274
Seq. No.
Seq. ID
                  LIB3166-029-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q2982262
BLAST score
                   327
E value
                   2.0e-30
Match length
                  107
% identity
                   60
```

NCBI Description (AF051214) probable glutathione S-transferase [Picea

mariana]

Seq. No. 225275

Seq. ID LIB3166-029-P1-K1-B4

E value

Match length

8.0e-12

70



```
Method
                  BLASTX
NCBI GI
                  q3047125
                  274
BLAST score
E value
                  2.0e-24
                  105
Match length
                  52
% identity
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.
                  225276
                  LIB3166-029-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  474
E value
                  6.0e-48
Match length
                  89
% identity
                  99
NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
Seq. No.
                  225277
Seq. ID
                  LIB3166-029-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g4530585
BLAST score
                  355
E value
                  8.0e-34
Match length
                  85
% identity
                  74
NCBI Description (AF130978) B12D protein [Ipomoea batatas]
                  225278
Seq. No.
Seq. ID
                  LIB3166-029-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  q466172
BLAST score
                  279
E value
                  5.0e-25
Match length
                  64
% identity
                  83
NCBI Description GTP-BINDING PROTEIN YPTM2 >gi 283056_pir__B38202 ypt family
                  - maize >gi_287835_emb_CAA44919 (X63278) yptm2 [Zea mays]
Seq. No.
                  225279
                  LIB3166-029-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1431629
BLAST score
                  291
E value
                  3.0e-26
Match length
                  82
% identity
                  66
NCBI Description (X99348) pectinacetylesterase precursor [Vigna radiata]
Seq. No.
                  225280
Seq. ID
                  LIB3166-029-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g1840425
BLAST score
                  127
```



```
% identity
NCBI Description (U36586) alcohol dehydrogenase [Vitis vinifera]
                  225281
Seq. No.
                  LIB3166-029-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3080389
BLAST score
                  310
E value
                  1.0e-47
Match length
                  125
% identity
                  81
NCBI Description (AL022603) putative membrane associated protein
                  [Arabidopsis thaliana]
Seq. No.
                  225282
                  LIB3166-029-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3047092
BLAST score
                  216
E value
                  2.0e-17
Match length
                  115
                  49
% identity
NCBI Description (AF058826) No definition line found [Arabidopsis thaliana]
                  225283
Seq. No.
Seq. ID
                  LIB3166-029-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q2661840
BLAST score
                  367
E value
                  3.0e - 35
Match length
                  96
                  70
% identity
NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]
Seq. No.
                  225284
                  LIB3166-029-P1-K1-E5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3297816
BLAST score
                  151
E value
                  9.0e-10
                  46
Match length
% identity
                  70
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
Seq. No.
                  225285
                  LIB3166-029-P1-K1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4056507
                  156
BLAST score
E value
                  2.0e-10
                  47
Match length
% identity
NCBI Description (AC005896) putative RNA binding protein [Arabidopsis
                  thaliana]
```

Seq. No. 225286

Seq. ID LIB3166-029-P1-K1-E8



```
Method
                  BLASTX
NCBI GI
                  g2088651
BLAST score
                  294
E value
                   1.0e-26
Match length
                  112
                   54
% identity
                  (AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  225287
                  LIB3166-029-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1922242
BLAST score
                  144
E value
                   4.0e-09
Match length
                  57
                   58
% identity
NCBI Description (Y10084) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  225288
Seq. ID
                  LIB3166-029-P1-K1-F6
Method
                  BLASTX
NCBI GI
                   q100203
BLAST score
                   302
E value
                   1.0e-27
Match length
                  102
                   62
% identity
NCBI Description
                  cysteine proteinase (EC 3.4.22.-) precursor - tomato
                  >gi 19195 emb CAA78403 (Z14028) pre-pro-cysteine
                  proteinase [Lycopersicon esculentum]
                   225289
Seq. No.
Seq. ID
                  LIB3166-029-P1-K1-F7
Method
                  BLASTX
NCBI GI
                   q833835
BLAST score
                   360
E value
                   1.0e-34
                  81
Match length
% identity
                   74
NCBI Description
                  (U26025) amygdalin hydrolase isoform AH I precursor [Prunus
                   serotina]
                   225290
Seq. No.
Seq. ID
                  LIB3166-029-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g1076746
BLAST score
                  207
E value
                   2.0e-16
                  86
Match length
                   59
% identity
NCBI Description heat shock protein 70 - rice (fragment)
                   >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
```

[Oryza sativa]

Seq. No. 225291

Seq. ID LIB3166-029-P1-K1-G12

Method BLASTX



```
NCBI GI
                   g4544443
BLAST score
                   373
                   5.0e-36
E value
                   115
Match length
                   33
% identity
                   (AC006592) putative mitochondrial uncoupling protein
NCBI Description
                   [Arabidopsis thaliana]
                   225292
Seq. No.
                  LIB3166-029-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g267069
BLAST score
                   501
                  7.0e-51
E value
Match length
                   97
                   96
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >qi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                   225293
Seq. No.
Seq. ID
                   LIB3166-029-P1-K1-G7
Method
                  BLASTX
                   g4006911
NCBI GI
BLAST score
                   302
                   1.0e-28
E value
Match length
                  71
% identity
                   93
NCBI Description
                  (Z99708) trichohyalin like protein [Arabidopsis thaliana]
                   225294
Seq. No.
                  LIB3166-029-P1-K1-G8
Seq. ID
Method
                   BLASTX
```

g136057 NCBI GI BLAST score 295 8.0e-27 E value Match length 85 67 % identity

TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) NCBI Description

>gi 99499 pir A32187 (S)-tetrahydroberberine oxidase -Coptis japonica >gi 556171 (J04121) triosephosphate

isomerase [Coptis japonica]

225295 Seq. No.

LIB3166-029-P1-K1-G9 Seq. ID

Method BLASTX NCBI GI g3877580 BLAST score 177 E value 6.0e-13 108 Match length 42 % identity

NCBI Description (Z67755) F54F7.1 [Caenorhabditis elegans]

225296 Seq. No.

LIB3166-029-P1-K1-H1 Seq. ID

Method BLASTX



```
g2832703
NCBI GI
BLAST score
                   316
E value
                   3.0e-29
Match length
                   97
                  56
% identity
NCBI Description
                  (AL021713) potassium channel protein KAT2 [Arabidopsis
                  thaliana]
                   225297
Seq. No.
                  LIB3166-029-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2347199
BLAST score
                   355
                  9.0e-34
E value
                  105
Match length
                  70
% identity
NCBI Description (AC002338) protein kinase isolog [Arabidopsis thaliana]
                  225298
Seq. No.
                  LIB3166-029-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g228210
BLAST score
                  405
E value
                  1.0e-39
                  101
Match length
                  77
% identity
NCBI Description granule-bound starch synthase [Solanum tuberosum]
                  225299
Seq. No.
Seq. ID
                  LIB3166-030-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g729051
BLAST score
                  247
E value
                   3.0e-21
Match length
                  89
% identity
                  63
NCBI Description CALTRACTIN (CENTRIN) >gi_444342_prf__1906390A
                  caltractin-like protein [Atriplex nummularia]
                  225300
Seq. No.
Seq. ID
                  LIB3166-030-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g1172001
BLAST score
                  439
E value
                   9.0e-44
Match length
                  102
% identity
                  83
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi_541843_pir__JQ2265
                  phenylalanine ammonia-lyase (EC 4.3.1.5) - western balsam
```

poplar x cottonwood >gi\_169454 (L11747) phenylalanine ammonia lyase [Populus trichocarpa x Populus deltoides]

Seq. No. 225301

Seq. ID LIB3166-030-P1-K1-A3

Method BLASTX NCBI GI g3080372 BLAST score 145



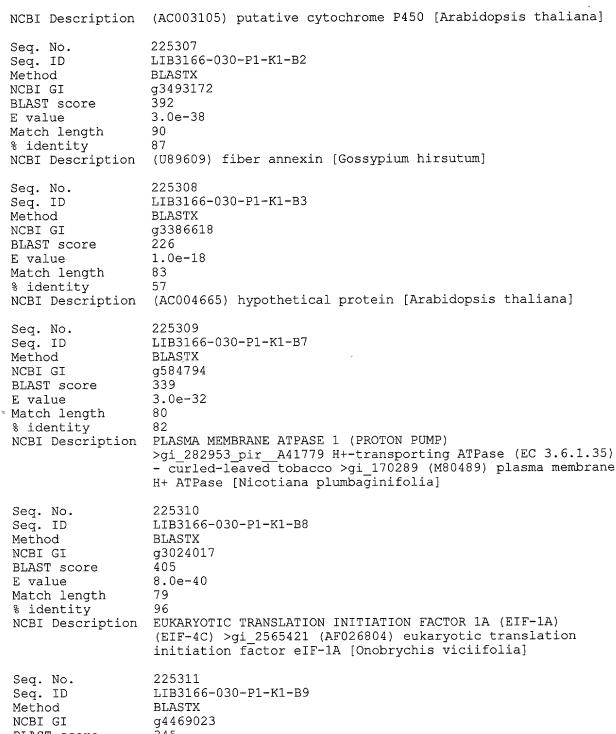
```
3.0e-09
E value
                  93
Match length
% identity
                  41
NCBI Description
                  (AL022580) putative pectinacetylesterase [Arabidopsis
                  thaliana]
                  225302
Seq. No.
                  LIB3166-030-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2661179
                  317
BLAST score
E value
                  2.0e-29
Match length
                  106
                  58
% identity
NCBI Description (U80984) AtZW10 [Arabidopsis thaliana]
                  225303
Seq. No.
Seq. ID
                  LIB3166-030-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g3298443
BLAST score
                  282
                  3.0e-25
E value
                  101
Match length
                  59
% identity
NCBI Description (AB010880) chloroplast ribosomal protein L17 [Nicotiana
                  tabacum]
Seq. No.
                  225304
                  LIB3166-030-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3193316
BLAST score
                  536
E value
                  5.0e-55
Match length
                  115
% identity
                  89
NCBI Description (AF069299) contains similarity to nucleotide sugar
                  epimerases [Arabidopsis thaliana]
                  225305
Seq. No.
                  LIB3166-030-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2218152
                  620
BLAST score
                  7.0e-65
E value
Match length
                  122
% identity
NCBI Description
                  (AF005279) type IIIa membrane protein cp-wap13 [Vigna
                  unguiculata]
                  225306
Seq. No.
```

Seq. ID LIB3166-030-P1-K1-B12

Method BLASTX NCBI GI q2760837 BLAST score 302

E value 1.0e-27 Match length 125 % identity 43





Method BLASTX
NCBI GI 94469023
BLAST score 345
E value 1.0e-32
Match length 109

% identity 72

NCBI Description (AL035602) putative protein [Arabidopsis thaliana]



Seq. No. 225312

Seq. ID LIB3166-030-P1-K1-C11

Method BLASTX
NCBI GI g3559805
BLAST score 449
E value 3.0e-49
Match length 119
% identity 78

NCBI Description (AJ006787) putative phytochelatin synthetase [Arabidopsis

thaliana]

Seq. No. 225313

Seq. ID LIB3166-030-P1-K1-C12

Method BLASTX
NCBI GI g2245108
BLAST score 487
E value 3.0e-49
Match length 118
% identity 73

NCBI Description (Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No. 225314

Seq. ID LIB3166-030-P1-K1-C2

Method BLASTX
NCBI GI g417592
BLAST score 166
E value 4.0e-18
Match length 78
% identity 54

NCBI Description RIBONUCLEIC ACID TRAFFICKING PROTEIN 1 (5'-3'

EXORIBONUCLEASE) (P116) >gi\_83014\_pir\_\_S20126

exoribonuclease RAT1 (EC 3.1.11.-) - yeast (Saccharomyces cerevisiae) >gi\_172365 (M95626) Rat1p [Saccharomyces cerevisiae] >gi\_386005\_bbs\_132577 (S61567) transcription activator=TAP1/RAT1 [Saccharomyces cerevisiae=yeast,

Peptide, 1006 aa] [Saccharomyces cerevisiae] >gi\_1420179\_emb\_CAA99240\_ (Z74956) ORF YOR048c

[Saccharomyces cerevisiae]

Seq. No. 225315

Seq. ID LIB3166-030-P1-K1-C5

Method BLASTX
NCBI GI g3647355
BLAST score 213
E value 4.0e-17
Match length 72
% identity 56

NCBI Description (Z97348) predicted using hexExon; MAL3P1.12 (PFC0150w),

Human hypothetical protein KIAA0249-related protein len: 1160 aa; Similarity to 2 human and an yeast hypothetical gene. Human hypothetical protein KIAA0249 (SW:Y249\_HUMA

Seq. No. 225316

Seq. ID LIB3166-030-P1-K1-C6

Method BLASTX
NCBI GI g3913518
BLAST score 202



```
7.0e-16
E value
Match length
                   60
                   68
% identity
NCBI Description
```

3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE

(3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE) (DPNPASE) >gi\_1103921 (U40433) 3'(2'),5'-bisphosphate

nucleotidase [Arabidopsis thaliana]

225317 Seq. No. LIB3166-030-P1-K1-C7 Seq. ID BLASTX Method NCBI GI q4468992 BLAST score 499 1.0e-50 E value 122 Match length

79 % identity

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

225318 Seq. No. LIB3166-030-P1-K1-D12 Seq. ID Method BLASTX NCBI GI g1621268 BLAST score 375 4.0e-36 E value

Match length 114 69 % identity

NCBI Description (Z81012) unknown [Ricinus communis]

225319 Seq. No.

LIB3166-030-P1-K1-D3 Seq. ID

Method BLASTX NCBI GI g3080389 405 BLAST score 1.0e-39 E value Match length 103 % identity 79

NCBI Description (AL022603) putative membrane associated protein

,[Arabidopsis thaliana]

225320 Seq. No.

Seq. ID LIB3166-030-P1-K1-D4

Method BLASTX NCBI GI g4539301 BLAST score 284 E value 5.0e - 30Match length 127 % identity

(AL049480) putative mitochondrial protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 225321

LIB3166-030-P1-K1-D6 Seq. ID

BLASTX Method NCBI GI g3218467 BLAST score 149 E value 1.0e-09 Match length 100

Match length

% identity

115 88



% identity NCBI Description (AJ006529) putative phosphatase [Gallus gallus] Seq. No. 225322 Seq. ID LIB3166-030-P1-K1-D9 Method BLASTX NCBI GI q3421087 BLAST score 420 E value 2.0e-41 Match length 88 % identity 95 NCBI Description (AF043524) 20S proteasome subunit PAE1 [Arabidopsis thaliana] Seq. No. 225323 Seq. ID LIB3166-030-P1-K1-E10 Method BLASTX NCBI GI q3281851 BLAST score 110 E value 2.0e-11 Match length 55 % identity 64 NCBI Description (AL031004) RNA lariat debranching enzyme - like protein [Arabidopsis thaliana] Seq. No. 225324 Seq. ID LIB3166-030-P1-K1-E5 Method ' BLASTX NCBI GI q121953 BLAST score 170 E value 4.0e-12 Match length 39 % identity 85 NCBI Description HISTONE H1 >gi\_81905\_pir\_\_S00033 histone H1.b - garden pea >gi\_20762\_emb\_CAA29123\_ (X05636) H1 histone (AA 1-263) [Pisum sativum] 225325 Seq. No. Seq. ID LIB3166-030-P1-K1-E7 Method BLASTX NCBI GI g1350680 BLAST score 261 E value 6.0e-23Match length 72 71 % identity NCBI Description 60S RIBOSOMAL PROTEIN L1 Seq. No. 225326 Seq. ID LIB3166-030-P1-K1-F1 Method BLASTX NCBI GI q3860264 BLAST score 560 E value 8.0e-58

32061

NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Method

NCBI GI

BLAST score

BLASTX

396

g4490321



```
Seq. No.
                   225327
                  LIB3166-030-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1220196
BLAST score
                  184
                   1.0e-13
E value
Match length
                  36
                  100
% identity
NCBI Description
                  (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
                  225328
Seq. No.
                  LIB3166-030-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2739365
BLAST score
                  567
E value
                   1.0e-58
                  126
Match length
% identity
                   81
                  (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
                  225329
Seq. No.
                  LIB3166-030-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3695383
BLAST score
                   621
                   6.0e-65
E value
Match length
                  126
% identity
                   89
                  (AF096370) similar to inorganic pyrophosphatase (Pfam:
NCBI Description
                   PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis
                  thaliana]
                   225330
Seq. No.
Seq. ID
                  LIB3166-030-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q3549666
BLAST score
                   199
E value
                   5.0e-16
Match length
                   53
% identity
NCBI Description (AL031394) putative protein [Arabidopsis thaliana]
                   225331
Seq. No.
Seq. ID
                  LIB3166-030-P1-K1-G12
Method
                  BLASTX
NCBI GI
                   q3668089
BLAST score
                   188
E value
                   3.0e-14
Match length
                   91
                   42
% identity
NCBI Description
                  (AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.
                   225332
                  LIB3166-030-P1-K1-G2
Seq. ID
```



```
E value
                   1.0e-38
Match length
                   113
                   71
% identity
NCBI Description
                  (AJ011604) nitrate transporter [Arabidopsis thaliana]
Seq. No.
                  225333
                  LIB3166-030-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4090533
BLAST score
                  457
E value
                   9.0e - 46
Match length
                  99
% identity
                  83
NCBI Description (U68215) ACC oxidase [Carica papaya]
Seq. No.
                  225334
                  LIB3166-030-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1871181
BLAST score
                  159
E value
                  8.0e-11
Match length
                  111
% identity
                  41
NCBI Description
                  (U90439) ring zinc finger protein isolog [Arabidopsis
                  thaliana]
Seq. No.
                  225335
Seq. ID
                  LIB3166-030-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g4512653
BLAST score
                  520
E value
                  4.0e-53
Match length
                  125
% identity
                  82
NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]
Seq. No.
                  225336
Seq. ID
                  LIB3166-030-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q1171642
BLAST score
                  384
E value
                  3.0e-37
Match length
                  103
% identity
                  68
NCBI Description
                  PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK
                  >gi_481206_pir S38326 protein kinase - Arabidopsis
                  thaliana >gi 166809 (L07248) protein kinase [Arabidopsis
                  thaliana]
                  225337
Seq. No.
Seq. ID
                  LIB3166-030-P1-K1-H12
```

Method BLASTX NCBI GI g541847 BLAST score 504 E value 3.0e-51 Match length 105 % identity 87



```
NCBI Description alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana
Seq. No.
                  225338
                  LIB3166-030-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1350981
BLAST score
                  337
E value
                  7.0e-41
                  114
Match length
% identity
                  78
                 40S RIBOSOMAL PROTEIN S3A (S PHASE SPECIFIC PROTEIN BIS289)
NCBI Description
                  >gi 480282_pir__S36622 hypothetical protein - turnip
                  >gi 387909 (L23553) S-phase-specific protein [Brassica
                  rapa] >gi_397401_emb_CAA81030_ (Z25769) putative product
                  [Brassica rapa]
                  225339
Seq. No.
                  LIB3166-031-P1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1710530
BLAST score
                  320
                  9.0e-30
E value
                  74
Match length
                  84
% identity
NCBI Description
                 60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256
                  ribosomal protein L27a - Arabidopsis thaliana
                  >gi 1107487 emb CAA63025_ (X91959) 60S ribosomal protein
                  L27a [Arabidopsis thaliana]
                  225340
Seq. No.
Seq. ID
                  LIB3166-031-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g2443329
                  520
BLAST score
                  4.0e-53
E value
Match length
                  116
% identity
NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]
                  225341
Seq. No.
Seq. ID
                  LIB3166-031-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g2245005
BLAST score
                  198
E value
                  1.0e-15
Match length
                  73
% identity
```

NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 225342

Seq. ID LIB3166-031-P1-K1-B11

Method BLASTX
NCBI GI g4249382
BLAST score 277
E value 4.0e-25
Match length 75
% identity 71



NCBI Description (AC005966) Strong similarity to gi\_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC

gb\_AC004481. [Arabidopsis thaliana]

Seq. No. 225343

Seq. ID LIB3166-031-P1-K1-B12

Method BLASTX
NCBI GI g3873408
BLAST score 148
E value 2.0e-09
Match length 113
% identity 40

NCBI Description (L76926) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 225344

Seq. ID LIB3166-031-P1-K1-B2

Method BLASTX
NCBI GI g2642448
BLAST score 381
E value 8.0e-37
Match length 112
% identity 28

NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana]

>gi 3169187 (AC004401) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 225345

Seq. ID LIB3166-031-P1-K1-B3

Method BLASTX
NCBI GI 94544427
BLAST score 409
E value 4.0e-40
Match length 83
% identity 89

NCBI Description (AC006955) putative ferredoxin-thioredoxin reductase

[Arabidopsis thaliana]

Seq. No. 225346

Seq. ID LIB3166-031-P1-K1-B4

Method BLASTX
NCBI GI g2262159
BLAST score 216
E value 1.0e-17
Match length 79
% identity 53

NCBI Description (AC002329) predicted protein similar to S.pombe protein

C5H10.03 [Arabidopsis thaliana]

Seq. No. 225347

Seq. ID LIB3166-031-P1-K1-B8

Method BLASTX
NCBI GI g3096944
BLAST score 228
E value 4.0e-19
Match length 68
% identity 59



NCBI Description (AL023094) putative protein [Arabidopsis thaliana] Seq. No. 225348 Seq. ID LIB3166-031-P1-K1-C1 BLASTX Method NCBI GI g3641647 BLAST score 408 E value 4.0e-40 103 Match length 72 % identity NCBI Description (AB006804) ACC synthase [Cucumis sativus] Seq. No. 225349 Seq. ID LIB3166-031-P1-K1-C2 Method BLASTX NCBI GI g2462834 BLAST score 146 E value 2.0e-09 50 Match length % identity 56 NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana] Seq. No. 225350 Seq. ID LIB3166-031-P1-K1-C3 Method BLASTX NCBI GI g1621268 BLAST score 483 E value 7.0e-49 111 Match length 79 % identity NCBI Description (Z81012) unknown [Ricinus communis] 225351 Seq. No. Seq. ID LIB3166-031-P1-K1-C5 Method BLASTX NCBI GI g3582328 BLAST score 204 E value 4.0e-16 Match length 85 % identity 47 NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana] Seq. No. 225352 Seq. ID LIB3166-031-P1-K1-C6

Method BLASTX NCBI GI q4559382 BLAST score 222 E value 3.0e-18 Match length 85 % identity 45

NCBI Description (AC006526) putative DNA binding protein [Arabidopsis

thaliana]

Seq. No. 225353

Seq. ID LIB3166-031-P1-K1-D1

Method BLASTX NCBI GI g4335755



BLAST score 188
E value 3.0e-14
Match length 99
% identity 44

NCBI Description (AC006284) putative hydroxyproline-rich glycoprotein

[Arabidopsis thaliana]

Seq. No. 225354

Seq. ID LIB3166-031-P1-K1-D10

Method BLASTX
NCBI GI g477280
BLAST score 244
E value 8.0e-21
Match length 56
% identity 75

NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) 55K

protein precursor - potato >gi\_410633\_bbs\_136740 cytochrome c reductase-processing peptidase subunit I, MPP subunit I, P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,

534 aa]

Seq. No. 225355

Seq. ID LIB3166-031-P1-K1-D11

Method BLASTX
NCBI GI g4538965
BLAST score 240
E value 2.0e-20
Match length 107
% identity 47

NCBI Description (AL049488) hypothetical protein [Arabidopsis thaliana]

Seq. No. 225356

Seq. ID LIB3166-031-P1-K1-D2

Method BLASTX
NCBI GI g4580523
BLAST score 247
E value 1.0e-21
Match length 69

% identity 72

NCBI Description (AF036305) scarecrow-like 8 [Arabidopsis thaliana]

Seq. No. 225357

Seq. ID LIB3166-031-P1-K1-E1

Method BLASTX
NCBI GI g3859598
BLAST score 311
E value 8.0e-52
Match length 125
% identity 83

NCBI Description (AF104919) contains similarity to Myb DNA-binding domains

(Pfam: PF00249, E=3.7e-27 N=3) [Arabidopsis thaliana]

Seq. No. 225358

Seq. ID LIB3166-031-P1-K1-E2

Method BLASTX NCBI GI g3915031 BLAST score 635



E value 1.0e-66 Match length 122 % identity 98 NCBI Description

ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi\_1217628 emb CAA65232

(X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase

[Gossypium hirsutum]

Seq. No. Seq. ID

225359

LIB3166-031-P1-K1-E7

Method BLASTX NCBI GI g4204277 BLAST score 280 3.0e-25 E value Match length 85 % identity 68

NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.

225360

Seq. ID LIB3166-031-P1-K1-E9

Method BLASTX NCBI GI g2194137 BLAST score 338 E value 8.0e-32 Match length 94 % identity 73

NCBI Description (AC002062) ESTs gb R29947, gb H76702 come from this gene.

[Arabidopsis thaliana]

Seq. No.

Seq. ID

LIB3166-031-P1-K1-F10

Method BLASTX NCBI GI g4206765 BLAST score 185 E value 6.0e-14Match length 76

% identity

NCBI Description (AF104329) putative type 1 membrane protein [Arabidopsis

thaliana]

Seq. No.

225362

225361

Seq. ID

LIB3166-031-P1-K1-F3

Method BLASTX NCBI GI g2275202 BLAST score 300 E value 2.0e-27 Match length 109 52 % identity

NCBI Description (AC002337) acyl-CoA synthetase isolog [Arabidopsis

thaliana]

Seq. No.

225363

Seq. ID

LIB3166-031-P1-K1-F4

Method BLASTX NCBI GI g1362008 BLAST score 179 E value 3.0e-13

· Match length

% identity

NCBI Description

115



```
Match length
% identity
                   13
NCBI Description ubiquitin-like protein 12 - Arabidopsis thaliana
                   225364
Seq. No.
Seq. ID
                  LIB3166-031-P1-K1-F7
Method
                  BLASTX
NCBI GI
                   q4006873
BLAST score
                   163
E value
                   3.0e-11
Match length
                   82
                   39
% identity
NCBI Description (Z99707) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  225365
Seq. ID
                  LIB3166-031-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g1076510
BLAST score
                   412
E value
                   2.0e-40
Match length
                  102
% identity
                   76
NCBI Description
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean
                  >gi_829119_emb_CAA52414_ (X74403) cyclophilin [Phaseolus
                  vulgaris]
                   225366
Seq. No.
Seq. ID
                  LIB3166-031-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  q3763916
BLAST score
                  143
E value
                   4.0e-09
Match length
                  84
% identity
                  38
NCBI Description
                  (AC004450) unknown protein [Arabidopsis thaliana]
                  >gi_4531439_gb_AAD22124.1_AC006224 6 (AC006224) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  225367
Seq. ID
                  LIB3166-031-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g3759184
BLAST score
                  328
E value
                  1.0e-30
Match length
                  125
% identity
                  54
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
                  225368
Seq. ID
                  LIB3166-031-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g2760606
BLAST score
                  534
E value
                  8.0e-55
```

32069

(AB001568) phospholipid hydroperoxide glutathione



peroxidase-like protein [Arabidopsis thaliana] >gi\_3004869 (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis thaliana] >gi\_4539451\_emb\_CAB39931.1\_ (AL049500) phospholipid hydroperoxide glutathione peroxidase [Arabidopsis thaliana]

LIB3166-031-P1-K1-G6 Seq. ID Method BLASTX q1694976 NCBI GI BLAST score 453 E value 2.0e-45 103 Match length % identity 84

(Y09482) HMG1 [Arabidopsis thaliana] NCBI Description

>gi\_2832361\_emb\_CAA74402\_ (Y14073) HMG protein [Arabidopsis

thaliana]

225370 Seq. No. Seq. ID

Seq. No.

LIB3166-031-P1-K1-G7

Method BLASTX NCBI GI q4539545 BLAST score [ 446 E value 2.0e-44 90 Match length % identity 97

NCBI Description (Y16644) PRCI [Nicotiana tabacum]

Seq. No. 225371

LIB3166-031-P1-K1-G8 Seq. ID

Method BLASTX NCBI GI g1944216 BLAST score 469 E value 3.0e-47Match length 98 % identity 88

NCBI Description (D84246) alcohol dehydrogenase [Arabidopsis thaliana]

225372 Seq. No.

LIB3166-031-P1-K1-G9 Seq. ID

Method BLASTX NCBI GI g4249385 BLAST score 364 E value 2.0e-37 Match length 81 % identity

NCBI Description (AC005966) T2K10.11 [Arabidopsis thaliana]

225373 Seq. No.

LIB3166-031-P1-K1-H10 Seq. ID

Method BLASTX NCBI GI g3132675 BLAST score 168 E value 2.0e-12 Match length 40 % identity

NCBI Description (AF061740) asparagine synthetase [Elaeagnus umbellata]



Seq. No.

```
Seq. ID
                     LIB3166-031-P1-K1-H12
  Method
                     BLASTX
  NCBI GI
                     g115492
  BLAST score
                     458
  E value
                     7.0e-46
  Match length
                     90
  % identity
                     51
  NCBI Description CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)
                     calmodulin-related protein [Petunia hybrida]
                     225375
  Seq. No.
  Seq. ID
                     LIB3166-031-P1-K1-H3
  Method
                     BLASTX
  NCBI GI
                     q3860249
  BLAST score
                     173
  E value
                     2.0e-12
  Match length
                     66
  % identity
                     58
  NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
  Seq. No.
                     225376
  Seq. ID
                     LIB3166-031-P1-K1-H7
  Method
                     BLASTX
  NCBI GI
                     g3114573
- BLAST score
                     577
  E value
                     8.0e-60°
  Match length
                     123
  % identity
  NCBI Description (AF019383) 1-deoxyxylulose-5-phosphate synthase [Mentha x
                     piperita]
  Seq. No.
                     225377
  Seq. ID
                     LIB3166-031-P1-K1-H8
  Method
                     BLASTX
  NCBI GI
                     q400923
  BLAST score
                     443
  E value
                     4.0e-44
  Match length
                     89
  % identity
                     97
  NCBI Description RAS-RELATED PROTEIN RAB7 >gi_485497_pir__S33531 GTP-binding protein rab - garden pea >gi_20756_emb_CAA46600 (X65650)
                     RAS-related GTP-binding protein [Pisum sativum]
  Seq. No.
                     225378
  Seq. ID
                     LIB3166-032-P1-K1-A1
  Method
                     BLASTX
  NCBI GI
                     q1944216
  BLAST score
                     432
  E value
                     6.0e-43
                     92
  Match length
                     87
  % identity
  NCBI Description (D84246) alcohol dehydrogenase [Arabidopsis thaliana]
  Seq. No.
                     225379
  Seq. ID
                     LIB3166-032-P1-K1-A2
```

Seq. ID

Method

NCBI GI



```
Method
                   BLASTX
NCBI GI
                   g2130149
BLAST score
                   614
E value
                   3.0e-64
Match length
                   120
                   98
% identity
                  translation elongation factor eEF-1 alpha chain - maize
NCBI Description
                   (fragment)
                   225380
Seq. No.
Seq. ID
                   LIB3166-032-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   q2665890
BLAST score
                   182
E value
                   5.0e-14
Match length
                   48
                   77
% identity
                   (AF035944) calcium-dependent protein kinase [Fragaria x
NCBI Description
                   ananassa]
                   225381
Seq. No.
Seq. ID
                   LIB3166-032-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   q231675
BLAST score
                   311
E value
                   1.0e-28
Match length
                   65
                   85
% identity
                   CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi_282955_pir__S23525 cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - common
NCBI Description
                    tobacco >gi 19839_emb CAA44216_ (X62343) cinnamyl-alcohol
                    dehydrogenase [Nicotiana tabacum]
Seq. No.
                    225382
Seq. ID
                   LIB3166-032-P1-K1-C2
Method
                   BLASTX
NCBI GI
                    g3603401
                   351
BLAST score
                    2.0e-33
E value
                   97
Match length
% identity
                    68
NCBI Description (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]
                    225383
Seq. No.
Seq. ID
                   LIB3166-032-P1-K1-D1
Method
                   BLASTX
NCBI GI
                    g3094012
BLAST score
                    426
E value
                    4.0e-42
                   99
Match length
                    77
% identity
NCBI Description (AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]
                    225384
Seq. No.
```

32072

LIB3166-032-P1-K1-D2

BLASTX

g82306



```
BLAST score
                   302
E value
                    1.0e-27
Match length
                   82
% identity
                   63
```

NCBI Description myb protein 305 - garden snapdragon

Seq. No. LIB3166-032-P1-K1-D6 Seq. ID Method BLASTX NCBI GI q417103 BLAST score 453 2.0e-45 E value 94 Match length % identity 96

NCBI Description HISTONE H3.2, MINOR >gi 282871 pir S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563 (U09458) histone H3.2 [Medicago sativa]  $>gi_488567$  ( $\overline{U}09460$ ) histone H3.2 [Medicago sativa] >gi\_488569 ( $\overline{\text{U}}$ 09461) histone H3.2 [Medicago sativa] >gi\_488575 ( $\overline{\text{U}}$ 09464) histone H3.2

[Medicago sativa] >gi\_488577 (U09465) histone H3.2 [Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445\_ (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum]

>gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >qi 3885890 (AF093633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 225386

Seq. ID LIB3166-032-P1-K1-E1

Method BLASTX NCBI GI q3860263 BLAST score 233 E value 1.0e-19 Match length 96 % identity

(AC005824) putative cytochrome p450 protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 225387

Seq. ID LIB3166-032-P1-K1-E2

BLASTX Method NCBI GI g4544403 BLAST score 350 E value 3.0e - 33Match length 103 % identity 68

NCBI Description (AC007047) putative glucan endo-1,3-beta-D-glucosidase

precursor [Arabidopsis thaliana]

Seq. No. 225388



```
LIB3166-032-P1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3493172
BLAST score
                   245
E value
                   3.0e-21
Match length
                   67
                   76
% identity
NCBI Description
                  (U89609) fiber annexin [Gossypium hirsutum]
                   225389
Seq. No.
Seq. ID
                   LIB3166-032-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   q1246823
BLAST score
                   185
E value
                   3.0e-18
                   70
Match length
                   67
% identity
NCBI Description (X89865) unknown [Phoenix dactylifera]
Seq. No.
                   225390
                   LIB3166-032-P1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1346526
BLAST score
                   461
                   3.0e-46
E value
Match length
                   89
                   97
% identity
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
                   ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)
                   >gi_1076533_pir__S52218 methionine adenosyltransferase (EC
                   2.5.1.6) - garden pea >gi_609225_emb_CAA57581_ (X82077) methionine adenosyltransferase [Pisum sativum] >gi_609559
                   (L36681) S-adenosylmethionine synthase [Pisum sativum]
Seq. No.
                   225391
Seq. ID
                   LIB3166-032-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   g4545262
BLAST score
                   215
E value
                   2.0e-17
Match length
                   48
                   85
% identity
                   (AF118230) metallothionein-like protein [Gossypium
NCBI Description
                   hirsutum]
Seq. No.
                   225392
Seq. ID
                   LIB3166-032-P1-K1-F12
                   BLASTX
Method
NCBI GI
                   q1361979
BLAST score
                   267
E value
                   2.0e-23
                   77
Match length
                   70
% identity
NCBI Description serine O-acetyltransferase (EC 2.3.1.30) - watermelon
```

serine acetyltransferase. [Citrullus lanatus]

>gi\_1350550\_dbj\_BAA12843\_ (D85624) serine acetyltransferase
[Citrullus lanatus] >gi\_1841312\_dbj\_BAA08479\_ (D49535)



>gi\_2337772\_dbj\_BAA21827\_ (AB006530) serine
acetyltransferase [Citrullus lanatus]

 Seq. No.
 225393

 Seq. ID
 LIB3166-032-P1-K1-F2

 Method
 BLASTX

 NCBI GI
 g3868857

 BLAST score
 408

E value 5.0e-40 Match length 93 % identity 82

NCBI Description (AB013886) RAV1 [Arabidopsis thaliana]

Seq. No. 225394

Seq. ID LIB3166-032-P1-K1-F7

Method BLASTX
NCBI GI g1168727
BLAST score 250
E value 1.0e-21
Match length 71
% identity 65

NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD)

>gi\_474300\_dbj\_BAA03099\_ (D13991) cinnamyl alcohol
dehydrogenase [Aralia cordata] >gi\_745086\_prf\_\_2015401A
cinnamoyl alcohol dehydrogenase [Aralia cordata]

Seq. No. 225395

Seq. ID LIB3166-032-P1-K1-G10

Method BLASTX
NCBI GI g3123264
BLAST score 411
E value 2.0e-40
Match length 86
% identity 88

NCBI Description 60S RIBOSOMAL PROTEIN L27 >gi\_2244857\_emb\_CAB10279\_ (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 225396

Seq. ID LIB3166-032-P1-K1-G12

Method BLASTX
NCBI GI g2981475
BLAST score 134
E value 2.0e-14
Match length 54
% identity 81

NCBI Description (AF053084) putative cinnamyl alcohol dehydrogenase [Malus

domestica]

Seq. No. 225397

Seq. ID LIB3166-032-P1-K1-G2

Method BLASTX
NCBI GI g3461848
BLAST score 203
E value 5.0e-16
Match length 118
% identity 44

NCBI Description (AC005315) putative ATPase [Arabidopsis thaliana]



NCBI Description ribosomal protein L7 [Solanum tuberosum]

% identity

```
225398
Seq. No.
                  LIB3166-032-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g625547
BLAST score
                  363
E value
                  8.0e-35
Match length
                  108
                  69
% identity
NCBI Description
                  chlorophyll a/b-binding protein type I - common tobacco
                  >gi_493723_emb_CAA45523_ (X64198) photosystem I
                  light-harvesting chlorophyll a/b-binding protein [Nicotiana
                  tabacum]
                  225399
Seq. No.
                  LIB3166-032-P1-K1-H12
Seq. ID
Method
                  BLASTX
                  g134777
NCBI GI
BLAST score
                  240
E value
                  2.0e-20
Match length
                  91
                  51
% identity
                  STAGE V SPORULATION PROTEIN K >gi_98485_pir__S16301 spoVJ
NCBI Description
                  protein - Bacillus subtilis >gi_40197_emb_CAA42049_
                   (X59412) spoVJ [Bacillus subtilis]
                  225400
Seq. No.
                  LIB3166-033-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3850111
BLAST score
                  172
                   2.0e-12
E value
                   78
Match length
% identity
                   46
                  (AL033388) hypothetical integral membrane protein, putative
NCBI Description
                  involvement in lipid metabolism [Schizosaccharomyces pombe]
                   225401
Seq. No.
                  LIB3166-033-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2529680
BLAST score
                   465
E value
                   1.0e-46
Match length
                   117
                   57
% identity
NCBI Description
                   (AC002535) putative protein disulfide-isomerase precursor
                   [Arabidopsis thaliana]
                   225402
Seq. No.
                  LIB3166-033-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g445613
BLAST score
                  147
E value
                   8.0e-10
Match length
                   47
```



```
Seq. No.
                   225403
Seq. ID
                   LIB3166-033-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   q1084321
BLAST score
                   241
E value
                   2.0e-20
Match length
                   68
% identity
                   68
                   protochlorophyllide reductase (EC 1.3.1.33) - cucumber
NCBI Description
                   >gi_2244614_dbj_BAA21089_ (D50085)
                   NADPH-protochlorophyllide oxidoreductase [Cucumis sativus]
                   225404
Seq. No.
Seq. ID
                   LIB3166-033-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   q1220196
BLAST score
                   541
E value
                   1.0e-55
Match length
                   122
                   87
% identity
                  (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
NCBI Description
                   225405
Seq. No.
                   LIB3166-033-P1-K1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244759
BLAST score
                   553
                   5.0e-57
E value
Match length
                   124
% identity
NCBI Description (Z97335) selenium-binding protein [Arabidopsis thaliana]
                   225406
Seq. No.
Seq. ID
                   LIB3166-033-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   q4154352
BLAST score
                   147
E value
                   4.0e-10
Match length
                   83
% identity
                   48
NCBI Description (AF110333) PrMC3 [Pinus radiata]
Seq. No.
                   225407
                   LIB3166-033-P1-K1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g587564
BLAST score
                   254
E value
                   2.0e-22
                   75
Match length
                   72
% identity
NCBI Description
                   (X80235) mitochondrial processing peptidase [Solanum
                   tuberosum]
```

225408

BLASTX

LIB3166-033-P1-K1-C10

Seq. No. Seq. ID

Method



```
q3617770
NCBI GI
BLAST score
                  147
                  1.0e-09
E value
Match length
                  34
                  79
% identity
                  (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
                  225409
Seq. No.
Seq. ID
                  LIB3166-033-P1-K1-C12
                  BLASTX
Method
NCBI GI
                  q4531443
                  484
BLAST score
                  6.0e-49
E value
                  126
Match length
                   75
% identity
                  (ACO06224) putative 50s ribosomal protein L3 [Arabidopsis
NCBI Description
                  thaliana]
                   225410
Seq. No.
Seq. ID
                  LIB3166-033-P1-K1-C2
Method
                  BLASTX
NCBI GI
                   g478673
BLAST score
                   291
E value
                   3.0e-26
                   125
Match length
% identity
                   50
                  proline-rich protein precursor - kidney bean
NCBI Description
                   >gi 21046_emb_CAA42942_ (X60391) proline-rich protein
                   [Phaseolus vulgaris]
Seq. No.
                   225411
                   LIB3166-033-P1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3559805
BLAST score
                   431
E value
                   6.0e-43
Match length
                   90
% identity
                   80
NCBI Description (AJ006787) putative phytochelatin synthetase [Arabidopsis
                   thaliana]
                   225412
Seq. No.
                   LIB3166-033-P1-K1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2781355
BLAST score
                   209
E value
                   1.0e-16
Match length
                   62
                   66
% identity
NCBI Description (AC003113) F2401.11 [Arabidopsis thaliana]
                   225413
Seq. No.
Seq. ID
                   LIB3166-033-P1-K1-D4
                   BLASTX
Method
NCBI GI
                   g4210948
```

534

9.0e-55

BLAST score E value



Match length 101
% identity 99
NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]
Seq. No. 225414
Seq. ID LIB3166-033-P1-K1-E2
Method BLASTX

Method BLASTX
NCBI GI g3249084
BLAST score 338
E value 8.0e-32
Match length 118
% identity 21
NCBI Description (AC004473

NCBI Description (AC004473) Similar to red-1 (related to thioredoxin) gene gb X92750 from Mus musculus. ESTs gb AA712687 and

gb\_Z37223 come from this gene [Arabidopsis thaliana]

Seq. No. 225415

Seq. ID LIB3166-033-P1-K1-E3

Method BLASTX
NCBI GI g2462762
BLAST score 255
E value 5.0e-22
Match length 85
% identity 59

NCBI Description (AC002292) Highly similar to auxin-induced protein

(aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 225416

Seq. ID LIB3166-033-P1-K1-E4

Method BLASTX
NCBI GI g2493318
BLAST score 230
E value 4.0e-19
Match length 88
% identity 50

NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi\_562779\_emb\_CAA80963\_

(Z25471) blue copper protein [Pisum sativum]

>gi 1098264 prf 2115352A blue Cu protein [Pisum sativum]

Seq. No. 225417

Seq. ID LIB3166-033-P1-K1-E6

Method BLASTX
NCBI GI g114339
BLAST score 532
E value 2.0e-54
Match length 128
% identity 84

NCBI Description PLASMA MEMBRANE ATPASE 3 (PROTON PUMP)

>gi\_67974\_pir\_\_PXMUP3 H+-transporting ATPase (EC 3.6.1.35)
type 3, plasma membrane - Arabidopsis thaliana >gi\_166625

(J04737) ATPase [Arabidopsis thaliana]

Seq. No. 225418

Seq. ID LIB3166-033-P1-K1-E7

Method BLASTX NCBI GI g3885515 BLAST score 264



```
1.0e-24
E value
Match length
                  68
                  88
% identity
NCBI Description
                  (AF084202) similar to ribosomal protein S26 [Medicago
                  sativa]
                  225419
Seq. No.
                  LIB3166-033-P1-K1-E8
Seq. ID
Method
                  BLASTX
                  g2499708
NCBI GI
BLAST score
                  143
E value
                  2.0e-09
                  39
Match length
                  77
% identity
NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
                  (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                  >gi 1020409 dbj BAA11135_ (D73410) phospholipase D [Zea
                  mays]
                  225420
Seq. No.
                  LIB3166-033-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2262170
BLAST score
                  391
                  5.0e-38
E value
Match length
                  124
% identity
                   60
                  (AC002329) predicted glycosyl hydrolase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  225421
                  LIB3166-033-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3928862
BLAST score
                   147
E value
                   2.0e-09
Match length
                   113
% identity
                  (AF089710) disease resistance protein RPP8 [Arabidopsis
NCBI Description
                   thaliana]
                   225422
Seq. No.
                   LIB3166-033-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2827714
BLAST score
                   248
E value
                   3.0e-21
Match length
                   114
% identity
                   46
```

NCBI Description (AL021684) receptor protein kinase - like protein

[Arabidopsis thaliana]

Seq. No. 225423

Seq. ID LIB3166-033-P1-K1-F2

Method BLASTX
NCBI GI g3252813
BLAST score 322



```
6.0e-30
E value
Match length
                  73
% identity
                  84
NCBI Description
                  (AC004705) vacuolar sorting receptor-like protein
                  [Arabidopsis thaliana] >gi_3810586 (AC005398) vacuolar
                  sorting receptor-like protein [Arabidopsis thaliana]
                  225424
Seq. No.
                  LIB3166-033-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1730109
BLAST score
                  452
                  4.0e-45
E value
                  108
Match length
                  81
% identity
                  LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN
NCBI Description
                  HYDROXYLASE) >gi 499022 emb_CAA53580_
                                                         (X75966)
                  leucoanthocyanidin dioxygenase [Vitis vinifera]
                  225425
Seq. No.
                  LIB3166-033-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1518540
BLAST score
                  616
E value
                  2.0e-64
Match length
                  128
% identity
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
Seq. No.
                  225426
Seq. ID
                  LIB3166-033-P1-K1-F5
                  BLASTX
Method
NCBI GI
                  g2341032
BLAST score
                  145
E value
                   1.0e-17
Match length
                  107
% identity
                   48
                  (AC000104) EST gb ATTS0956 comes from this gene.
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   225427
                   LIB3166-033-P1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4098128
BLAST score
                   472
E value
                   2.0e-47
Match length
                  96
                   97
% identity
```

NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]

Seq. No. 225428 Seq. ID LIB3166-033-P1-K1-G1

Method BLASTX
NCBI GI g3461817
BLAST score 288
E value 6.0e-26
Match length 65



% identity NCBI Description (AC004138) unknown protein [Arabidopsis thaliana] 225429 Seq. No. LIB3166-033-P1-K1-G2 Seq. ID Method BLASTX g3080398 NCBI GI BLAST score 312 E value 1.0e-28 Match length 123 26 % identity (AL022603) putative protein [Arabidopsis thaliana] NCBI Description 225430 Seq. No. LIB3166-033-P1-K1-G5 Seq. ID Method BLASTX NCBI GI q3860245 BLAST score 360 E value 2.0e-34 Match length 119 % identity 60 (AC005824) putative argonaute protein [Arabidopsis NCBI Description thaliana] Seq. No. 225431 LIB3166-033-P1-K1-G9 Seq. ID Method BLASTX g2392771 NCBI GI 350 BLAST score 3.0e - 33E value Match length 100 71 % identity (AC002534) putative kinesin-like protein [Arabidopsis NCBI Description thaliana] Seq. No. 225432 Seq. ID LIB3166-033-P1-K1-H1 Method BLASTX NCBI GI q1518540 BLAST score 600 E value 2.0e-62 Match length 125 % identity 94 NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max] 225433 Seq. No. Seq. ID LIB3166-033-P1-K1-H12 Method BLASTX NCBI GI g4545262 BLAST score 163 3.0e-11 E value

Match length 43 67 % identity

(AF118230) metallothionein-like protein [Gossypium NCBI Description

hirsutum]

Seq. No. 225434



```
Seq. ID
                  LIB3166-033-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q4218535
BLAST score
                   387
E value
                  2.0e-37
Match length
                  96
                   68
% identity
NCBI Description
                 (AJ010829) GRAB1 protein [Triticum sp.]
                  225435
Seq. No.
Seq. ID
                  LIB3166-033-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q2407800
BLAST score
                  363
E value
                   1.0e-34
Match length
                  98
                   78
% identity
NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
Seq. No.
                  225436
Seq. ID
                  LIB3166-033-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  q4538903
BLAST score
                  264
E value
                   4.0e-23
Match length
                  55
                  87
% identity
NCBI Description (AL049482) putative protein [Arabidopsis thaliana]
Seq. No.
                  225437
                  LIB3166-033-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3763917
BLAST score
                   226
E value
                   9.0e-19
Match length
                   94
% identity
                   49
                  (AC004450) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4531438 gb AAD22123.1 AC006224 5 (AC006224)
                  hypothetical protein [Arabidopsis thaliana]
                   225438
Seq. No.
Seq. ID
                  LIB3166-034-P1-K1-A10
                  BLASTX
Method
NCBI GI
                  g4559342
BLAST score
                   475
E value
                   7.0e-48
                  125
Match length
% identity
                   66
                  (AC007087) putative copper methylamine oxidase [Arabidopsis
NCBI Description
                  thaliana]
                   225439
Seq. No.
Seq. ID
                  LIB3166-034-P1-K1-A12
Method
                  BLASTX
```

g2842744

304

NCBI GI BLAST score



E value 7.0e-28 Match length 70 % identity 79

NCBI Description ENHANCER OF RUDIMENTARY HOMOLOG >gi\_1595812 (U67398)

enhancer of rudimentary homolog ATER [Arabidopsis thaliana]

Seq. No. 225440

Seq. ID LIB3166-034-P1-K1-A2

Method BLASTX
NCBI GI g1170373
BLAST score 537
E value 3.0e-55
Match length 118
% identity 88

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi\_1072473\_pir\_\_S46302

heat shock cognate protein 70-1 - Arabidopsis thaliana >gi\_397482\_emb\_CAA52684\_ (X74604) heat shock protein 70

cognate [Arabidopsis thaliana]

Seq. No. 225441

Seq. ID LIB3166-034-P1-K1-A4

Method BLASTX
NCBI GI g3287693
BLAST score 384
E value 2.0e-37
Match length 87
% identity 82

NCBI Description (AC003979) Similar to LIM17 gene product gb\_1653769 from

the genome of Synechocystis sp. gb D90916. [Arabidopsis

thaliana]

Seq. No. 225442

Seq. ID LIB3166-034-P1-K1-A9

Method BLASTX
NCBI GI g1362093
BLAST score 157
E value 1.0e-10
Match length 37
% identity 81

NCBI Description hypothetical protein (clone TPP15) - tomato (fragment)

>gi 924632 (U20595) unknown [Solanum lycopersicum]

Seq. No. 225443

Seq. ID LIB3166-034-P1-K1-B1

Method BLASTX
NCBI GI g2980795
BLAST score 420
E value 2.0e-41
Match length 89
% identity 89

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 225444

Seq. ID LIB3166-034-P1-K1-B10

Method BLASTX NCBI GI g2809255 BLAST score 279



E value 6.0e-25 Match length 73 . % identity 74

NCBI Description (AC002560) F21B7.24 [Arabidopsis thaliana]

225445 Seq. No.

Seq. ID LIB3166-034-P1-K1-B11

Method BLASTX NCBI GI q1703446 BLAST score 190 1.0e-14 E value Match length 94 45 % identity

L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) NCBI Description

> >gi\_1076292\_pir\_\_S53127 asparaginase - Arabidopsis thaliana >gi\_735918\_emb\_CAA84367\_ (Z34884) asparaginase [Arabidopsis

thaliana]

225446 Seq. No.

Seq. ID LIB3166-034-P1-K1-B12

Method BLASTX NCBI GI q1351272 BLAST score 141 E value 3.0e-09 Match length 28 % identity 89

TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi\_414550 NCBI Description

(U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi\_742408\_prf\_\_2009415A triose phosphate

isomerase [Arabidopsis thaliana]

Seq. No. 225447

Seq. ID LIB3166-034-P1-K1-B4

Method BLASTX NCBI GI g1076515 BLAST score 329 E value 9.0e-31 Match length 129 56 % identity

NCBI Description pectinesterase precursor - kidney bean

>gi 732913 emb CAA59482 (X85216) pectinesterase [Phaseolus

vulgaris]

Seq. No. 225448

Seq. ID LIB3166-034-P1-K1-B5

Method BLASTX NCBI GI g1928981 BLAST score 304 E value 6.0e-28 Match length 91 % identity 68

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

225449 Seq. No.

Seq. ID LIB3166-034-P1-K1-B6

Method BLASTX

NCBI Description



```
NCBI GI
                   q3123271
BLAST score
                   356
                   1.0e-40
E value
Match length
                   98
                   85
% identity
                   40S RIBOSOMAL PROTEIN S6 >gi 2224751 emb CAA74381 (Y14052)
NCBI Description
                   ribosomal protein S6 [Arabidopsis thaliana]
Seq. No.
                   225450
                   LIB3166-034-P1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4539330
                   377
BLAST score
                   2.0e-36
E value
Match length
                   104
% identity
                   68
NCBI Description
                   (AL035679) putative receptor-like protein kinase (fragment)
                   [Arabidopsis thaliana]
                   225451
Seq. No.
                   LIB3166-034-P1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2642448
BLAST score
                   168
E value
                   7.0e-12
Match length
                   122
                   37
% identity
                   (AC002391) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3169187 (AC004401) hypothetical protein [Arabidopsis
                   thaliana]
                   225452
Seq. No.
                   LIB3166-034-P1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1170938
BLAST score
                   507
E value
                   1.0e-51
Match length
                   118
% identity
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
                   ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_481566_pir__S38875 methionine adenosyltransferase (EC
                   2.5.1.6) - tomato >gi 429106 emb CAA80866 (Z24742)
                   S-adenosyl-L-methionine synthetase [Lycopersicon
                   esculentum]
Seq. No.
                   225453
                   LIB3166-034-P1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4263711
BLAST score
                   230
E value
                   3.0e-19
Match length
                   58
% identity
```

[Arabidopsis thaliana]

(AC006223) putative CCR4-associated transcription factor

E value

Match length

6.0e-40

104



```
225454
 Seq. No.
 Seq. ID
                   LIB3166-034-P1-K1-C10
Method
                   BLASTX
 NCBI GI
                   q4262250
                   265
 BLAST score
                   2.0e-23
E value
                   87
Match length
                   69
 % identity
 NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]
 Seq. No.
                   225455
 Seq. ID
                   LIB3166-034-P1-K1-C2
                   BLASTX
 Method
 NCBI GI
                   q1518540
 BLAST score
                   144
                   4.0e-09
 E value
 Match length
                   33
                   82
 % identity
 NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
                   225456
 Seq. No.
                   LIB3166-034-P1-K1-C3
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g4514716
                   178
BLAST score
                   5.0e-13
 E value
                   84
 Match length
                   37
 % identity
 NCBI Description (AB017533) EPc [Nicotiana tabacum]
 Seq. No.
                   225457
 Seq. ID
                   LIB3166-034-P1-K1-C5
 Method
                   BLASTX
 NCBI GI
                   q4426565
 BLAST score
                   211
 E value
                   7.0e-17
 Match length
                   112
 % identity
                    40
 NCBI Description (AF031483) unknown [Rattus norvegicus]
 Seq. No.
                    225458
                   LIB3166-034-P1-K1-C6
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g4490297
 BLAST score
                   147
 E value
                    2.0e-09
                   76
 Match length
 % identity
 NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
                    225459
 Seq. No.
                   LIB3166-034-P1-K1-C7
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g1495804
 BLAST score
                    406
```



```
% identity
                  (X96406) 13-lipoxygenase [Solanum tuberosum]
NCBI Description
                  225460
Seq. No.
                  LIB3166-034-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3676818
BLAST score
                  215
                  2.0e-17
E value
Match length
                  55
                   71
% identity
NCBI Description
                  (AF091514) metallothionein homolog [Elaeagnus umbellata]
Seq. No.
                  225461
                  LIB3166-034-P1-K1-D10
Seq. ID
                  BLASTX
Method
                  g3080437
NCBI GI
BLAST score
                  142
E value
                  1.0e-08
                  50
Match length
                   66
% identity
                  (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
                  225462
Seq. No.
                  LIB3166-034-P1-K1-D11
Seq. IĐ
Method
                  BLASTX
                  g1778376
NCBI GI
BLAST score
                   566
E value
                   2.0e-58
                  130
Match length
                   81
% identity
NCBI Description
                  (U81288) PsRT17-1 [Pisum sativum]
                   225463
Seq. No.
                  LIB3166-034-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1707008
                   319
BLAST score
                   1.0e-29
E value
Match length
                   91
                   73
% identity
NCBI Description
                   (U78721) 30S ribosomal protein S5 isolog [Arabidopsis
                   thaliana]
                   225464
Seq. No.
Seq. ID
                   LIB3166-034-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   q3759184
BLAST score
                   398
E value
                   7.0e-39
Match length
                   116
% identity
NCBI Description
                  (AB018441) phi-1 [Nicotiana tabacum]
```

Seq. No. 225465

Seq. ID LIB3166-034-P1-K1-D7

Method BLASTX

E value

2.0e-67



```
g533084
NCBI GI
                   376
BLAST score
E value
                   2.0e-36
Match length
                   92
                   75
% identity
                  (U07597) delta-9 stearoyl-acyl carrier protein desaturase
NCBI Description
                  precursor [Thunbergia alata]
                   225466
Seq. No.
                   LIB3166-034-P1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1944216
BLAST score
                   410
E value
                   2.0e-40
                   91
Match length
                   86
% identity
                  (D84246) alcohol dehydrogenase [Arabidopsis thaliana]
NCBI Description
                   225467
Seq. No.
                   LIB3166-034-P1-K1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2055374
                   501
BLAST score
E value
                   7.0e-51
Match length
                   127
% identity
                   78
NCBI Description
                  (U29095) serine-threonine protein kinase [Triticum
                   aestivum]
Seq. No.
                   225468
                   LIB3166-034-P1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1709846
BLAST score
                   264
E value
                   4.0e-23
Match length
                   127
% identity
                   43
NCBI Description
                  PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >qi 706853 (U04336)
                   22 kDa component of photosystem II [Lycopersicon
                   esculentum]
Seq. No.
                   225469
Seq. ID
                   LIB3166-034-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   g3493172
BLAST score
                   551
E value
                   8.0e-57
Match length
                   110
                   98
% identity
NCBI Description
                  (U89609) fiber annexin [Gossypium hirsutum]
Seq. No.
                   225470
Seq. ID
                   LIB3166-034-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g1351202
BLAST score
                   643
```



```
Match length
                  129
                  94
% identity
                  TUBULIN BETA CHAIN >gi 312989 emb CAA42777 (X60216)
NCBI Description
                  beta-tubulin [Glycine max]
                  225471
Seq. No.
                  LIB3166-034-P1-K1-E8
Seq. ID
                  BLASTX
Method
                  g3885334
NCBI GI
                  371
BLAST score
                  1.0e-35
E value
Match length
                  125
% identity
                   62
                  (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                  thaliana]
                   225472
Seq. No.
                  LIB3166-034-P1-K1-E9
Seq. ID
                  BLASTX
Method
                   q464849
NCBI GI
                   524
BLAST score
                   1.0e-53
E value
                   99
Match length
                   98
% identity
                 TUBULIN ALPHA CHAIN >gi_486847_pir__$36232 tubulin alpha
NCBI Description
                   chain - almond >gi 20413 emb_CAA47635_ (X67162)
                   alpha-tubulin [Prunus dulcis]
                   225473
Seq. No.
                   LIB3166-034-P1-K1-F1
Seq. ID
                   BLASTX
Method
                   g2160166
NCBI GI
                   170
BLAST score
                   5.0e-12
E value
                   70
Match length
                   50
% identity
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
                   225474
Seq. No.
                   LIB3166-034-P1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3868853
                   240
BLAST score
                   2.0e-20
E value
                   71
Match length
% identity
NCBI Description (AB013853) GPI-anchored protein [Vigna radiata]
                   225475
Seq. No.
Seq. ID
                   LIB3166-034-P1-K1-F7
                   BLASTX
Method
NCBI GI
                   q3286721
BLAST score
                   187 .
                   2.0e-14
E value
                   53
Match length
 % identity
```

NCBI Description (AJ007449) trans-cinnamic 4-monooxygenase [Cicer arietinum]

Seq. ID

Method



```
225476
Seq. No.
Seq. ID
                  LIB3166-034-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g3901012
BLAST score
                  231
                  1.0e-27
E value
Match length
                  97
% identity
                  70
                  (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
NCBI Description
                  sylvatica]
                  225477
Seq. No.
Seq. ID
                  LIB3166-034-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q2507281
BLAST score
                  273
                  2.0e-24
E value
Match length
                  56
% identity
                  93
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_
                   (X97380) atran2 [Arabidopsis thaliana]
                  225478
Seq. No.
                  LIB3166-034-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2194128
BLAST score
                   296
E value
                   7.0e-27
Match length
                  113
% identity
                   54
                  (AC002062) Strong similarity to Arabidopsis receptor-like
NCBI Description
                   kinase (gb_ATLECGENE) and F20P5.15. [Arabidopsis thaliana]
                   225479
Seq. No.
                  LIB3166-034-P1-K1-G3
Seq. ID
Method
                  BLASTX
                   g4557062
NCBI GI
BLAST score
                   256
                   2.0e-22
E value
Match length
                   99
                   58
% identity
NCBI Description (AC007045) hypothetical protein [Arabidopsis thaliana]
                   225480
Seq. No.
Seq. ID
                   LIB3166-034-P1-K1-G4
Method
                  BLASTX
NCBI GI
                   g228210
BLAST score
                   504
E value
                   3.0e-51
Match length
                  117
                   77
% identity
NCBI Description granule-bound starch synthase [Solanum tuberosum]
                   225481
Seq. No.
```

32091

LIB3166-034-P1-K1-G9

BLASTX



g3367534 NCBI GI BLAST score 481 1.0e-48 E value Match length 107 86 % identity (AC004392) Strong similarity to coatamer alpha subunit NCBI Description (HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis thaliana] 225482 Seq. No. LIB3166-034-P1-K1-H1 Seq. ID BLASTX Method q3286691 NCBI GI 367 BLAST score 3.0e-35 E value Match length 94 74 % identity (AJ007450) auxilin-like protein [Arabidopsis thaliana] NCBI Description 225483 Seq. No. LIB3166-034-P1-K1-H10 Seq. ID BLASTX Method NCBI GI g1351271 BLAST score 314 2.0e-29 E value 70 Match length 83 % identity TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) NCBI Description >gi\_1084309\_pir\_\_S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi\_806312 (L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea] 225484 Seq. No. LIB3166-034-P1-K1-H2 Seq. ID BLASTX Method NCBI GI g113461 BLAST score 259 3.0e-26 E value 72 Match length 86 % identity NCBI Description ADP, ATP CARRIER PROTEIN PRECURSOR (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT) >gi\_100423\_pir\_\_S14874 ADP,ATP carrier protein, ACC potato >gi\_21405\_emb\_CAA40782\_ (X57557) adenine nucleotide translocator [Solanum tuberosum] Seq. No. 225485 Seq. ID LIB3166-034-P1-K1-H5 Method BLASTX q3080437 NCBI GI 202 BLAST score

Method BLASTX
NCBI GI g3080437
BLAST score 202
E value 8.0e-16
Match length 50
% identity 84

NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

Method

NCBI GI

BLASTX

g4220474



```
Seq. No.
                  225486
Seq. ID
                  LIB3166-034-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g2864614
BLAST score
                  366
E value
                  4.0e-35
Match length
                  119
                  56
% identity
                 (AL021811) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  225487
                  LIB3166-034-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3063396
BLAST score
                  349
E value
                  2.0e-33
                  77
Match length
% identity
                  86
NCBI Description (AB012947) vcCyP [Vicia faba]
                  225488
Seq. No.
Seq. ID
                  LIB3166-035-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q542125
BLAST score
                  201
E value
                  1.0e-16
Match length
                  52
% identity
                  94
                  translation elongation factor eEF-1 alpha chain - barley
NCBI Description
                  >gi_396134_emb_CAA80666_ (Z23130) protein synthesis
                  elongation factor-1 alpha [Hordeum vulgare]
                  225489
Seq. No.
                  LIB3166-035-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3309243
BLAST score
                  461
E value
                  3.0e-46
                  93
Match length
                   92
% identity
                 (AF073507) aconitase-iron regulated protein 1 [Citrus
NCBI Description
                  limon]
                  225490
Seq. No.
Seq. ID
                  LIB3166-035-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g4567245
BLAST score
                  231
E value
                  2.0e-19
Match length
                  77
                   62
% identity
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
                  225491
Seq. No.
Seq. ID
                  LIB3166-035-P1-K1-A4
```



```
BLAST score
                  208
                  1.0e-16
E value
Match length
                  104
                  54
% identity
                  (AC006069) putative myosin heavy chain [Arabidopsis
NCBI Description
                  thaliana]
                  225492
Seq. No.
                  LIB3166-035-P1-K1-A5
Seq. ID
                  BLASTX
Method
                  g1220196
NCBI GI
BLAST score
                  293
                  4.0e-29
E value
                  80
Match length
                  85
% identity
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
                  225493
Seq. No.
                  LIB3166-035-P1-K1-A6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4262250
                  524
BLAST score
                  1.0e-53
E value
                  105
Match length
                  92
% identity
NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]
                  225494
Seq. No.
                  LIB3166-035-P1-K1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2431769
BLAST score
                  227
                   7.0e-19
E value
                  56
Match length
                   77
% identity
NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]
                  225495
Seq. No.
                  LIB3166-035-P1-K1-B11
Seq. ID
Method
                  BLASTX
                  q421989
NCBI GI
BLAST score
                   292
                   2.0e-26
E value
Match length
                  89
                   60
% identity
                  serpin - barley >gi 19071 emb CAA78822 (Z15116) protein zx
NCBI Description
                   [Hordeum vulgare] >gi_444778_prf_ 1908213A protein Zx
                   [Hordeum vulgare]
                   225496
Seq. No.
                   LIB3166-035-P1-K1-B2
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g3935184
BLAST score 264
E value 4.0e-23
Match length 120
% identity 53



NCBI Description (AC004557) F17L21.27 [Arabidopsis thaliana] Seq. No. 225497 Seq. ID LIB3166-035-P1-K1-B3 Method BLASTX NCBI GI g2213610 BLAST score 167 E value 1.0e-11 Match length 102 20 % identity

NCBI Description (AC000103) F21J9.4 [Arabidopsis thaliana]

225498 Seq. No.

Seq. ID LIB3166-035-P1-K1-B8

Method BLASTX NCBI GI q547683 BLAST score 604 E value 6.0e-63 Match length 126 % identity 94

NCBI Description HEAT SHOCK COGNATE PROTEIN 80 >gi\_170456 (M96549) heat

shock cognate protein 80 [Solanum lycopersicum] >gi\_445601\_prf\_\_1909348A heat shock protein hsp80

[Lycopersicon esculentum]

Seq. No. 225499

Seq. ID LIB3166-035-P1-K1-C12

Method BLASTX NCBI GI g3242723 BLAST score 401 E value 4.0e-39 Match length 125 % identity

NCBI Description (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis

thaliana]

Seq. No. 225500

Seq. ID LIB3166-035-P1-K1-C3

Method BLASTX NCBI GI g4335764 BLAST score 477 E value 4.0e-48 Match length 117 % identity 46

NCBI Description (AC006284) putative WRKY DNA-binding protein [Arabidopsis

thaliana]

225501 Seq. No.

Seq. ID LIB3166-035-P1-K1-C8

Method BLASTX NCBI GI g729442 BLAST score 385 E value 2.0e-37 Match length 105 % identity 73

NCBI Description PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR

>gi 166380 (M80235) glucose-regulated endoplasmic reticular



## protein precursor [Medicago sativa]

```
Seq. No.
                  225502
                  LIB3166-035-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2088651
BLAST score
                  143
E value
                  5.0e-09
Match length
                  50
% identity
                  64
                  (AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
                  [Arabidopsis thaliana]
                  225503
Seq. No.
                  LIB3166-035-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3176965
BLAST score
                  500
E value
                  9.0e-51
Match length
                  122
% identity
                  84
NCBI Description (AF067967) pyrroline-5-carboxylate synthetase
                  [Mesembryanthemum crystallinum]
Seq. No.
                  225504
                  LIB3166-035-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832629
BLAST score
                  143
E value
                  3.0e-10
Match length
                  118
% identity
                  33
NCBI Description (AL021711) 4-coumarate-CoA ligase - like [Arabidopsis
                  thaliana]
                  225505
Seq. No.
                  LIB3166-035-P1-K1-E1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3036840
BLAST score
                  298
E value
                  4.0e-27
                  118
Match length
% identity
                  49
                  (AJ222967) cystinosin [Homo sapiens]
NCBI Description
                  >gi 3036851 emb CAA75882 (Y15924) cystinosin [Homo
                  sapiens]
                  225506
Seq. No.
Seq. ID
                  LIB3166-035-P1-K1-E12
Method
                  BLASTX
                  g586318
NCBI GI
BLAST score
                  153
                  4.0e-10
E value
                  70
Match length
% identity
                  47
NCBI Description HYPOTHETICAL 30.3 KD PROTEIN IN MBA1-RPS13 INTERGENIC
```

REGION >gi\_626233\_pir\_\_S46059 probable membrane protein



YBR187w - yeast (Saccharomyces cerevisiae) >gi\_536548\_emb\_CAA85148\_ (Z36056) ORF YBR187w

[Saccharomyces cerevisiae] >gi\_575915 (U02073) unknown

[Saccharomyces cerevisiae]

Seq. No. 225507

Seq. ID LIB3166-035-P1-K1-E5

Method BLASTX
NCBI GI g4508073
BLAST score 288
E value 5.0e-26
Match length 86
% identity 63

NCBI Description (AC005882) 43220 [Arabidopsis thaliana]

Seq. No. 225508

Seq. ID LIB3166-035-P1-K1-E7

Method BLASTX
NCBI GI g4220481
BLAST score 193
E value 5.0e-15
Match length 89
% identity 44

- NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 225509

Seq. ID LIB3166-035-P1-K1-F11

Method BLASTX
NCBI GI g2896801
BLAST score 151
E value 2.0e-10
Match length 61
% identity 52

NCBI Description (AC004155) ERCC4 MOUSE [Mus musculus]

Seq. No. 225510

Seq. ID LIB3166-035-P1-K1-F12

Method BLASTX
NCBI GI g2558664
BLAST score 200
E value 1.0e-15
Match length 112
% identity 38

NCBI Description (AC002354) hypothetical protein [Arabidopsis thaliana]

Seq. No. 225511

Seq. ID LIB3166-035-P1-K1-F5

Method BLASTX
NCBI GI g1208776
BLAST score 155
E value 8.0e-11
Match length 38
% identity 68

NCBI Description (U48367) alcohol dehydrogenase [Pinus banksiana]

>gi 1208788 (U48373) alcohol dehydrogenase [Pinus

banksiana]

Seq. No.

Seq. ID

225517

LIB3166-035-P1-K1-G9



```
Seq. No.
                  225512
Seq. ID
                  LIB3166-035-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q1174162
BLAST score
                  501
                  6.0e-51
E value
Match length
                  95
                  91
% identity
NCBI Description
                  (U44976) ubiquitin-conjugating enzyme [Arabidopsis
                  thaliana] >gi_3746915 (AF091106) E2
                  ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
Seq. No.
                  225513
Seq. ID
                  LIB3166-035-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q131772
BLAST score
                  536
                  5.0e-55
E value
Match length
                  116
% identity
                  92
NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
                  >gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) -
                  maize
Seq. No.
                  225514
Seq. ID
                  LIB3166-035-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g2275201
BLAST score
                  228
                  5.0e-19
E value
Match length
                  92
                  47
% identity
NCBI Description (AC002337) unknown protein [Arabidopsis thaliana]
Seq. No.
                  225515
Seq. ID
                  LIB3166-035-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  q4572674
BLAST score
                  235
E value
                  5.0e-20
Match length
                  78
% identity
NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]
                  225516
Seq. No.
Seq. ID
                  LIB3166-035-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g2275204
BLAST score
                  296
E value
                  6.0e-27
Match length
                  73
                  70
% identity
NCBI Description
                  (AC002337) DNA binding protein isolog [Arabidopsis
                  thaliana]
```

Match length

NCBI Description

% identity

64

84



```
Method
                   BLASTX
 NCBI GI
                   q99893
 BLAST score
                   456
 E value
                   1.0e-45
 Match length
                   95
                   93
 % identity
 NCBI Description chlorophyll a/b-binding protein 4 - soybean
 Seq. No.
                   225518
 Seq. ID
                   LIB3166-035-P1-K1-H1
 Method
                   BLASTX
 NCBI GI
                   q4218535
 BLAST score
                   220
                   4.0e-18
 E value
 Match length
                   58
 % identity
                   66
 NCBI Description
                  (AJ010829) GRAB1 protein [Triticum sp.]
 Seq. No.
                   225519
 Seq. ID
                   LIB3166-035-P1-K1-H10
 Method
                   BLASTX
 NCBI GI
                   q3552003
 BLAST score
                   496
 E value
                   2.0e-50
 Match length
                   120
 % identity
                   81
 NCBI Description
                   (AF085083) alcohol dehydrogenase A [Gossypium hirsutum]
                   >gi_3552005 (AF085084) alcohol dehydrogenase A [Gossypium
                   hirsutum] >gi_3552007 (AF085085) alcohol dehydrogenase A
                   [Gossypium hirsutum] >gi 4140632 (AF090165) alcohol
                   dehydrogenase A [Gossypium hirsutum] >gi 4140634 (AF090166)
                   alcohol dehydrogenase A [Gossypium hirsutum] >gi_4140636
                   (AF090167) alcohol dehydrogenase A [Gossypium hirsutum]
                   >gi_4140638 (AF090168) alcohol dehydrogenase A [Gossypium
                   hirsutum]
 Seq. No.
                   225520
 Seq. ID
                   LIB3166-035-P1-K1-H2
 Method
                   BLASTX
 NCBI GI
                   q4469026
 BLAST score
                   182
 E value
                   2.0e-17
                   59
 Match length
 % identity
 NCBI Description
                   (AL035602) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   225521
 Seq. ID
                   LIB3166-035-P1-K1-H9
 Method
                   BLASTX
 NCBI GI
                   g3023190
 BLAST score
                   268
 E value
                   7.0e-24
```

14-3-3 protein [Solanum tuberosum]

14-3-3-LIKE PROTEIN 16R >gi 1888459 emb CAA72381 (Y11685)



Seq. No. 225522 Seq. ID

LIB3166-036-P1-K1-A1

Method BLASTX NCBI GI q4220512 BLAST score 279 7.0e-25E value 107 Match length % identity 51

NCBI Description (AL035356) putative pectate lyase [Arabidopsis thaliana]

Seq. No. 225523

LIB3166-036-P1-K1-A10 Seq. ID

BLASTX Method NCBI GI q4538911 BLAST score 432 7.0e-43E value 107 Match length 81 % identity

NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No. 225524

LIB3166-036-P1-K1-A12 Seq. ID

Method BLASTX NCBI GI g586069 155. BLAST score E value 2.0e-10 Match length 58 45 % identity

VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) NCBI Description

>gi\_541424\_pir\_\_S41420 valine--tRNA ligase (EC 6.1.1.9) -

Bacillus subtilis >gi\_452309\_emb\_CAA54458\_ (X77239) valyl-tRNA synthetase [Bacillus subtilis]

>qi 2635274 emb CAB14769 (Z99118) valyl-tRNA synthetase

[Bacillus subtilis]

Seq. No. 225525

LIB3166-036-P1-K1-A2 Seq. ID

Method BLASTX NCBI GI q120673 BLAST score 389 E value 6.0e-38 Match length 95 79 % identity

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description

>gi\_66013\_pir\_\_DEPJG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - garden petunia >gi\_20551\_emb\_CAA42904\_ (X60346) glyceraldehyde 3-phosphate dehydrogenase [Petunia x hybrida]

Seq. No. 225526

Seq. ID LIB3166-036-P1-K1-A4

Method BLASTX NCBI GI g4105772 BLAST score 442 E value 5.0e-44Match length 116 % identity 43



NCBI Description (AF049917) PGP9B [Petunia x hybrida]
Seq. No. 225527
Seq. ID LIB3166-036-P1-K1-A8
Method BLASTX

Method BLASTX
NCBI GI g2760345
BLAST score 539
E value 2.0e-55
Match length 115
% identity 26

NCBI Description (U84967) ubiquitin [Arabidopsis thaliana]

Seq. No. 225528

Seq. ID LIB3166-036-P1-K1-B1

Method BLASTX
NCBI GI g3451078
BLAST score 207
E value 2.0e-16
Match length 112
% identity 38

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 225529

Seq. ID LIB3166-036-P1-K1-B11

Method BLASTX
NCBI GI g3522938
BLAST score 166
E value 1.0e-11
Match length 73
% identity 41

NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]

Seq. No. 225530

Seq. ID LIB3166-036-P1-K1-B3

Method BLASTX
NCBI GI g2507421
BLAST score 283
E value 2.0e-25
Match length 61
% identity 89

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi 1800277 (U81042) translation initiation factor [Arabidopsis thaliana] >gi 4490709 emb CAB38843.1 (AL035680) translation initiation factor [Arabidopsis thaliana]

Seq. No. 225531

Seq. ID LIB3166-036-P1-K1-B8

Method BLASTX
NCBI GI g401322
BLAST score 295
E value 8.0e-27
Match length 64
% identity 92

NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD

SUBUNIT) >gi\_167313 (L03186) vacuolar H+-ATPase catalytic

subunit [Gossypium hirsutum]



```
Seq. No.
                   225532
Seq. ID
                   LIB3166-036-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   g3033400
BLAST score
                   344
E value
                   2.0e-32
Match length
                   119
% identity
                   60
NCBI Description
                   (AC004238) putative Ser/Thr protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   225533
Seq. ID
                   LIB3166-036-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   g4210948
BLAST score
                   307
E value
                   2.0e-28
Match length
                   67
% identity
                   91
NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]
Seq. No.
                   225534
Seq. ID
                  LIB3166-036-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   g1263291
BLAST score
                   448
E value
                   4.0e-47
Match length
                   105
% identity
                   89
NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]
Seq. No.
                   225535
Seq. ID
                  LIB3166-036-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q4115936
BLAST score
                  158
E value
                   9.0e-11
Match length
                  55
% identity
NCBI Description (AF118223) No definition line found [Arabidopsis thaliana]
Seq. No.
                  225536
Seq. ID
                  LIB3166-036-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q266946
BLAST score
                  226
```

E value 8.0e-19 Match length 57 % identity 81

NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN PO (LIGHT-INDUCED 34 KD

PROTEIN) >gi\_71143\_pir\_\_R5UBPO acidic ribosomal protein PO

- red goosefoot >gi 18141\_emb\_CAA33276\_ (X15206) 34kD

light-induced protein [Chenopodium rubrum]

Seq. No. 225537

Seq. ID LIB3166-036-P1-K1-D8

Method BLASTX



```
NCBI GI
                   q3249088
 BLAST score
                   196
 E value
                   3.0e-15
 Match length
                   67
 % identity
                   48
NCBI Description (AC004473) Contains similarity to goliath protein gb_M97204
                   from D. melanogster. [Arabidopsis thaliana]
 Seq. No.
                   225538
 Seq. ID
                   LIB3166-036-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   q4336426
BLAST score
                   164
E value
                   3.0e-12
Match length
                   81
% identity
                   49
NCBI Description (AF090835) Ca2+-dependent protein kinase [Mesembryanthemum
                   crystallinum]
Seq. No.
                   225539
Seq. ID
                   LIB3166-036-P1-K1-E11
Method
                  BLASTX
NCBI GI
                   q416922
BLAST score
                   222
E value
                   3.0e-18
Match length
                   94
% identity
                   52
NCBI Description DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (DUTPASE)
                  (DUTP PYROPHOSPHATASE) (P18) >gi_282947_pir__JQ1599 dUTP
                  pyrophosphatase (EC 3.6.1.23) - tomato
                  >gi_251897_bbs_109276 (S40549) deoxyuridine triphosphatase,
                  dUTPase, P18 (EC 3.6.1.23) [tomatoes, Tint Tim cultivar
                  LA154, Peptide, 169 aa] [Lycopersicon esculentum]
Seq. No.
                  225540
Seq. ID
                  LIB3166-036-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g2853087
BLAST score
                  234
E value
                  5.0e-20
Match length
                  64
% identity
                  75
NCBI Description (AL021768) putative protein [Arabidopsis thaliana]
Seq. No.
                  225541
Seq. ID
                  LIB3166-036-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  q2688824
BLAST score
                  276
E value
                  1.0e-24
Match length
                  70
% identity
                  79
NCBI Description
                 (U93273) putative auxin-repressed protein [Prunus
                  armeniaca]
```

225542 Seq. ID LIB3166-036-P1-K1-E3

Seq. No.

```
Method
                  BLASTX
NCBI GI
                  g3860274
BLAST score
                  144
E value
                  3.0e-09
Match length
                  32
% identity
                  81
NCBI Description
                 (AC005824) unknown protein [Arabidopsis thaliana]
                  >gi_4314397_gb_AAD15607_ (AC006232) putative zinc finger
                  protein [Arabidopsis thaliana]
```

Seq. No. 225543 Seq. ID LIB3166-036-P1-K1-E6

Method BLASTX
NCBI GI g3169182
BLAST score 178
E value 2.0e-13
Match length 69
% identity 42

NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]

Seq. No. 225544 Seq. ID LIB3166-036-P1-K1-F1 Method BLASTX NCBI GI q3142300 BLAST score 162 E value 1.0e-17 Match length 112 % identity 59

NCBI Description (AC002411) Contains similarity to pre-mRNA processing

protein PRP39 gb\_L29224 from S. cerevisiae. ESTs gb\_R64908 and gb\_T88158, gb\_N38703 and gb\_AA651043 come from this

gene. [Arabidopsis thaliana]

Seq. No. 225545

Seq. ID LIB3166-036-P1-K1-F12

Method BLASTX
NCBI GI g1729860
BLAST score 255
E value 4.0e-22
Match length 80
% identity 66
NCBI Description 26S PROT.

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) (MG(2+)-DEPENDENT ATPASE 1)

PROTEIN HOMOLOG 1) (TBP-1) (MG(2+)-DEPENDENT ATPASE 1) (LEMA-1) >gi\_1362099\_pir\_\_S56672 probable 26S proteinase chain MA-1 - tomato >gi\_732815\_emb\_CAA52445 (X74426)

Mg-dependent ATPase 1 [Lycopersicon esculentum]

Seq. No. 225546

Seq. ID LIB3166-036-P1-K1-F2

Method BLASTX
NCBI GI 9462195
BLAST score 351
E value 2.0e-33
Match length 77
% identity 88

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)

>gi\_100682\_pir\_\_S21636 GOS2 protein - rice

E value

Match length

1.0e-08

41

```
>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza sativa]
```

```
Seq. No.
                  225547
                  LIB3166-036-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3901012
BLAST score
                  248
E value
                  8.0e-27
Match length
                  102
% identity
                  68
                  (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
NCBI Description
                  sylvatica]
                  225548
Seq. No.
Seq. ID
                  LIB3166-036-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g485518
BLAST score
                  247
                  1.0e-26
E value
                  80
Match length
                  78
% identity
NCBI Description
                  ubiquitin / ribosomal protein CEP52 - rice
                  >gi_303857_dbj_BAA02154_ (D12629) ubiquitin/ribosomal
                  polyprotein [Oryza sativa]
Seq. No.
                  225549
Seq. ID
                  LIB3166-036-P1-K1-F9
Method
                  BLASTX
                  g3915021
NCBI GI
                  379
BLAST score
                  8.0e-37
E value
                  92
Match length
                  78
% identity
NCBI Description SUCROSE-PHOSPHATE SYNTHASE 1
                  (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1)
                  >gi_2190348_emb_CAA72506_ (Y11821) sucrose-phosphate
                   synthase [Craterostigma plantagineum]
Seq. No.
                  225550
Seq. ID
                  LIB3166-036-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g20729
BLAST score
                  169
E value
                  6.0e-12
Match length
                  55
% identity
NCBI Description (X15190) precursor (AA -68 to 337) [Pisum sativum]
Seq. No.
                  225551
Seq. ID
                  LIB3166-036-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q4544431
BLAST score
                  141
```



% identity NCBI Description (AC006955) hypothetical protein [Arabidopsis thaliana] Seq. No. 225552 Seq. ID LIB3166-036-P1-K1-G12 Method BLASTX NCBI GI g119350 BLAST score 533 E value 1.0e-54 Match length 113 % identity 90 NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi 81608 pir JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi\_16271\_emb\_CAA41114 (X58107) enolase [Arabidopsis thaliana] Seq. No. 225553 Seq. ID LIB3166-036-P1-K1-G3 Method BLASTX NCBI GI g2190548 BLAST score 307 E value 2.0e-28 Match length 72 % identity 78 NCBI Description (AC001229) EST gb ATTS1121 comes from this gene. [Arabidopsis thaliana] Seq. No. 225554 Seq. ID LIB3166-036-P1-K1-G6 Method BLASTX NCBI GI q464981 BLAST score 292 E value 1.0e-26 Match length 70 % identity 80 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum] Seq. No. 225555 Seq. ID LIB3166-036-P1-K1-H10 Method BLASTX NCBI GI g2194142 BLAST score 414 E value 1.0e-40 Match length 122 % identity NCBI Description (AC002062) ESTs gb\_N38288,gb\_T43486,gb\_AA395242 come from this gene. [Arabidopsis thaliana]

Seq. No. 225556

Seq. ID LIB3166-036-P1-K1-H11

Method BLASTX
NCBI GI g2894599
BLAST score 455
E value 2.0e-45

```
Match length
                    95
 % identity
                    81
 NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
 Seq. No.
                    225557
 Seq. ID
                    LIB3166-036-P1-K1-H12
Method
                    BLASTX
NCBI GI
                    q4539460
BLAST score
                    227
E value
                    9.0e-19
Match length
                    122
% identity
NCBI Description (AL049500) putative protein [Arabidopsis thaliana]
Seq. No.
                    225558
Seq. ID
                    LIB3166-036-P1-K1-H5
Method
                    BLASTX
NCBI GI
                    g543905
BLAST score
                    407
E value
                    7.0e-40
Match length
                    102
% identity
                    79
NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162)
                   brassinosteroid-regulated protein [Glycine max]
Seq. No.
                    225559
Seq. ID
                   LIB3166-036-P1-K1-H8
Method
                   BLASTX
NCBI GI
                    g3914666
BLAST score
                    175
E value
                    1.0e-12
Match length
                    61
% identity
                    57
NCBI Description CHLOROPLAST 50S RIBOSOMAL PROTEIN L4 PRECURSOR
                   >gi_2791998_emb_CAA74895_ (Y14566) ribosomal protein L4
[Arabidopsis thaliana] >gi_2792000_emb_CAA74894_ (Y14565)
                   ribosomal protein L4 [Arabidopsis thaliana]
Seq. No.
                   225560
Seq. ID
                   LIB3166-037-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   g1170747
BLAST score
                   194
E value
                   5.0e-15
Match length
                   56
% identity
                   73
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi_167345
                   (M88324) late embryogenesis-abundant protein [\overline{G}ossypium]
                   hirsutum] >gi_167347 (M37697) Lea5-A late
```

Seq. No. 225561

Seq. ID LIB3166-037-P1-K1-A3

Method BLASTX
NCBI GI g4490732
BLAST score 341
E value 2.0e-32

embryogenesis-abundant protein [Gossypium hirsutum]

```
Match length
                      73
   % identity
   NCBI Description
                     (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
                      protein [Arabidopsis thaliana]
   Seq. No.
                      225562
   Seq. ID
                      LIB3166-037-P1-K1-A4
   Method
                      BLASTX
   NCBI GI
                      q464986
   BLAST score
                      286
   E value
                      6.0e-26
  Match length
                      69
   % identity
                      81
   NCBI Description
                     UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
                      LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                     >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana
                      >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                      enzyme homolog [Arabidopsis thaliana] >gi 349211 (L00639)
                      ubiquitin conjugating enzyme [Arabidopsis thaliana]
                      >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating
                      enzyme E2 [Arabidopsis thaliana]
                      >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein
                     ligase UBC9 [Arabidopsis thaliana]
  Seq. No.
                     225563
  Seq. ID
                     LIB3166-037-P1-K1-A5
  Method
                     BLASTX
  NCBI GI
                     g2072356
  BLAST score
                     245
  E value
                     7.0e-21
  Match length
                     62
  % identity
                     74
  NCBI Description (U96713) aminoalcoholphosphotransferase [Brassica rapa]
  Seq. No.
                     225564
  Seq. ID
                     LIB3166-037-P1-K1-A8
  Method
                     BLASTX
  NCBI GI
                     g3128168
  BLAST score
                     361
  E value
                     1.0e-34
  Match length
                     87
  % identity
  NCBI Description
                    (AC004521) putative carboxyl-terminal peptidase
                     [Arabidopsis thaliana]
  Seq. No.
                     225565
  Seq. ID
                     LIB3166-037-P1-K1-B1
  Method
                     BLASTX
  NCBI GI
                     g1174749
  BLAST score
                     547
  E value
                     3.0e-56
  Match length
                     127
% identity
  NCBI Description
                    TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
                     >gi_1362177_pir__S53760 triose-phosphate isomerase (EC
                     5.3.1.1), cytosolic - rye >gi_407525_emb_CAA81487_ (Z26875)
```



225566

triosephosphate isomerase [Secale cereale]
>gi\_1095493\_prf\_\_2109226A triosephosphate isomerase [Secale cereale]

 Seq. ID
 LIB3166-037-P1-K1-B11

 Method
 BLASTX

 NCBI GI
 g3355465

 BLAST score
 432

 E value
 7.0e-43

 Match length
 120

NCBI Description (AC004218) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

68

Seq. No. 225567

Seq. No.

% identity

Seq. ID LIB3166-037-P1-K1-B2

Method BLASTX
NCBI GI g3763930
BLAST score 341
E value 4.0e-32
Match length 98
% identity 63

NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]

Seq. No. 225568

Seq. ID LIB3166-037-P1-K1-B7

Method BLASTX
NCBI GI g3482977
BLAST score 277
E value 1.0e-24
Match length 86
% identity 62

NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

Seq. No. 225569

Seq. ID LIB3166-037-P1-K1-B8

Method BLASTX
NCBI GI g2497543
BLAST score 512
E value 3.0e-52
Match length 115

% identity 85
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 542061 pir \$41379

pyruvate kinase - common tobacco >gi\_444023\_emb\_CAA82628

(Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No. 225570

Seq. ID LIB3166-037-P1-K1-C10

Method BLASTX
NCBI GI 94538963
BLAST score 462
E value 1.0e-50
Match length 110
% identity 71

NCBI Description (AL049488) chlorophyll a/b-binding protein-like

[Arabidopsis thaliana]

NCBI GI

BLAST score

Seq. No.

225571

```
Seq. ID
                    LIB3166-037-P1-K1-C11
 Method
                    BLASTX
 NCBI GI
                    g19184
 BLAST score
                    137
 E value
                    1.0e-08
 Match length
                    64
 % identity
                    50
 NCBI Description (X61287) Type I (26 kD) CP29 polypeptide [Lycopersicon
                    esculentum]
 Seq. No.
                    225572
 Seq. ID
                   LIB3166-037-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   g1174867
BLAST score
                    331
E value
                    6.0e - 31
Match length
                   72
% identity
                   86
NCBI Description
                   UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING
                   PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2
                   KD PROTEIN) >gi_633687_emb_CAA55862_ (X79275)
                   ubiquinol--cytochrome c reductase [Solanum tuberosum] >gi_1094912_prf__2107179A cytochrome c
                   oxidase:SUBUNIT=8.2kD [Solanum tuberosum]
Seq. No.
                   225573
Seq. ID
                   LIB3166-037-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g2833375
BLAST score
                   350
E value
                   3.0e-33
Match length
                   71
% identity
                   90
NCBI Description DNA-DIRECTED RNA POLYMERASE II 8.2 KD POLYPEPTIDE (RPB10)
                   (RP10) (ABC10) >gi_533690 (U12133) RNA polymerase II
                   subunit RPB10 homolog; similar to yeast RNA polymerase II
                   subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica
                   napus]
Seq. No.
                   225574
Seq. ID
                   LIB3166-037-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   q441457
BLAST score
                   551
E value
                   1.0e-56
Match length
                   104
% identity
NCBI Description
                  (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
                   esculentum]
Seq. No.
                   225575
Seq. ID
                   LIB3166-037-P1-K1-C5
Method
                   BLASTX
```

32110

g2088651



E value 7.0e-28 Match length 110 % identity 50

NCBI Description (AF002109) hypersensitivity-related gene 201 isolog

[Arabidopsis thaliana]

Seq. No. 225576

Seq. ID LIB3166-037-P1-K1-C6

Method BLASTX
NCBI GI g3123745
BLAST score 525
E value 1.0e-53
Match length 123
% identity 80

NCBI Description (AB013447) aluminum-induced [Brassica napus]

Seq. No. 225577

Seq. ID LIB3166-037-P1-K1-C7

Method BLASTX
NCBI GI g1076515
BLAST score 212
E value 5.0e-17
Match length 112
% identity 42

NCBI Description pectinesterase precursor - kidney bean

>gi\_732913 emb\_CAA59482 (X85216) pectinesterase [Phaseolus

vulgaris]

Seq. No. 225578

Seq. ID LIB3166-037-P1-K1-C8

Method BLASTX
NCBI GI g421826
BLAST score 138
E value 1.0e-08
Match length 29
% identity 90

NCBI Description chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana

>gi\_298036\_emb\_CAA50712\_ (X71878) CP29 [Arabidopsis

thaliana]

Seq. No. 225579

Seq. ID LIB3166-037-P1-K1-C9

Method BLASTX
NCBI GI g122007
BLAST score 282
E value 3.0e-25
Match length 81
% identity 70

NCBI Description HISTONE H2A >gi\_100161 pir\_ S11498 histone H2A - parsley

>gi\_20448\_emb\_CAA37828 (X53831) H2A histone protein (AA 1

- 149) [Petroselinum crispum]

Seq. No. 225580

Seq. ID LIB3166-037-P1-K1-D1

Method BLASTX
NCBI GI g2511693
BLAST score 334

```
E value
                  3.0e-31
Match length
                  88
% identity
NCBI Description (Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
Seq. No.
                  225581
                  LIB3166-037-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3164222
BLAST score
                  180
E value
                  3.0e-13
Match length
                  44
% identity
NCBI Description (AB008518) RMA1 [Arabidopsis thaliana] >gi_4206205
                  (AF071527) RMA1 RING zinc finger protein [Arabidopsis
                  thaliana]
```

Seq. No. 225582

Seq. ID LIB3166-037-P1-K1-D11

Method BLASTX
NCBI GI g2194142
BLAST score 219
E value 8.0e-18
Match length 67
% identity 58

NCBI Description (AC002062) ESTs gb\_N38288,gb\_T43486,gb\_AA395242 come from

this gene. [Arabidopsis thaliana]

 Seq. No.
 225583

 Seq. ID
 LIB3166-037-P1-K1-D12

 Method
 BLASTX

 NCBI GI
 g4097915

 BLAST score
 164

BLAST score 164
E value 2.0e-11
Match length 116
% identity 34
NCBI Description (U72147)

NCBI Description (U72147) unknown [Anabaena sp. CA]

Seq. No. 225584

Seq. ID LIB3166-037-P1-K1-D2

Method BLASTX
NCBI GI g2262170
BLAST score 194
E value 7.0e-15
Match length 125
% identity 40

NCBI Description (AC002329) predicted glycosyl hydrolase [Arabidopsis

thaliana]

Seq. No. 225585

Seq. ID LIB3166-037-P1-K1-D3

Method BLASTX
NCBI GI g1402877
BLAST score 165
E value 1.0e-11
Match length 75
% identity 57

NCBI Description (X98130) unknown [Arabidopsis thaliana] >gi\_1495257\_emb\_CAA66117\_ (X97485) orf03 [Arabidopsis thaliana] Seq. No. 225586 Seq. ID LIB3166-037-P1-K1-D6 Method BLASTX NCBI GI g4193382 BLAST score 382 E value 5.0e-37 Match length 86 % identity 81 NCBI Description (AF083336) ribosomal protein S27 [Arabidopsis thaliana] >gi 4193384 (AF083337) ribosomal protein S27 [Arabidopsis thaliana] Seq. No. 225587 Seq. ID LIB3166-037-P1-K1-D7 Method BLASTX NCBI GI g289920 BLAST score 348 E value 3.0e-33 Match length 95 % identity 78 NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium hirsutum] Seq. No. 225588 Seq. ID LIB3166-037-P1-K1-D8 BLASTX

Method BLASTX
NCBI GI g4415908
BLAST score 164
E value 2.0e-11
Match length 71
% identity 49

NCBI Description (AC006282) unknown protein [Arabidopsis thaliana]

Seq. No. 225589

Seq. ID LIB3166-037-P1-K1-D9

Method BLASTX
NCBI GI g3924609
BLAST score 310
E value 2.0e-28
Match length 118
% identity 56

NCBI Description (AF069442) putative polyprotein of LTR transposon

[Arabidopsis thaliana]

Seq. No. 225590

Seq. ID LIB3166-037-P1-K1-E1

Method BLASTX
NCBI GI g2506139
BLAST score 395
E value 2.0e-38
Match length 99
% identity 77

NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)

```
(ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa] 225591
```

Seq. ID LIB3166-037-P1-K1-E12
Method BLASTX
NCBI GI g3158376
BLAST score 442
E value 6.0e-44
Match length 120
% identity 75

Seq. No.

NCBI Description (AF035385) unknown [Arabidopsis thaliana]

 Seq. No.
 225592

 Seq. ID
 LIB3166-037-P1-K1-E5

 Method
 BLASTX

 NCBI GI
 g2961385

 BLAST score
 215

 E value
 2.0e-17

E value 2.0
Match length 72
% identity 62

NCBI Description (AL022141) putative protein [Arabidopsis thaliana]

Seq. No. 225593

Seq. ID LIB3166-037-P1-K1-E6

Method BLASTX
NCBI GI g4490736
BLAST score 584
E value 1.0e-60
Match length 125
% identity 50

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 225594

Seq. ID LIB3166-037-P1-K1-E7

Method BLASTX
NCBI GI g167367
BLAST score 237
E value 3.0e-20
Match length 49
% identity 90

NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 225595

Seq. ID LIB3166-037-P1-K1-E9

Method BLASTX
NCBI GI 9726334
BLAST score 602
E value 1.0e-62
Match length 127
% identity 90

NCBI Description (U22533) NADP-malate dehydrogenase [Flaveria trinervia]

Seq. No. 225596

Seq. ID LIB3166-037-P1-K1-F1

Method BLASTX NCBI GI g1172571

E value

Match length

5.0e-23

110



```
BLAST score
                    616
 E value
                    2.0e-64
 Match length
                    126
 % identity
                    91
 NCBI Description
                   PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP)
                   >gi_1076277_pir__S52637 phosphoenolpyruvate carboxykinase
                    (ATP) (EC 4.1.1.49) - cucumber >gi_567102 (L31899)
                   phosphoenolpyruvate carboxykinase [Cucumis sativus]
 Seq. No.
                   225597
 Seq. ID
                   LIB3166-037-P1-K1-F10
 Method
                   BLASTX
 NCBI GI
                   g3688191
 BLAST score
                   204
 E value
                   5.0e-16
Match length
                   91
 % identity
                   51
NCBI Description
                   (AJ010090) MAP3K alpha protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   225598
Seq. ID
                   LIB3166-037-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   q170131
BLAST score
                   253
E value
                   8.0e-22
Match length
                   68
% identity
                   74
NCBI Description (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
Seq. No.
                   225599
Seq. ID
                   LIB3166-037-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   q4218535
BLAST score
                   449
E value
                   9.0e-45
Match length
                   117
% identity
                   67
NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]
Seq. No.
                   225600
Seq. ID
                   LIB3166-037-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   g2739387
BLAST score
                   152
E value
                   6.0e-10
Match length
                   57
% identity
                   47
NCBI Description
                 (AC002505) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   225601
Seq. ID
                  LIB3166-038-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g1906830
BLAST score
                  263
```



% identity 47
NCBI Description (Y11829) heat shock protein [Arabidopsis thaliana]
Seq. No. 225602
Seq. ID LIB3166-038-P1-K1-A11
Method BLASTX
NCBI GI g2494111
BLAST score 403
E value 2.0e-39

% identity 77
NCBI Description (AC002376) Contains similarity to Glycine protein kinase 6
(gb\_M67449). [Arabidopsis thaliana]

Seq. No. 225603

Match length

Seq. ID LIB3166-038-P1-K1-A2

97

Method BLASTX
NCBI GI g730463
BLAST score 294
E value 1.0e-26
Match length 100
% identity 57

NCBI Description 60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)

>gi\_630323\_pir\_\_S44069 ribosomal protein L35a.e.c15 - yeast
(Saccharomyces cerevisiae) >gi\_484241 (L23923) ribosomal

protein L37 [Saccharomyces cerevisiae]

>gi\_1420537\_emb\_CAA99454\_ (Z75142) ORF YOR234c

[Saccharomyces cerevisiae]

Seq. No. 225604

Seq. ID LIB3166-038-P1-K1-A5

Method BLASTX
NCBI GI 94557078
BLAST score 244
E value 9.0e-21
Match length 123
% identity 41

NCBI Description (AC007045) putative Tall-1 pol polyprotein, 5' partial

[Arabidopsis thaliana]

Seq. No. 225605

Seq. ID LIB3166-038-P1-K1-A8

Method BLASTX
NCBI GI g537313
BLAST score 363
E value 1.0e-34
Match length 96
% identity 75

NCBI Description (L36159) unknown protein [Medicago sativa]

Seq. No. 225606

Seq. ID LIB3166-038-P1-K1-B10

Method BLASTX
NCBI GI g3881976
BLAST score 368
E value 3.0e-35
Match length 109



% identity NCBI Description (AJ012409) hypothetical protein [Homo sapiens] Seq. No. 225607 Seq. ID LIB3166-038-P1-K1-B2 Method BLASTX NCBI GI q4406816 BLAST score 562 E value 5.0e-58 Match length 113 % identity 93 NCBI Description (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana] Seq. No. 225608 Seq. ID LIB3166-038-P1-K1-B3 Method BLASTX NCBI GI g2982320 BLAST score 229 E value 5.0e-19 Match length 98 % identity 47 NCBI Description (AF051245) hypothetical protein [Picea mariana] Seq. No. 225609 Seq. ID LIB3166-038-P1-K1-B4 Method BLASTX NCBI GI g100490 BLAST score 589 E value 3.0e-61 Match length 120 % identity 28 NCBI Description polyubiquitin - garden snapdragon (fragment) >gi\_16071\_emb\_CAA48140\_ (X67957) ubiquitin [Antirrhinum majus] Seq. No. 225610 Seq. ID LIB3166-038-P1-K1-B8 Method BLASTX NCBI GI g464986 BLAST score 423 E value 9.0e-42Match length 79 % identity 97 UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN NCBI Description LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi\_421857\_pir\_\_S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi\_297884\_emb\_CAA78714\_ (Z14990) ubiquitin conjugating
enzyme homolog [Arabidopsis thaliana] >gi\_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi\_600391\_emb\_CAA51201\_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi\_4455355\_emb\_CAB36765.1\_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No. 225611

Seq. ID LIB3166-038-P1-K1-B9

```
BLASTX
Method
NCBI GI
                  g2347199
BLAST score
                  514
                  2.0e-52
E value
Match length
                  120
% identity
                  75
NCBI Description (AC002338) protein kinase isolog [Arabidopsis thaliana]
Seq. No.
                  225612
                  LIB3166-038-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2980768
                  298
BLAST score
                  4.0e-27
E value
Match length
                  93
% identity
                  72
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]
                  225613
Seq. No.
                  LIB3166-038-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2459424
BLAST score
                  395
E value
                  2.0e-38
Match length
                  108
% identity
                  71
NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]
Seq. No.
                  225614
Seq. ID
                  LIB3166-038-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g3885515
BLAST score
                  199
E value
                  2.0e-15
Match length
                  54
                  69
% identity
NCBI Description (AF084202) similar to ribosomal protein S26 [Medicago
                  sativa]
                  225615
Seq. No.
Seq. ID
                  LIB3166-038-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q3024020
BLAST score
                  418
E value
                  3.0e-41
Match length
                  89
% identity
                  89
NCBI Description INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)
                  >gi 2225881 dbj BAA20877 (AB004824) eukaryotic initiation
                  factor 5A3 [Solanum tuberosum]
Seq. No.
                  225616
```

Seq. ID LIB3166-038-P1-K1-D1

Method BLASTX NCBI GI q3264767 BLAST score 372 E value 9.0e-36

Match length 74 % identity 92

NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No. 225617

Seq. ID LIB3166-038-P1-K1-D2

Method BLASTX
NCBI GI g3892054
BLAST score 514
E value 2.0e-52
Match length 123
% identity 71

NCBI Description (AC002330) putative glycosyltransferase [Arabidopsis

thaliana]

Seq. No. 225618

Seq. ID LIB3166-038-P1-K1-D4

Method BLASTX
NCBI GI g1173256
BLAST score 540
E value 2.0e-55
Match length 104
% identity 99

NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi\_629496\_pir\_\_S45026 ribosomal

protein S4 - upland cotton >gi\_488739\_emb\_CAA55882\_ (X79300) ribosomal protein, small subunit 4e (RS4e)

[Gossypium hirsutum]

Seq. No. 225619

Seq. ID LIB3166-038-P1-K1-D5

Method BLASTX
NCBI GI g927025
BLAST score 271
E value 6.0e-24
Match length 127
% identity 44

NCBI Description (L44134) SPF1-like DNA-binding protein [Cucumis sativus]

Seq. No. 225620

Seq. ID LIB3166-038-P1-K1-D6

Method BLASTX
NCBI GI g115765
BLAST score 387
E value 2.0e-37
Match length 103
% identity 71

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR

(CAB-7) >gi\_100201\_pir\_\_S07408 chlorophyll a/b-binding protein type II (cab-7) - tomato >gi\_19180\_emb\_CAA32197\_ (X14036) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi\_170431 (M20241) chlorophyll a/b-binding protein [Lycopersicon esculentum] >gi\_226546\_prf\_\_1601518A

chlorophyll a/b binding protein II [Lycopersicon

esculentum]

Seq. No. 225621

Seq. ID LIB3166-038-P1-K1-D7

BLAST score

Match length

E value

146

45

3.0e-09

```
Method
                   BLASTX
 NCBI GI
                   g3123295
 BLAST score
                   194
 E value
                   7.0e-15
Match length
                   114
 % identity
                   38
NCBI Description CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi_2583169
                   (AF026473) calmodulin-related protein [Arabidopsis
                   thaliana]
Seq. No.
                   225622
Seq. ID
                   LIB3166-038-P1-K1-D9
Method
                  BLASTX
NCBI GI
                   g2791834
BLAST score
                  488
E value
                  2.0e-49
Match length
                  111
% identity
                  86
NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta]
Seq. No.
                  225623
Seq. ID
                  LIB3166-038-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g2245108
BLAST score
                  156
E value
                  2.0e-10
Match length
                  46
% identity
                  63
NCBI Description (Z97343) EREBP-4 homolog [Arabidopsis thaliana]
Seq. No.
                  225624
Seq. ID
                  LIB3166-038-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g3608485
BLAST score
                  504
E value
                  3.0e-51
Match length
                  103
% identity
                  92
NCBI Description (AF088915) proteasome beta subunit [Petunia x hybrida]
Seq. No.
                  225625
Seq. ID
                  LIB3166-038-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g3928086
BLAST score
                  198
E value
                  2.0e-15
Match length
                  60
% identity
                  65
NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]
Seq. No.
                  225626
Seq. ID
                  LIB3166-038-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g2388963
```



% identity NCBI Description (Z98979) hypothetical protein [Schizosaccharomyces pombe] Seq. No. 225627 Seq. ID LIB3166-038-P1-K1-E2 Method BLASTX NCBI GI g3869088 BLAST score 566 E value 2.0e-58 Match length 108 % identity 100 NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata] Seq. No. 225628 Seq. ID LIB3166-038-P1-K1-E3 Method BLASTX NCBI GI g3860249 BLAST score 359 E value 3.0e-34 Match length 124 % identity 64 NCBI Description (AC005824) unknown protein [Arabidopsis thaliana] Seg. No. 225629 Seq. ID LIB3166-038-P1-K1-E5 Method BLASTX NCBI GI q4056568 BLAST score 184 E value 7.0e-20 Match length 80 % identity 61 NCBI Description (U90944) PDI-like protein [Zea mays] Seq. No. 225630 Seq. ID LIB3166-038-P1-K1-F11 Method BLASTX NCBI GI g4263519 BLAST score 107 E value 3.0e-10 Match length 73 % identity NCBI Description (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana] Seq. No. 225631 Seq. ID LIB3166-038-P1-K1-F12 Method BLASTX NCBI GI g3024126 BLAST score 487

E value 3.0e-49 Match length 96 % identity 96

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi\_1655576\_emb\_CAA95856\_ (Z71271) S-adenosyl-L-methionine

synthetase 1 [Catharanthus roseus]



```
Seq. No.
                   225632
Seq. ID
                   LIB3166-038-P1-K1-F6
Method
                   BLASTX
NCBI GI
                   g1345698
BLAST score
                   640
E value
                   3.0e-67
Match length
                   126
% identity
                   96
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR
                   (CAB-151) (LHCP) >gi_99601_pir__S20917 chlorophyll a/b-binding protein - upland cotton
                   >gi_452314_emb_CAA38025_ (X54090) chlorophyll ab binding
                   protein [Gossypium hirsutum]
Seq. No.
                   225633
Seq. ID
                   LIB3166-038-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   q465921
BLAST score
                   268
E value
                   1.0e-23
Match length
                   82
% identity
                   65
NCBI Description
                   PROBABLE VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D
                   SUBUNIT) >gi_482192_pir__S40985 hypothetical protein
                   F55H2.2 - Caenorhabditis elegans >gi_3877608_emb_CAA81600_
                   (Z27080) similar to membrane-associated atpase gamma chain;
                   cDNA EST CEMSA49R comes from this gene; cDNA EST yk466a12.5
                   comes from this gene [Caenorhabditis elegans]
Seq. No.
                   225634
Seq. ID
                   LIB3166-038-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   q4006873
BLAST score
                   366
E value
                   4.0e-35
Match length
                   116
% identity
                   60
NCBI Description (Z99707) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   225635
Seq. ID
                   LIB3166-038-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   g3236259
BLAST score
                   248
                   3.0e-30
E value
Match length
                   94
% identity
NCBI Description
                  (AC004684) putative alcohol dehydrogenase [Arabidopsis
                   thaliana]
Seq. No.
                   225636
Seq. ID
                  LIB3166-038-P1-K1-G3
```

Method BLASTX

NCBI GI g3287695
BLAST score 424
E value 8.0e-42
Match length 127

NCBI Description

demissum]

```
% identity
 NCBI Description
                   (AC003979) Similar to hypothetical protein C34B7.2
                    gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis
                   thaliana]
 Seq. No.
                   225637
 Seq. ID
                   LIB3166-038-P1-K1-G5
 Method
                   BLASTX
 NCBI GI
                   g4455246
 BLAST score
                   204
 E value
                   4.0e-16
Match length
                   50
 % identity
                   74
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
Seq. No.
                   225638
Seq. ID
                   LIB3166-038-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g4102861
BLAST score
                   475
                   7.0e-48
E value
Match length
                   95
% identity
                   91
NCBI Description (AF016893) copper/zinc-superoxide dismutase [Populus
                   tremuloides]
Seq. No.
                   225639
Seq. ID
                   LIB3166-038-P1-K1-H11
Method
                   BLASTX
NCBI GI
                   g1332579
BLAST score
                   574
E value
                   2.0e-59
Match length
                   124
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
Seq. No.
                   225640
Seq. ID
                   LIB3166-038-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   g3860263
BLAST score
                   220
E value
                   6.0e-24
Match length
                  114
% identity
                  (AC005824) putative cytochrome p450 protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   225641
Seq. ID
                  LIB3166-038-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g1370589
BLAST score
                  223
E value
                  3.0e-18
Match length
                  98
% identity
```

32123

(X98304) protein induced upon tuberization [Solanum

```
Seq. No.
                       225642
   Seq. ID
                       LIB3166-038-P1-K1-H3
   Method
                       BLASTX
   NCBI GI
                       g2582381
   BLAST score
                       628
   E value
                       1.0e-65
   Match length
                       120
   % identity
                       91
  NCBI Description (AF021220) cation-chloride co-transporter [Nicotiana
                       tabacum]
   Seq. No.
                       225643
   Seq. ID
                      LIB3166-038-P1-K1-H4
  Method
                      BLASTX
  NCBI GI
                      g3641868
  BLAST score
                      127
  E value
                      1.0e-13
                      74
  Match length
  % identity
                      61
  NCBI Description (AJ011012) hypothetical protein [Cicer arietinum]
  Seq. No.
                      225644
  Seq. ID
                      LIB3166-038-P1-K1-H6
  Method
                      BLASTX
  NCBI GI
                      g2275196
  BLAST score
                      554
  E value
                      3.0e-57
  Match length
                      110
  % identity
                      88
  NCBI Description (AC002337) water stress-induced protein, WSI76 isolog
                      [Arabidopsis thaliana]
  Seq. No.
                      225645
  Seq. ID
                      LIB3166-038-P1-K1-H8
  Method
                      BLASTX
  NCBI GI
                      q119194
  BLAST score
                      160
  E value
                      5.0e-15
  Match length
                      61
  % identity
                      72
  NCBI Description ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
                      >gi_81607_pir__S09152 translation elongation factor Tu
                      precursor, chloroplast - Arabidopsis thaliana

>gi_22565_emb_CAA36498_ (X52256) elongation factor Tu

precursor [Arabidopsis thaliana] >gi_226817_prf__1607332A
                      elongation factor Tu [Arabidopsis thaliana]
  Seq. No.
                      225646
  Seq. ID
                      LIB3166-039-P1-K1-A1
  Method
                     BLASTX
  NCBI GI
                     g3033389
- BLAST score
                     248
  E value
                      3.0e-21
 Match length
                     116
  % identity
 NCBI Description (AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
```

```
Seq. No.
                   225647
 Seq. ID
                   LIB3166-039-P1-K1-A10
 Method
                   BLASTX
 NCBI GI
                   g2618698
 BLAST score
                   140
 E value
                   1.0e-08
Match length
                   34
 % identity
                   79
NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]
Seq. No.
                   225648
Seq. ID
                   LIB3166-039-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   g3122071
BLAST score
                   479
E value
                   2.0e-48
Match length
                   97
% identity
                   95
NCBI Description
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                   >gi_2130148_pir__S66339 translation elongation factor eEF-1
                   alpha chain - maize >gi 1321656_dbj_BAA08249 (D45408)
                   alpha subunit of tlanslation elongation factor 1 [Zea mays]
Seq. No.
                   225649
Seq. ID
                   LIB3166-039-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   q1888557
BLAST score
                   596
E value
                   5.0e-62
Match length
                   126
% identity
                   83
NCBI Description (U89841) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase
                   [Lupinus angustifolius]
Seq. No.
                   225650
Seq. ID
                  LIB3166-039-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g1771381
BLAST score
                  324
E value
                   4.0e-30
Match length
                  102
% identity
NCBI Description (X95877) phosphoinositide-specific phospholipase C
                  [Nicotiana rustica]
Seq. No.
                  225651
Seq. ID
                  LIB3166-039-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g133872
BLAST score
                  420
E value
                  2.0e-41
Match length
                  114
% identity
                  77
                  30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)
NCBI Description
                  >gi_282838_pir__S26494 ribosomal protein S1, chloroplast -
                  spinach >gi_322404_pir__A44121 small subunit ribosomal
```

```
protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_(X66135) ribosomal protein S1 [Spinacia oleracea] >gi_170143 (M82923) chloroplast ribosomal protein S1
```

Seq. No. 225652

Seq. ID LIB3166-039-P1-K1-A9

Method BLASTX
NCBI GI g2895510
BLAST score 203
E value 3.0e-16
Match length 81
% identity 48

NCBI Description (AF033204) putative pectin methylesterase [Arabidopsis

thaliana]

Seq. No. 225653

Seq. ID LIB3166-039-P1-K1-B1

Method BLASTX
NCBI GI g3309620
BLAST score 169
E value 6.0e-12
Match length 125
% identity 40

NCBI Description (AF074916) resistance to Pseudomonas syringae protein 5

[Arabidopsis thaliana]

[Spinacia oleracea]

Seq. No. 225654

Seq. ID LIB3166-039-P1-K1-B11

Method BLASTX
NCBI GI g4127688
BLAST score 298
E value 4.0e-27
Match length 84
% identity 68

NCBI Description (AJ006065) isochorismate synthase [Catharanthus roseus]

Seq. No. 225655

Seq. ID LIB3166-039-P1-K1-B2

Method BLASTX
NCBI GI g1621268
BLAST score 370
E value 2.0e-35
Match length 112
% identity 69

NCBI Description (Z81012) unknown [Ricinus communis]

Seq. No. 225656

Seq. ID LIB3166-039-P1-K1-B3

Method BLASTX
NCBI GI g2244847
BLAST score 301
E value 1.0e-27
Match length 97
% identity 65

NCBI Description (Z97337) hydroxyproline-rich glycoprotein homolog

[Arabidopsis thaliana]



Seq. No. 225657 Seq. ID LIB3166-039-P1-K1-B6 Method BLASTX

NCBI GI g2833386 BLAST score 452 E value 4.0e-45 Match length 111 % identity 84

NCBI Description RIBULOSE-PHOSPHATE 3-EPIMERASE PRECURSOR

> (PENTOSE-5-PHOSPHATE 3-EPIMERASE) (PPE) (RPE) (R5P3E) >gi\_2129493\_pir\_\_S62724 ribulose-phosphate 3-epimerase (EC 5.1.3.1) precursor - spinach >gi\_1162980 (L42328) ribulose-5-phosphate 3-epimerase [Spinacia oleracea] >gi\_3264788 (AF070941) ribulose-phosphate 3-epimerase

[Spinacia oleracea] >gi\_1587969\_prf\_\_2207382A D-ribulose-5-phosphate 3-epimerase [Sorghum bicolor]

Seq. No. 225658

Seq. ID LIB3166-039-P1-K1-B7

Method BLASTX NCBI GI g464987 BLAST score 554 E value 4.0e-57 Match length 107 % identity 95

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN

LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)

>gi\_421858\_pir\_\_S32672 ubiquitin--protein ligase (EC
6.3.2.19) UBC10 - Arabidopsis thaliana

>gi\_297878\_emb\_CAA78715 (Z14991) ubiquitin conjugating
enzyme [Arabidopsis thaliana] >gi\_349213 (L00640) ubiquitin

conjugating enzyme [Arabidopsis thaliana]

Seq. No. 225659

Seq. ID LIB3166-039-P1-K1-B9

Method BLASTX NCBI GI g417103 BLAST score 464 E value 1.0e-46 Match length 93 % identity 100

NCBI Description HISTONE H3.2, MINOR >gi\_282871\_pir\_ S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563 (U09458) histone H3.2 [Medicago sativa] >gi 488567 ( $\overline{\text{U}}$ 09460) histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2 [Medicago sativa] >gi\_488577 (U09465) histone H3.2 [Medicago sativa] >gi\_488577 (U09465) histone H3.2 [Medicago sativa] >gi\_510911 emb\_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi\_1435157 emb\_CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AF093633) histone H3 [Oryza sativa]

```
>gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_
```

```
(AL035708) Histon H3 [Arabidopsis thaliana]
Seq. No.
                   225660
Seq. ID
                   LIB3166-039-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g1237250
BLAST score
                   461
E value
                   3.0e-46
Match length
                   109
% identity
                   80
NCBI Description (X96784) cytochrome P450 [Nicotiana tabacum]
Seq. No.
                   225661
Seq. ID
                   LIB3166-039-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   g3687246
BLAST score
                   176
E value
                   8.0e-13
Match length
                   88
% identity
                   38
NCBI Description (AC005169) putative suppressor protein [Arabidopsis
                   thaliana]
Seq. No.
                   225662
Seq. ID
                   LIB3166-039-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g2827139
BLAST score
                   612
E value
                   6.0e-64
Match length
                  127
% identity
                   88
NCBI Description (AF027172) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567)
                  cellulose synthase catalytic subunit (RSW1) [Arabidopsis
                  thaliana]
Seq. No.
                  225663
Seq. ID
                  LIB3166-039-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g4056487
BLAST score
                  397
E value
                  1.0e-38
Match length
                  105
% identity
NCBI Description (AC005896) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  225664
Seq. ID
                  LIB3166-039-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g2088647
BLAST score
                  150
                  9.0e-10
E value
Match length
                  71
```

```
NCBI Description
                    (AF002109) hypothetical protein [Arabidopsis thaliana]
                    >gi_3158394 (AF036340) LRR-containing F-box protein
                    [Arabidopsis thaliana]
 Seq. No.
                    225665
 Seq. ID
                    LIB3166-039-P1-K1-C9
 Method
                    BLASTX
 NCBI GI
                    q1495804
 BLAST score
                    420
 E value
                    2.0e-41
 Match length
                   112
 % identity
                    73
NCBI Description (X96406) 13-lipoxygenase [Solanum tuberosum]
 Seq. No.
                   225666
 Seq. ID
                   LIB3166-039-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   g422418
BLAST score
                   206
E value
                   3.0e-16
Match length
                   98
 % identity
                   42
NCBI Description
                   pol protein - fruit fly (Drosophila ananassae) transposon
                   Tom (fragment) >gi_394705_emb_CAA80824_ (Z24451) pol
                   protein [Drosophila ananassae]
Seq. No.
                   225667
Seq. ID
                   LIB3166-039-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   g4490715
BLAST score
                   187
E value
                   4.0e-14
Match length
                   122
% identity
                   35
NCBI Description (AL035680) putative protein [Arabidopsis thaliana]
Seq. No.
                   225668
                   LIB3166-039-P1-K1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g421843
BLAST score
                   458
E value
                   8.0e-46
Match length
                   126
% identity
NCBI Description
                  protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana
                   >gi_217861_dbj_BAA01715_ (D10909) serine/threonine protein
                   kinase [Arabidopsis thaliana]
Seq. No.
                   225669
Seq. ID
                   LIB3166-039-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   g1161575
BLAST score
                   390
E value
                  7.0e-38
Match length
                  113
% identity
NCBI Description
```

(X94947) homeobox [Lycopersicon esculentum]
32129

```
Seq. No.
                  ~ 225670
Seq. ID
                   LIB3166-039-P1-K1-D8
Method
                   BLASTX
NCBI GI
                    g1781348
BLAST score
                   473
E value
                    1.0e-47
Match length
                    101
% identity
                    90
NCBI Description (Y10380) homologous to plastidic aldolases [Solanum
                    tuberosum]
Seq. No.
                    225671
Seq. ID
                   LIB3166-039-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   g2983447
BLAST score
                   245
E value
                   7.0e-21
Match length
                   123
% identity
                    41
NCBI Description (AE000714) large subunit of isopropylmalate isomerase
                    [Aquifex aeolicus]
Seq. No.
                   225672
Seq. ID
                   LIB3166-039-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g2815246
BLAST score
                   225
E value
                   2.0e-18
Match length
                   55
% identity
                   73
NCBI Description (X95709) class I type 2 metallothionein [Cicer arietinum]
Seq. No.
                   225673
Seq. ID
                   LIB3166-039-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   g3913047
BLAST score
                   494
E value
                   4.0e-50
Match length
                   105
% identity
                   91
NCBI Description FLORAL HOMEOTIC PROTEIN APETALA1 (MADS C)
                   >gi_1076477_pir__S52236 Saap1 protein - white mustard
>gi_609253_emb_CAA57233_ (X81480) Saap1 [Sinapis alba]
Seq. No.
                   225674
Seq. ID
                   LIB3166-039-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   g1781299
BLAST score
                   251
E value
                   1.0e-21
Match length
                   114
% identity
                   46
NCBI Description
                  (Y09506) transformer-SR ribonucleoprotein [Nicotiana
                   tabacum]
Seq. No.
                   225675
```

Method

NCBI GI

BLAST score

BLASTX

564

g1483150

```
LIB3166-039
BLASTX
```

```
Seq. ID
                   LIB3166-039-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   g1944216
BLAST score
                   526
E value
                   8.0e-54
Match length
                   117
% identity
NCBI Description (D84246) alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.
                   225676
Seq. ID
                   LIB3166-039-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   q1771160
BLAST score
                   475
E value
                   7.0e-48
Match length
                   121
% identity
                   75
NCBI Description
                  (X98929) SBT1 [Lycopersicon esculentum]
                   >gi_3687305_emb_CAA06999_ (AJ006378) subtilisin-like
                  protease [Lycopersicon esculentum]
Seq. No.
                   225677
Seq. ID
                  LIB3166-039-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g2213592
BLAST score
                  226
E value
                  1.0e-18
Match length
                  123
% identity
                  51
NCBI Description (AC000348) T7N9.12 [Arabidopsis thaliana]
Seq. No.
                  225678
Seq. ID
                  LIB3166-039-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g2213600
BLAST score
                  465
E value
                  1.0e-46
Match length
                  127
% identity
                  70
NCBI Description (AC000348) T7N9.20 [Arabidopsis thaliana]
Seq. No.
                  225679
Seq. ID
                  LIB3166-039-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g4309698
BLAST score
                  466
E value
                  1.0e-48
Match length
                  113
% identity
                  87
NCBI Description
                 (AC006266) putative glucosyltransferase [Arabidopsis
                  thaliana]
Seq. No.
                  225680
Seq. ID
                  LIB3166-039-P1-K1-F10
```



E value 3.0e-58
Match length 120
% identity 85
NCBI Description (D84417

NCBI Description (D84417) monodehydroascorbate reductase [Arabidopsis

thaliana]

Seq. No.

225681

Seq. ID LIB3166-039-P1-K1-F12

Method BLASTX
NCBI GI g289920
BLAST score 641
E value 3.0e-67
Match length 122
% identity 98

NCBI Description (L07119) chlorophyll A/B binding protein [Gossypium

hirsutum]

Seq. No.

225682

Seq. ID LIB3166-039-P1-K1-F2

Method BLASTX
NCBI GI g4455210
BLAST score 214
E value 3.0e-17
Match length 97
% identity 58
NCBI Description (ALGS: 144

NCBI Description (AL035440) putative aspartate-tRNA ligase [Arabidopsis

thaliana]

Seq. No.

225683

Seq. ID LIB3166-039-P1-K1-F3

Method BLASTX
NCBI GI g2833388
BLAST score 528
E value 4.0e-54
Match length 126
% identity 79

NCBI Description GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR

>gi\_629660\_pir\_\_S43341 ADPglucose--starch

glucosyltransferase (EC 2.4.1.21) precursor - cassava >gi\_437042 emb\_CAA52273 (X74160) starch (bacterial

glycogen) synthase [Manihot esculenta]

Seq. No. 225684

Seq. ID LIB3166-039-P1-K1-F4

Method BLASTX
NCBI GI g2388689
BLAST score 458
E value 7.0e-46
Match length 128
% identity 70

NCBI Description (AF016633) GH1 protein [Glycine max]

Seq. No. 225685

Seq. ID LIB3166-039-P1-K1-F7

Method BLASTX
NCBI GI g3702321
BLAST score 530



E value 3.0e-54 Match length 125 % identity 45

NCBI Description (AC005397) putative TGF-beta receptor interacting protein

[Arabidopsis thaliana]

Seq. No. 225686

Seq. ID LIB3166-039-P1-K1-G1

Method BLASTX
NCBI GI g4455201
BLAST score 456
E value 1.0e-45
Match length 113
% identity 78

NCBI Description (AL035440) grpE like protein [Arabidopsis thaliana]

Seq. No. 225687

Seq. ID LIB3166-039-P1-K1-G10

Method BLASTX
NCBI GI g1373125
BLAST score 297
E value 6.0e-27
Match length 106
% identity 60

NCBI Description (U43709) similar to the metB gene product of Escherichia

coli; cloned by functional complementation of a metB mutant strain of Escherichia coli LE392 [Arabidopsis thaliana]

Seq. No. 225688

Seq. ID LIB3166-039-P1-K1-G11

Method BLASTX
NCBI GI g2500047
BLAST score 639
E value 4.0e-67
Match length 127
% identity 91

NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE

PHOSPHO-HYDROLASE) (PPASE) >gi\_534916\_emb\_CAA85362\_(Z36894) soluble inorganic pyrophosphatase [Solanum

tuberosum]

Seq. No. 225689

Seq. ID LIB3166-039-P1-K1-G2

Method BLASTX
NCBI GI 94572679
BLAST score 335
E value 2.0e-31
Match length 74
% identity 84

NCBI Description (AC006954) RSZp22 splicing factor; contains RNA recognition

motif [Arabidopsis thaliana]

Seq. No. 225690

Seq. ID LIB3166-039-P1-K1-G4

Method BLASTX NCBI GI g3123295 BLAST score 223



```
E value
                    3.0e-18
Match length
                    118
% identity
                    41
NCBI Description
                    CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >qi 2583169
                    (AF026473) calmodulin-related protein [Arabidopsis
                    thaliana]
Seq. No.
                    225691
Seq. ID
                    LIB3166-039-P1-K1-G5
Method
                    BLASTX
NCBI GI
                    q2088651
BLAST score
                    395
E value
                    2.0e-38
Match length
                    128
% identity
                    58
NCBI Description
                    (AF002109) hypersensitivity-related gene 201 isolog
                    [Arabidopsis thaliana]
Seq. No.
                    225692
Seq. ID
                   LIB3166-039-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   q3183088
BLAST score
                   209
E value
                    1.0e-16
Match length
                   71
% identity
                    56
NCBI Description PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
                   (LTP) >gi_629658_pir__S47084 lipid transfer like protein -cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer
                   like protein [Vigna unguiculata]
Seq. No.
                   225693
Seq. ID
                   LIB3166-039-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g4099914
BLAST score
                   271
E value
                   5.0e-24
                   79
Match length
                   70
% identity
NCBI Description
                   (U91857) ethylene-responsive element binding protein
                   homolog [Stylosanthes hamata]
Seq. No.
                   225694
Seq. ID
                   LIB3166-039-P1-K1-H11
Method
                   BLASTX
NCBI GI
                   g3341687
BLAST score
                   179
E value
                   4.0e-13
Match length
                   86
% identity
                   47
NCBI Description
                  (AC003672) putative ras protein [Arabidopsis thaliana]
```

Seq. No. 225695

Seq. ID LIB3166-039-P1-K1-H12

Method BLASTX NCBI GI g1743354 BLAST score 504

```
E value
                   3.0e-51
Match length
                   130
% identity
                   74
NCBI Description (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
Seq. No.
                   225696
Seq. ID
                   LIB3166-039-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   q1084482
BLAST score
                   166
E value
                   5.0e-16
Match length
                   90
% identity
                   60
NCBI Description heat shock protein 70 - Maize
Seq. No.
                   225697
Seq. ID
                   LIB3166-039-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   g1169013
BLAST score
                   473
E value
                   1.0e-47
Match length
                   116
% identity
                   72
                  COP9 PROTEIN (FUSCA PROTEIN FUS7) >gi_625971_pir__A54842
NCBI Description
                   COP9 protein - Arabidopsis thaliana >gi_530870 (\overline{L3}2874)
                   COP9 [Arabidopsis thaliana] >gi_2244767_emb_CAB10190_
                   (Z97335) COP9 protein [Arabidopsis thaliana]
Seq. No.
                   225698
Seq. ID
                  LIB3166-040-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g2541876
BLAST score
                  189
E value
                   3.0e-14
Match length
                  105
```

NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No. 225699

Seq. ID LIB3166-040-P1-K1-A4

Method BLASTX NCBI GI g2541876 BLAST score 164 E value 2.0e-11 Match length 94 % identity 35

NCBI Description (D26015): CND41, chloroplast nucleoid DNA binding protein

[Nicotiana tabacum]

Seq. No. 225700

Seq. ID LIB3166-040-P1-K1-A5

Method BLASTX NCBI GI g135449 BLAST score 295 E value 5.0e-30 Match length 88



NCBI Description TUBULIN BETA-1 CHAIN >gi\_100932\_pir\_\_S14701 tubulin beta-1

chain - maize >gi\_295851\_emb\_CAA37060\_ (X52878) beta 1

tubulin [Zea mays]

Seq. No. 225701

Seq. ID LIB3166-040-P1-K1-A8

Method BLASTX
NCBI GI g1362093
BLAST score 266
E value 1.0e-23
Match length 66
% identity 74

NCBI Description hypothetical protein (clone TPP15) - tomato (fragment)

>gi\_924632 (U20595) unknown [Solanum lycopersicum]

Seq. No. 225702

Seq. ID LIB3166-040-P1-K1-B10

Method BLASTX
NCBI GI g3915031
BLAST score 643
E value 1.0e-67
Match length 122
% identity 98

NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR

(STEAROYL-ACP DESATURASE) >gi\_1217628\_emb\_CAA65232

(X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase

[Gossypium hirsutum]

Seq. No. 225703

Seq. ID LIB3166-040-P1-K1-B11

Method BLASTX
NCBI GI g2464855
BLAST score 179
E value 4.0e-13
Match length 43

% identity 74

NCBI Description (Z99707) myb-related protein [Arabidopsis thaliana]

Seq. No. 225704

Seq. ID LIB3166-040-P1-K1-B12

Method BLASTX
NCBI GI g3643085
BLAST score 392
E value 4.0e-38
Match length 112
% identity 65

NCBI Description (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum

crystallinum]

Seq. No. 225705

Seq. ID LIB3166-040-P1-K1-B3

Method BLASTX
NCBI GI g2245125
BLAST score 197
E value 3.0e-15
Match length 61



NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.

225706

Seq. ID

LIB3166-040-P1-K1-B7

Method NCBI GI BLAST score BLASTX g3242785 528

E value Match length

4.0e-54 119

79

% identity NCBI Description

(AF055355) respiratory burst oxidase protein C [Arabidopsis

thaliana]

Seq. No.

225707

Seq. ID Method

LIB3166-040-P1-K1-B8

NCBI GI BLAST score E value

BLASTX g2970641 343 1.0e-32

Match length 84 % identity 74

NCBI Description (AF052194) xyloglucan endotransglycosylase precursor

[Actinidia deliciosa]

Seq. No.

225708

Seq. ID

LIB3166-040-P1-K1-B9

Method BLASTX NCBI GI g4220535 BLAST score 515 E value 1.0e-52 Match length 121 % identity 81

NCBI Description (AL035356) clathrin coat assembly like protein [Arabidopsis

thaliana]

Seq. No.

225709

Seq. ID

LIB3166-040-P1-K1-C1

Method BLASTX NCBI GI g3550454 BLAST score 573 E value 2.0e-59 Match length 106 % identity 98

NCBI Description

(AF085820) alcohol dehydrogenase A [Gossypium barbadense] >gi\_3550458 (AF085821) alcohol dehydrogenase A [Gossypium barbadense] >gi 3551965 (AF085064) alcohol dehydrogenase A

[Gossypium hirsutum] >gi 3551967 (AF085065) alcohol

dehydrogenase A [Gossypium hirsutum] >gi 3551971 (AF085067) alcohol dehydrogenase A [Gossypium hirsutum] >qi 3551975 (AF085069) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_3551977 (AF085070) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140594 (AF090146) alcohol dehydrogenase A [Gossypium hirsutum] >gi 4140604 (AF090151) alcohol

dehydrogenase A [Gossypium hirsutum] >gi\_4140606 (AF090152) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140608 (AF090153) alcohol dehydrogenase A [Gossypium hirsutum]



>gi\_4140610 (AF090154) alcohol dehydrogenase A [Gossypium hirsutum]

Seq. ID LIB3166-040-P1-K1-C11
Method BLASTX
NCBI GI g3327275
BLAST score 359
E value 3.0e-34
Match length 114
% identity 63

Seq. No.

NCBI Description (AB016002) PKn3 [Ipomoea nil]

Seq. No. 225711

Seq. ID LIB3166-040-P1-K1-C12

Method BLASTX
NCBI GI g1737218
BLAST score 206
E value 8.0e-17
Match length 47
% identity 77

NCBI Description (U79959) vacuolar sorting receptor homolog [Arabidopsis

thalianal

Seq. No. 225712

Seq. ID LIB3166-040-P1-K1-C2

Method BLASTX
NCBI GI 9436307
BLAST score 174
E value 1.0e-12
Match length 71
% identity 61

NCBI Description (S66686) synaptic vesicle protein=n-syb [Drosophila, head,

Peptide, 181 aa] [Drosophila sp.] >gi\_738733\_prf\_\_2001392A

synaptic vesicle protein [Drosophila melanogaster]

Seq. No. 225713

Seq. ID LIB3166-040-P1-K1-C7

Method BLASTX
NCBI GI g2129630
BLAST score 294
E value 1.0e-26
Match length 76
% identity 66

NCBI Description lamin - Arabidopsis thaliana >gi\_1262754\_emb\_CAA65750

(X97023) lamin [Arabidopsis thaliana]  $>gi_3395760$  (U77721)

unknown [Arabidopsis thaliana]

Seq. No. 225714

Seq. ID LIB3166-040-P1-K1-C8

Method BLASTX
NCBI GI g2583117
BLAST score 240
E value 3.0e-20
Match length 74
% identity 65

NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. ID

Method

NCBI GI

E value

BLAST score

225720

BLASTX

146

g2465923

3.0e-09

LIB3166-040-P1-K1-D7

```
Seq. No.
                   225715
Seq. ID
                   LIB3166-040-P1-K1-C9
Method
                   BLASTX
NCBI GI
                   g3451068
BLAST score
                   320
E value
                   1.0e-29
Match length
                   85
                   74
% identity
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]
Seq. No.
                   225716
Seq. ID
                  LIB3166-040-P1-K1-D10
Method
                  BLASTX
NCBI GI
                   g1171579
BLAST score
                   526
E value
                   8.0e-54
Match length
                  124
% identity
                  81
NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum]
Seq. No.
                  225717
Seq. ID
                  LIB3166-040-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g4263787
BLAST score
                  432
E value
                  6.0e-43
Match length
                  107
% identity
                  76
NCBI Description (AC006068) unknown protein [Arabidopsis thaliana]
Seq. No.
                  225718
Seq. ID
                  LIB3166-040-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g3269284
BLAST score
                  269
E value
                  9.0e-24
Match length
                  92
% identity
                  62
NCBI Description (AL030978) histone H2A- like protein [Arabidopsis thaliana]
Seq. No.
                  225719
Seq. ID
                  LIB3166-040-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q4468813
BLAST score
                  224
E value
                  3.0e-23
Match length
                  104
% identity
                  47
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]
```

32139



```
Match length
                   105
% identity
                   27
NCBI Description
                   (AF024648) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
                   225721
Seq. No.
Seq. ID
                   LIB3166-040-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g3540181
BLAST score
                   233
E value
                   2.0e-19
Match length
                   87
% identity
                   52
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   225722
Seq. ID
                   LIB3166-040-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   q1777443
BLAST score
                   156
E value
                   2.0e-10
Match length
                   123
% identity
                   39
                   (U28422) CCA1 [Arabidopsis thaliana] >gi_3510263 (AC005310)
NCBI Description
                   DNA-binding protein CCA1 [Arabidopsis thaliana] >gi 4090569
                   (U79156) CCA1 [Arabidopsis thaliana]
Seq. No.
                   225723
Seq. ID
                  LIB3166-040-P1-K1-E4
Method
                  BLASTX
NCBI GI
                   g3868758
BLAST score
                   223
E value
                   3.0e-18
Match length
                   42
% identity
                   90
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
Seq. No.
                  225724
Seq. ID
                  LIB3166-040-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g4204575
BLAST score
                  342
E value
                   3.0e-32
Match length
                  101
% identity
                   64
NCBI Description (AF098510) cytochrome b5 DIF-F [Petunia x hybrida]
Seq. No.
                  225725
Seq. ID
```

LIB3166-040-P1-K1-E6

Method BLASTX NCBI GI g4220482 BLAST score 226 E value 1.0e-18 Match length 88 % identity

NCBI Description (AC006069) hypothetical protein [Arabidopsis thaliana]



```
225726
Seq. No.
Seq. ID
                  LIB3166-040-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  q3776005
BLAST score
                  218
E value
                  1.0e-17
Match length
                  81
% identity
                  56
NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]
                  225727
Seq. No.
                  LIB3166-040-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4193388
BLAST score
                  367
E value
                  3.0e - 35
Match length
                  91
                  79
% identity
NCBI Description (AF091455) translationally controlled tumor protein [Hevea
                  brasiliensis]
                  225728
Seq. No.
                  LIB3166-040-P1-K1-F10
Seq. ID
Method
                  BLASTX
                  g1762945
NCBI GI
BLAST score
                  308
E value
                  3.0e-28
Match length
                  117
% identity
                  52
NCBI Description
                  (U66269) ORF; able to induce HR-like lesions [Nicotiana
                  tabacum]
Seq. No.
                  225729
Seq. ID
                  LIB3166-040-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q3861068
BLAST score
                  141
E value
                   1.0e-08
Match length
                  65
% identity
                   43
NCBI Description (AJ235272) unknown [Rickettsia prowazekii]
Seq. No.
                   225730
                  LIB3166-040-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462754
BLAST score
                  282
E value
                  3.0e-25
                  103
Match length
% identity
                  57
NCBI Description (AC002292) Unknown protein [Arabidopsis thaliana]
```

Seq. ID LIB3166-040-P1-K1-F5

Method BLASTX NCBI GI g3334661 BLAST score 283



```
E value
                    2.0e-25
 Match length
                    101
 % identity
                    54
 NCBI Description (Y10490) putative cytochrome P450 [Glycine max]
                    225732
 Seq. No.
 Seq. ID
                    LIB3166-040-P1-K1-F8
 Method
                    BLASTX
 NCBI GI
                    g289920
 BLAST score
                    557
 E value
                    2.0e-57
 Match length
                    103
                    97
 % identity
 NCBI Description
                    (L07119) chlorophyll A/B binding protein [Gossypium
                    hirsutum]
 Seq. No.
                    225733
 Seq. ID
                    LIB3166-040-P1-K1-F9
 Method
                    BLASTX
 NCBI GI
                    g3132476
 BLAST score
                    257
 E value
                    3.0e-22
 Match length
                    80
 % identity
                    68
NCBI Description (AC003096) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    225734
 Seq. ID
                    LIB3166-040-P1-K1-G1
 Method
                    BLASTX
 NCBI GI
                    g4559372
 BLAST score
                    294
 E value
                    1.0e-26
                    75
 Match length
 % identity
                    73
 NCBI Description (AC006585) putative CONSTANS protein [Arabidopsis thaliana]
                    225735
 Seq. No.
 Seq. ID
                    LIB3166-040-P1-K1-G10
 Method
                    BLASTX
 NCBI GI
                    g2464855
 BLAST score
                    436
 E value
                    3.0e-43
 Match length
                    100
 % identity
                    76
 NCBI Description (Z99707) myb-related protein [Arabidopsis thaliana]
 Seq. No.
                    225736
 Seq. ID
                    LIB3166-040-P1-K1-G11
 Method
                    BLASTX
 NCBI GI
                    g1531674
 BLAST score
                    638
 E value
                    5.0e-67
 Match length
                    119
                    99
 % identity
```

NCBI Description (U68462) actin [Striga asiatica]

```
Seq. ID LIB3166-040-P1-K1-G4 Method BLASTX NCBI GI g2369714 BLAST score 157 E value 1.0e-10
```

57

% identity 58
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

 Seq. No.
 225738

 Seq. ID
 LIB3166-040-P1-K1-G6

 Method
 BLASTX

 NCBI GI
 g4432857

 BLAST score
 365

 E value
 6.0e-35

E value 6.0e-35
Match length 124
% identity 54

Match length

NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No. 225739 Seq. ID LIB3166-040-P1-K1-G7 Method BLASTX NCBI GI g2494144 BLAST score 216 2.0e-17 E value Match length 120 % identity 25

NCBI Description (AC002329) predicted leucine-rich protein [Arabidopsis

thaliana]

Seq. No. 225740

Seq. ID LIB3166-040-P1-K1-G9

Method BLASTX
NCBI GI g1220196
BLAST score 539
E value 2.0e-55
Match length 111 ...
% identity 89

NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No. 225741

Seq. ID LIB3166-040-P1-K1-H11

Method BLASTX
NCBI GI g3915083
BLAST score 605
E value 4.0e-63
Match length 123
% identity 93

NCBI Description TUBULIN BETA CHAIN >gi 1403143\_emb CAA67056 (X98406)

beta-tubulin [Cicer arietinum]

Seq. No. 225742

Seq. ID LIB3166-040-P1-K1-H12

Method BLASTX
NCBI GI g131015
BLAST score 334
E value 2.0e-31



```
Match length
% identity
                    73
NCBI Description PATHOGENESIS-RELATED PROTEIN R MAJOR FORM PRECURSOR
                    (THAUMATIN-LIKE PROTEIN E22) >gi_100385_pir__JH0230
                   pathogenesis-related protein R precursor - common tobacco
                   >gi_19855_emb_CAA33293 (X15224) thaumatin-like protein [Nicotiana tabacum] >gi_19980_emb_CAA31235 (X12739)
                   pathogenesis-related protein R (AA 1 - 226) [Nicotiana
                   tabacum]
Seq. No.
                   225743
Seq. ID
                   LIB3166-040-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   q2244965
BLAST score
                   315
E value
                   3.0e-29
Match length
                   84
% identity
                   71
NCBI Description (Z97340) unnamed protein product [Arabidopsis thaliana]
Seq. No.
                   225744
Seq. ID
                   LIB3166-040-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   q1200205
BLAST score
                   314
E value
                   6.0e-29
Match length
                   60
% identity
                   97
NCBI Description (X95753) DAG [Antirrhinum majus]
Seq. No.
                   225745
Seq. ID
                   LIB3166-040-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   g2738248
BLAST score
                   325
                   2.0e-30
E value
Match length
                   93
% identity
                   75
NCBI Description (U97200) cobalamin-independent methionine synthase
                   [Arabidopsis thaliana]
Seq. No.
                   225746
Seq. ID
                   LIB3166-040-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   q2244965
BLAST score
                   300
E value
                   2.0e-27
Match length
                   121
% identity
NCBI Description (Z97340) unnamed protein product [Arabidopsis thaliana]
Seq. No.
                   225747
```

Seq. ID LIB3166-042-P1-K1-A1

Method BLASTX NCBI GI g2062174 BLAST score 194

E value 7.0e-15



```
Match length
                   118
% identity
                   35
NCBI Description
                 (AC001645) transcription factor (TINY) isolog [Arabidopsis
                  thaliana]
                  225748
Seq. No.
Seq. ID
                  LIB3166-042-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g2738915
BLAST score
                  299
E value
                  4.0e-27
Match length
                  118
% identity
                  50
NCBI Description (AF020760) serine protease [Homo sapiens]
Seq. No.
                  225749
Seq. ID
                  LIB3166-042-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g3252807
BLAST score
                  215
E value
                  2.0e-17
Match length
                  71
% identity
                  54
NCBI Description (AC004705) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  225750
Seq. ID
                  LIB3166-042-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g4008006
BLAST score
                  169
E value
                  5.0e-12
Match length
                  61
% identity
                  61
NCBI Description (AF084034) receptor-like protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  225751
Seq. ID
                  LIB3166-042-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g4206124
BLAST score
                  597
E value
                  4.0e-62
Match length
                  129
% identity
                  89
NCBI Description (AF097668) T-complex protein 1 epsilon subunit
                  [Mesembryanthemum crystallinum]
Seq. No.
                  225752
Seq. ID
                  LIB3166-042-P1-K1-A5
Method
                  BLASTX
                  g2384669
NCBI GI
BLAST score
                  400
```

Method BLASTX
NCBI GI g2384669
BLAST score 400
E value 5.0e-39
Match length 104
% identity 73

NCBI Description (AF012656) putative potassium transporter AtKT1p

[Arabidopsis thaliana]



```
225753
Seq. No.
                   LIB3166-042-P1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2208903
BLAST score
                   295
E value
                   7.0e-27
Match length
                   107
% identity
                   54
NCBI Description
                   (AB004798) ascorbate oxidase [Arabidopsis thaliana]
                   225754
Seq. No.
Seq. ID
                   LIB3166-042-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   q1220196
BLAST score
                   661
E value
                   1.0e-69
Match length
                   129
                   98
% identity
NCBI Description
                   (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
                   225755
Seq. No.
                   LIB3166-042-P1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3779218
BLAST score
                   300
E value
                   3.0e-27
Match length
                   94
                   62
% identity
                  (AF030879) protein kinase CPK1 [Solanum tuberosum]
NCBI Description
                   225756
Seq. No.
Seq. ID
                   LIB3166-042-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   g2342685
BLAST score
                   418
E value
                    4.0e-41
Match length
                   123
% identity
                    63
NCBI Description
                    (AC000106) Contains similarity to Rhodococcus amidase
                   (gb_D16207). ESTs gb_T20504,gb_H36650,gb_N97423,gb_H36595 come from this gene. [Arabidopsis thaliana]
                   225757
Seq. No.
Seq. ID
                   LIB3166-042-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   g2160694
BLAST score
                   422
E value
                   1.0e-41
Match length
                   123
% identity
                   64
NCBI Description
                    (U73528) B' regulatory subunit of PP2A [Arabidopsis
                   thaliana]
```

Seq. ID LIB3166-042-P1-K1-B7

Method BLASTX



```
g1458245
NCBI GI
                  143
BLAST score
E value
                  7.0e-09
Match length
                  111
% identity
                  33
                  (U64834) coded for by C. elegans cDNA cm17a1; coded for by
NCBI Description
                  C. elegans cDNA cm7g1; coded for by C. elegans cDNA
                  CEMSE26F; similar to methyltransferases [Caenorhabditis
                  elegans]
                  225759
Seq. No.
Seq. ID
                  LIB3166-042-P1-K1-C11
Method
                  BLASTX
                  g3242789
NCBI GI
BLAST score
                  271
E value
                  6.0e-24
                  118
Match length
                  59
% identity
                  (AF055357) respiratory burst oxidase protein D [Arabidopsis
NCBI Description
                  thaliana]
                  225760
Seq. No.
                  LIB3166-042-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4406770
BLAST score
                  177
E value
                  7.0e-13
Match length
                  42
                  79
% identity
NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]
Seq. No.
                  225761
                  LIB3166-042-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4262378
BLAST score
                  164
E value ·
                  2.0e-11
Match length
                  86
% identity
                  37
NCBI Description (AF092910) stage specific peptide 24 [Trypanosoma cruzi]
Seq. No.
                  225762
Seq. ID
                  LIB3166-042-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g2194138
BLAST score
                  151
E value
                  7.0e-10
Match length
                  66
% identity
                  48
NCBI Description
                   (AC002062) Similar to Arabidopsis receptor-like protein
                  kinase precursor (gb M84659). [Arabidopsis thaliana]
```

Seq. ID LIB3166-042-P1-K1-D4

Method BLASTX NCBI GI g1871194 BLAST score 227



```
E value
                  9.0e-19
Match length
                  95
% identity
                  49
NCBI Description
                  (U90439) DNA binding protein isolog [Arabidopsis thaliana]
                  >gi 2335092 (AC002339) putative DNA binding protein
                  [Arabidopsis thaliana]
Seq. No.
                  225764
Seq. ID
                  LIB3166-042-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g4557078
BLAST score
                  272
E value
                  5.0e-24
Match length
                  103
% identity
                  49
NCBI Description (AC007045) putative Tall-1 pol polyprotein, 5' partial
                  [Arabidopsis thaliana]
Seq. No.
                  225765
Seq. ID
                  LIB3166-042-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g2827715
BLAST score
                  311
E value
                  1.0e-28
Match length
                  84
                  7
% identity
NCBI Description (AL021684) receptor protein kinase - like protein
                  [Arabidopsis thaliana]
Seq. No.
                  225766
Seq. ID
                  LIB3166-042-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q4388818
BLAST score
                  241
E value
                  1.0e-20
Match length
                  87
% identity
NCBI Description (AC006528) putative pol polyprotein with a Zn-finger CCHC
                  type domain (prosite:QDOC50158) and a DDE integrase
                  signature motif [Arabidopsis thaliana]
Seq. No.
                  225767
Seq. ID
                  LIB3166-042-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q4455246
BLAST score
                  521
E value
                  3.0e-53
Match length
                  130
% identity
                  74
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
```

Seq. ID LIB3166-042-P1-K1-E1

Method BLASTX
NCBI GI g1518540
BLAST score 602
E value 9.0e-63



Match length % identity 93

NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No. 225769

Seq. ID LIB3166-042-P1-K1-E10

Method BLASTX NCBI GI g2829910 BLAST score 376 E value 3.0e-36 Match length 102 % identity 64

NCBI Description (AC002291) Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana]

Seq. No. 225770

Seq. ID LIB3166-042-P1-K1-E11

Method BLASTX NCBI GI g1197461 BLAST score 656 E value 5.0e-69 Match length 130 % identity 95

NCBI Description (X78819) casein kinase I [Arabidopsis thaliana]

Seq. No. 225771

Seq. ID LIB3166-042-P1-K1-E2

Method BLASTX NCBI GI g3834302 BLAST score 473 E value 1.0e-47 Match length 127 % identity 79

NCBI Description (AC005679) Similar to gb D45384 vacuolar H+-pyrophosphatase from Oryza sativa. ESTs gb\_F14272 and gb F14273 come from

this gene. [Arabidopsis thaliana]

Seq. No. 225772

Seq. ID LIB3166-042-P1-K1-E3

Method BLASTX NCBI GI g115492 BLAST score 559 E value 1.0e-57 Match length 109 % identity 52

NCBI Description CALMODULIN-RELATED PROTEIN >gi 169205 (M80831) calmodulin-related protein [Petunia.hybrida]

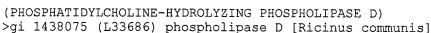
Seq. No. 225773

Seq. ID LIB3166-042-P1-K1-E4

Method BLASTX NCBI GI q2499710 BLAST score 577 E value 8.0e-60 Match length 124 % identity 87

NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)





Seq. ID LIB3166-042-P1-K1-F1

Method BLASTX
NCBI GI g547683
BLAST score 343
E value 2.0e-32
Match length 122
% identity 58

NCBI Description HEAT SHOCK COGNATE PROTEIN 80 >gi\_170456 (M96549) heat

shock cognate protein 80 [Solanum lycopersicum]
>gi\_445601\_prf\_\_1909348A heat shock protein hsp80

[Lycopersicon esculentum]

Seq. No. 225775

Seq. ID LIB3166-042-P1-K1-F10

Method BLASTX
NCBI GI g2829751
BLAST score 187
E value 5.0e-14
Match length 110
% identity 36

NCBI Description MACROPHAGE MIGRATION INHIBITORY FACTOR HOMOLOG (BMMIF)

>gi\_1850559 (U88035) macrophage migration inhibitory factor
[Brugia malayi] >gi\_2190976 (AF002699) macrophage migration

inhibitory factor [Brugia malayi]

Seq. No. 225776

Seq. ID LIB3166-042-P1-K1-F11

Method BLASTX
NCBI GI g2828280
BLAST score 149
E value 1.0e-09
Match length 33
% identity 85

NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

>gi\_2832633\_emb\_CAA16762\_ (AL021711) putative protein

[Arabidopsis thaliana]

Seq. No. 225777

Seq. ID LIB3166-042-P1-K1-F12

Method BLASTX
NCBI GI g4539453
BLAST score 297
E value 6.0e-27
Match length 88
% identity 61

NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 225778

Seq. ID LIB3166-042-P1-K1-F2

Method BLASTX
NCBI GI g509810
BLAST score 523
E value 2.0e-53

% identity



```
Match length
                  126
% identity
                  79
NCBI Description (L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]
                  225779
Seq. No.
Seq. ID
                  LIB3166-042-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g1931655
BLAST score
                  313
E value
                  7.0e-29
Match length
                  109
% identity
                  61
NCBI Description (U95973) receptor-kinase isolog [Arabidopsis thaliana]
Seq. No.
                  225780
Seq. ID
                  LIB3166-042-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g485514
BLAST score
                  145
E value
                  4.0e-09
Match length
                  33
% identity
                  79
NCBI Description ADR11-2 protein - soybean (fragment)
                  >gi 296443 emb CAA49341 (X69640) auxin down regulated
                  [Glycine max]
                  225781
Seq. No.
Seq. ID
                  LIB3166-042-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g1150406
BLAST score
                  194
E value
                  7.0e-15
Match length
                  100
% identity
                  39
NCBI Description (Z46868) exo-1,3-beta-glucanase/1,3-beta-D-glucan
                  glucanohydrolase [Pichia angusta]
                  225782
Seq. No.
Seq. ID
                  LIB3166-042-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g3258647
BLAST score
                  228
E value
                  7.0e-19
Match length
                  125
% identity
NCBI Description
                  (AF044677) retinitis pigmentosa GTPase regulator [Mus
                  musculus]
                  225783
Seq. No.
Seq. ID
                  LIB3166-042-P1-K1-G1
                  BLASTX
Method
NCBI GI
                  g3548802
                  207
BLAST score
E value
                  2:0e-16
Match length
                  66
```

32151

NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana]

% identity

NCBI Description





## >gi 4335769 gb AAD17446 (AC006284) putative axi1 protein [Nicotiana tabacum] [Arabidopsis thaliana]

225784 Seq. No. Seq. ID LIB3166-042-P1-K1-G12 Method BLASTX NCBI GI g3236253 BLAST score 301 E value 2.0e-27 Match length 120 % identity 52 NCBI Description (AC004684) receptor-like protein kinase [Arabidopsis thaliana] Seq. No. 225785 LIB3166-042-P1-K1-G2 Seq. ID Method BLASTX NCBI GI g167367 BLAST score 494 E value 4.0e-50 Match length 125 % identity 77 NCBI Description (L08199) peroxidase [Gossypium hirsutum] Seq. No. 225786 LIB3166-042-P1-K1-G3 Seq. ID Method BLASTX NCBI GI q2760320 BLAST score 345 E value 1.0e-32 Match length 104 % identity 68 NCBI Description (AC002130) F1N21.4 [Arabidopsis thaliana] Seq. No. 225787 Seq. ID LIB3166-042-P1-K1-G4 BLASTX Method NCBI GI q4193382 386 BLAST score E value 2.0e-37 Match length 86 83 % identity (AF083336) ribosomal protein S27 [Arabidopsis thaliana] NCBI Description >gi 4193384 (AF083337) ribosomal protein S27 [Arabidopsis thaliana] 225788 Seq. No. Seq. ID LIB3166-042-P1-K1-G5 Method BLASTX NCBI GI g4006924 BLAST score 589 E value 3.0e-61 Match length 126 83

thaliana]

(Z99708) beta-galactosidase like protein [Arabidopsis



```
Seq. No.
                   225789
Seq. ID
                  LIB3166-042-P1-K1-G6
Method
                  BLASTX
NCBI GI
                   g1084321
BLAST score
                  521
E value
                   3.0e-53
Match length
                  123
% identity
                   80
NCBI Description
                  protochlorophyllide reductase (EC 1.3.1.33) - cucumber
                   >gi_2244614_dbj_BAA21089_ (D50085)
                  NADPH-protochlorophyllide oxidoreductase [Cucumis sativus]
Seq. No.
                   225790
Seq. ID
                  LIB3166-042-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g2764941
BLAST score
                  348
E value
                   6.0e-33
Match length
                  90
% identity
                   68
NCBI Description
                  (X98255) transcriptionally stimulated by gibberellins;
                   expressed in meristematic region, and style [Arabidopsis
                  thaliana]
Seq. No.
                   225791
Seq. ID
                  LIB3166-042-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g2804278
BLAST score
                  553
E value
                  6.0e-57
Match length
                  129
% identity
                  81
NCBI Description (AB003516) squalene epoxidase [Panax ginseng]
Seq. No.
                  225792
Seq. ID
                  LIB3166-042-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g2088653
BLAST score
                  214
E value
                  3.0e-17
Match length
                  109
% identity
                  41
NCBI Description (AF002109) Hslpro-1 related protein isolog [Arabidopsis
                  thaliana]
Seq. No.
                  225793
Seq. ID
                  LIB3166-042-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q3868758
BLAST score
                  418
E value
                  4.0e-41
Match length
                  101
% identity
                  75
```

Seq. ID LIB3166-042-P1-K1-H2

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]



Method BLASTX
NCBI GI g3319345
BLAST score 117
E value 2.0e-09
Match length 82
% identity 49

NCBI Description (AF077407) contains similarity to maize transposon MuDR

(GB:M76978) [Arabidopsis thaliana]

Seq. No. 225795

Seq. ID LIB3166-042-P1-K1-H5

Method BLASTX
NCBI GI g2088653
BLAST score 214
E value 3.0e-17
Match length 109
% identity 41

NCBI Description (AF002109) Hs1pro-1 related protein isolog [Arabidopsis

thaliana]

Seq. No. 225796

Seq. ID LIB3166-042-P1-K1-H7

Method BLASTX
NCBI GI g113621
BLAST score 470
E value 3.0e-47
Match length 105
% identity 89

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi\_68196\_pir\_ ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi\_168420 (M16220) aldolase
[Zea mays] >gi\_295850\_emb\_CAA31366\_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi\_225624\_prf\_\_1307278A

cytoplasmic aldolase [Zea mays]

Seq. No. 225797

Seq. ID LIB3166-042-P1-K1-H8

Method BLASTX
NCBI GI g3122139
BLAST score 375
E value 4.0e-36
Match length 122
% identity 55

NCBI Description GLYCEROL KINASE (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE)

(GLYCEROKINASE) (GK) (ATP-STIMULATED

GLUCOCORTICOID-RECEPTOR TRANSLOCATON PROMOTER) (ASTP)

 $>gi_484372_pir_JN0606$  ATP-stimulated

glucocorticoid-receptor translocation promoter protein - rat >gi\_433211\_dbj\_BAA03677\_ (D16102) ATP-stimulated glucocorticoid-receptor translocaton promoter [Rattus

rattus]

Seq. No. 225798

Seq. ID LIB3166-043-P1-K1-A11

Method BLASTX NCBI GI g3913413 BLAST score 390



```
E value
                   7.0e-38
Match length
                   85
% identity
                  89
NCBI Description
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME 1 (ADOMETDC 1)
                   (SAMDC 1) (SAMDC9) >gi_1155240 (U38526)
                  S-adenosylmethionine decarboxylase 1 [Dianthus
                  caryophyllus] >gi 2406585 (U94786) S-adenosylmethionine
                  decarboxylase [Dianthus caryophyllus]
Seq. No.
                  225799
Seq. ID
                  LIB3166-043-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g1730502
BLAST score
                  215
E value
                  2.0e-17
Match length
                  87
                  45
% identity
NCBI Description TRANSMEMBRANE PROTEIN PFT27 >gi_110903 pir A31351 probable
                  transmembrane protein FT27 - mouse >gi_535682 (M23568)
                  transmembrane protein [Mus musculus]
                  225800
Seq. No.
Seq. ID
                  LIB3166-043-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q4062934
BLAST score
                  491
E value
                  8.0e-50
Match length
                  110
% identity
                  82
NCBI Description (D88272) formate dehydrogenase [Hordeum vulgare]
Seq. No.
                  225801
Seq. ID
                  LIB3166-043-P1-K1-A4
                  BLASTX
Method
NCBI GI
                  q3746069
BLAST score
                  160
E value
                  6.0e-11
Match length
                  108
% identity
                  31
NCBI Description (AC005311) putative reverse transcriptase [Arabidopsis
                  thaliana]
Seq. No.
                  225802
Seq. ID
                  LIB3166-043-P1-K1-A9
Method
                  BLASTX
                  q4218120
                  347
```

NCBI GI BLAST score E value 7.0e-33 Match length 101 % identity

NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis

thaliana]

Seq. No. 225803

Seq. ID LIB3166-043-P1-K1-B2

Method BLASTX NCBI GI q3201680

BLAST score

E value

464

1.0e-46



```
BLAST score
E value
                   7.0e - 30
Match length
                   127
% identity
                   55
NCBI Description (AF060941) extra-large G-protein [Arabidopsis thaliana]
Seq. No.
                   225804
Seq. ID
                  LIB3166-043-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g4220533
BLAST score
                   333
E value
                   4.0e-31
Match length
                   108
% identity
                   34
NCBI Description (AL035356) putative mitochondrial uncoupling protein
                   [Arabidopsis thaliana]
                   225805
Seq. No.
Seq. ID
                   LIB3166-043-P1-K1-B8
Method
                   BLASTX
NCBI GI
                   g1928981
BLAST score
                   532
E value
                   1.0e-54
Match length
                   120
% identity
                   89
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                   oleracea var. botrytis]
                   225806
Seq. No.
Seq. ID
                   LIB3166-043-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g1710124
BLAST score
                   181
E value
                   2.0e-13
Match length
                   117
                   37
% identity
NCBI Description (U62279) leucine-rich repeat-containing extracellular
                   glycoprotein; contains six N-glycosylation sites [NX(S/T)]
                   [Sorghum bicolor]
                   225807
Seq. No.
Seq. ID
                   LIB3166-043-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   g4006924
BLAST score
                   197
E value
                   2.0e-15
Match length
                   46
% identity
                   76
NCBI Description
                  (Z99708) beta-galactosidase like protein [Arabidopsis
                   thaliana]
Seq. No.
                   225808
                   LIB3166-043-P1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4455208
```

BLAST score

E value Match length 407 7.0e-40

122



```
Match length
                  115
                  79
% identity
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  225809
                  LIB3166-043-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4325324
BLAST score
                  627
E value
                  1.0e-65
Match length
                  125
% identity
                  93
NCBI Description (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis
                  thaliana]
                  225810
Seq. No.
                  LIB3166-043-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4325324
BLAST score
                  258
E value
                  2.0e-22
Match length
                  103
% identity
NCBI Description (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis
                  thaliana]
Seq. No.
                  225811
Seq. ID
                  LIB3166-043-P1-K1-C3
Method
                  BLASTX
                  g2979552
NCBI GI
BLAST score
                  435
E value
                  4.0e-43
Match length
                  123
% identity
                  71
NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]
Seq. No.
                  225812
Seq. ID
                  LIB3166-043-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g2499611
BLAST score
                  468
E value
                  6.0e-47
Match length
                  117
                  79
% identity
NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7)
                  (ATMPK7) >gi_629548_pir__S40473 mitogen-activated protein
                  kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana
                  >gi 457406 dbj BAA04870 (D21843) MAP kinase [Arabidopsis
                  thaliana]
                  225813
Seq. No.
Seq. ID
                  LIB3166-043-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g130600
```

32157



% identity

NCBI Description ENZYMATIC POLYPROTEIN [CONTAINS: ASPARTIC PROTEASE;

ENDONUCLEASE; REVERSE TRANSCRIPTASE ] >gi 76782 pir S01283

hypothetical protein 5 - figwort mosaic virus >gi\_58813\_emb\_CAA29527 (X06166) ORF V (AA 1-666) [Figwort

mosaic virus]

Seq. No.

225814

Seq. ID LIB3166-043-P1-K1-C8

Method BLASTX NCBI GI q393707 BLAST score 509 E value 8.0e-52 Match length 117

% identity 84

NCBI Description (X67696) acetyl-CoA acyltransferase [Cucumis sativus]

Seq. No.

225815

Seq. ID LIB3166-043-P1-K1-D1

Method BLASTX NCBI GI g3063396 BLAST score 349 E value 2.0e-33 Match length 87 % identity 77

NCBI Description (AB012947) vcCyP [Vicia faba]

225816 Seq. No.

Seq. ID LIB3166-043-P1-K1-D10

Method BLASTX NCBI GI g1531758 BLAST score 605 E value 4.0e-63 Match length 124 % identity 94

NCBI Description (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028)

unknown protein [Arabidopsis thaliana]

Seq. No. 225817

LIB3166-043-P1-K1-D11 Seq. ID

Method BLASTX NCBI GI g3858935 BLAST score 522 E value 2.0e-53 Match length 119 % identity 82

NCBI Description (AL021636) synaptobrevin-like protein [Arabidopsis

thaliana] >gi 4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis

thaliana]

Seq. No. 225818

Seq. ID LIB3166-043-P1-K1-D12

Method BLASTX NCBI GI g3858935 BLAST score 225 E value 5.0e-19

32158



```
Match length
                  71
% identity
NCBI Description
                  (AL021636) synaptobrevin-like protein [Arabidopsis
                  thaliana] >gi 4103357 (AF025332) vesicle-associated
                  membrane protein 7C; synaptobrevin 7C [Arabidopsis
                  thaliana]
Seq. No.
                  225819
Seq. ID
                  LIB3166-043-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g4455276
BLAST score
                  167
E value
                  1.0e-11
Match length
                  71
% identity
                  (AL035527) peptide transporter-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  225820
Seq. ID
                  LIB3166-043-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g1220196
BLAST score
                  543
E value
                  8.0e-56
Match length
                  111
% identity
                  90
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.
                  225821
                  LIB3166-043-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1332411
BLAST score
                  505
E value
                  2.0e-51
Match length
                  109
% identity
                  88
NCBI Description (D85102) dihydroflavonol 4-reductase [Rosa hybrida]
Seq. No.
                  225822
                  LIB3166-043-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244780
BLAST score
                  266
E value
                  2.0e-23
Match length
                  57
% identity
                  93
NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  225823
Seq. ID
                  LIB3166-043-P1-K1-E1
Method
                  BLASTX
```

Method BLASTX
NCBI GI g1170621
BLAST score 355
E value 7.0e-34
Match length 103
% identity 67

NCBI Description KINESIN-LIKE PROTEIN C >gi 1084342 pir S48020

Match length

% identity

115

64



kinesin-related protein katC - Arabidopsis thaliana >gi\_1438844\_dbj\_BAA04674\_ (D21138) heavy chain polypeptide of kinesin-like protein [Arabidopsis thaliana]

Seq. No. 225824 Seq. ID LIB3166-043-P1-K1-E10 Method BLASTX NCBI GI g2995384 BLAST score 177 E value 3.0e-13 Match length 65 63 % identity NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays] Seq. No. 225825 Seq. ID LIB3166-043-P1-K1-E12 Method BLASTX NCBI GI g1408471 BLAST score 153 E value 4.0e-12 Match length 59 % identity 66 NCBI Description (U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi\_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana] Seq. No. 225826 Seq. ID LIB3166-043-P1-K1-E2 Method BLASTX NCBI GI g4558661 BLAST score 368 E value 3.0e-35 Match length 114 % identity 66 NCBI Description (AC007063) putative malate oxidoreductase (NAD) [Arabidopsis thaliana] 225827 Seq. No. Seq. ID LIB3166-043-P1-K1-E4 Method BLASTX NCBI GI g832876 BLAST score 535 E value 7.0e-55 Match length 119 % identity 87 NCBI Description (L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi\_1097368\_prf\_\_2113407A ascorbate free radical reductase [Lycopersicon esculentum] Seq. No. 225828 Seq. ID LIB3166-043-P1-K1-E5 Method BLASTX NCBI GI g3914002 BLAST score 367 E value 3.0e-35

32160



NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >qi 2935279 (AF033862) Lon protease [Arabidopsis thaliana]

Seq. No. 225829

Seq. ID LIB3166-043-P1-K1-E7

Method BLASTX NCBI GI g1173256 BLAST score 526 E value 8.0e-54 Match length 125 % identity 83

NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi 629496 pir S45026 ribosomal

protein S4 - upland cotton >gi 488739 emb CAA55882 (X79300) ribosomal protein, small subunit 4e (RS4e)

[Gossypium hirsutum]

225830 Seq. No.

LIB3166-043-P1-K1-E8 Seq. ID

Method BLASTX NCBI GI g2654868 154 BLAST score 7.0e-13 E value Match length 52 % identity 77

NCBI Description (AF015301) RbohAp108 [Arabidopsis thaliana]

225831 Seq. No.

LIB3166-043-P1-K1-F1 Seq. ID

Method BLASTX NCBI GI q2098705 BLAST score 294 E value 1.0e-26 Match length 118

% identity

NCBI Description (U82973) pectinesterase [Citrus sinensis]

Seq. No. 225832

LIB3166-043-P1-K1-F10 Seq. ID

Method BLASTX NCBI GI g3643607 BLAST score 470 E value 3.0e-47Match length 113 % identity 43

NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 225833

Seq. ID LIB3166-043-P1-K1-F11

Method BLASTX NCBI GI g2253442 BLAST score 188 E value 3.0e-14 Match length 46 % identity 67

NCBI Description (AF007784) LTCOR11 [Lavatera thuringiaca]

Seq. No. 225834

Seq. ID

Method



```
LIB3166-043-P1-K1-F12
Seq. ID
Method
                  BLASTX
                  q2829868
NCBI GI
BLAST score
                  187
                  4.0e-14
E value
                  50
Match length
                  68
% identity
                 (AC002396) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  225835
                  LIB3166-043-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2288981
                  310
BLAST score
                  2.0e-28
E value
                  97
Match length
                  40
% identity
                  (AC002335) calcium binding protein isolog [Arabidopsis
NCBI Description
                  thaliana] >gi 3763938 (AC004450) putative calcium binding
                  protein [Arabidopsis thaliana]
                  225836
Seq. No.
                  LIB3166-043-P1-K1-F4
Seq. ID
                  BLASTX
Method
                  g3929545
NCBI GI
                   281
BLAST score
E value
                   4.0e-25
Match length
                  126
                   49
% identity
                  (AF067194) S-adenosylmethionine decarboxylase [Oryza
NCBI Description
                  sativa]
                   225837
Seq. No.
Seq. ID
                   LIB3166-043-P1-K1-F5
Method
                  BLASTX
NCBI GI
                   q2583123
BLAST score
                   318
E value
                   2.0e-29
Match length
                   98
% identity
                   63
NCBI Description
                  (AC002387) putative nucleotide sugar epimerase [Arabidopsis
                   thaliana]
                   225838
Seq. No.
                   LIB3166-043-P1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3643085
BLAST score
                   246
E value
                   4.0e-21
Match length
                   109
% identity
                   50
NCBI Description (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum
                   crystallinum]
                   225839 `
Seq. No.
```

LIB3166-043-P1-K1-F8

BLASTX



```
NCBI GI
                  q4220533
BLAST score
                  317
E value
                  2.0e-29
Match length
                  126
% identity
                  56
                  (AL035356) putative mitochondrial uncoupling protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  225840
Seq. ID
                  LIB3166-043-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q3355468
BLAST score
                  507
E value
                  1.0e-51
Match length
                  122
% identity
                  (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  225841
Seq. ID
                  LIB3166-043-P1-K1-G10
                  BLASTX
Method
NCBI GI
                  q3646340
BLAST score
                  536
                  5.0e-55
E value
Match length
                  119
                  87
% identity
NCBI Description (AJ000763) MADS-box protein [Malus domestica]
Seq. No.
                  225842
                  LIB3166-043-P1-K1-G11
Seq. ID
Method
                  BLASTX
                  q4090535
NCBI GI
BLAST score
                  366
E value
                  3.0e-35
Match length
                  82
                  79
% identity
NCBI Description (U68216) ACC synthase [Carica papaya]
                  225843
Seq. No.
Seq. ID
                  LIB3166-043-P1-K1-G12
                  BLASTX
Method
NCBI GI
                  g1702983
BLAST score
                  231
E value
                  2.0e-19
                  96
Match length
                   48
% identity
NCBI Description AUXIN-REPRESSED 12.5 KD PROTEIN >gi 99855 pir__S11850
                  hypothetical protein - garden strawberry
```

>gi\_22573\_emb\_CAA36676\_ (X52429) 12.5 kDa protein [Fragaria
x ananassa] >gi\_927034 (L44142) auxin-repressed protein

[Fragaria ananassa]

225844 Seq. No.

Seq. ID LIB3166-043-P1-K1-G2

Method BLASTX NCBI GI g1169544



BLAST score 228 E value 1.0e-32 Match length 121 % identity 69

ERD1 protein [Arabidopsis thaliana]

Seq. No. 225845

Seq. ID LIB3166-043-P1-K1-G3

Method BLASTX
NCBI GI g3087805
BLAST score 203
E value 9.0e-25
Match length 81
% identity 78

NCBI Description (AJ223038) latex allergen [Hevea brasiliensis]

Seq. No. 225846

Seq. ID LIB3166-043-P1-K1-G4

Method BLASTX
NCBI GI g3236240
BLAST score 325
E value 3.0e-30
Match length 103
% identity 65

NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No. 225847

Seq. ID LIB3166-043-P1-K1-G6

Method BLASTX
NCBI GI g1263291
BLAST score 457
E value 9.0e-46
Match length 97
% identity 88

NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No. 225848

Seq. ID LIB3166-043-P1-K1-G7

Method BLASTX
NCBI GI g729335
BLAST score 153
E value 4.0e-10
Match length 65
% identity 48

NCBI Description SUCCINATE DEHYDROGENASE (UBIQUINONE) IRON-SULFUR PROTEIN

PRECURSOR (IP) >gi 508849 (L27705) succinate dehydrogenase

iron-protein subunit [Drosophila melanogaster]

Seq. No. 225849

Seq. ID LIB3166-043-P1-K1-G8

Method BLASTX
NCBI GI g3023190
BLAST score 426
E value 4.0e-42
Match length 104



```
% identity
NCBI Description
                  14-3-3-LIKE PROTEIN 16R >gi 1888459 emb CAA72381 (Y11685)
                  14-3-3 protein [Solanum tuberosum]
Seq. No.
                  225850
Seq. ID
                  LIB3166-043-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g4415942
BLAST score
                  219
E value
                  6.0e-22
Match length
                  122
% identity
                  52
NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  225851
Seq. ID
                  LIB3166-043-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g3548810
BLAST score
                  160
E value
                  6.0e-11
                  98
Match length
% identity
                  43
NCBI Description (AC005313) putative chloroplast nucleoid DNA binding
                  protein [Arabidopsis thaliana]
                  225852
Seq. No.
Seq. ID
                  LIB3166-043-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g4455340
BLAST score
                  211
E value
                  7.0e-17
Match length
                  105
% identity
                  43
NCBI Description (AL035522) putative protein [Arabidopsis thaliana]
Seq. No.
                  225853
Seq. ID
                  LIB3166-043-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g1871182
BLAST score
                  494
E value
                  4.0e-50
Match length
                  119
% identity
                  75
NCBI Description (U90439) phospholipase D isolog [Arabidopsis thaliana]
Seq. No.
                  225854
Seq. ID
                  LIB3166-043-P1-K1-H9
                  BLASTX
Method
```

NCBI GI q2980760 BLAST score 242 2.0e-20 E value Match length 85 % identity

NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 225855

Seq. ID LIB3166-044-P1-K1-A1

32165



```
Method
                  BLASTX
                   g3668089
NCBI GI
BLAST score
                   138
E value
                   7.0e-09
Match length
                   67
% identity
                   36
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.
                  225856
                  LIB3166-044-P1-K1-A12
Seq. ID
Method
                  BLASTX
                  g2558938
NCBI GI
BLAST score
                  241
                   2.0e-20
E value
Match length
                  76
% identity
                   61
NCBI Description (AF024625) arm repeat containing protein [Brassica napus]
                  225857
Seq. No.
Seq. ID
                  LIB3166-044-P1-K1-A2
Method
                  BLASTX
                  g3668089
NCBI GI
BLAST score
                  344
E value
                  2.0e-32
Match length
                  126
                  50
% identity
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
                  225858
Seq. No.
Seq. ID
                  LIB3166-044-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q4455192
BLAST score
                   498
E value
                   2.0e-50
Match length
                  129
% identity
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                   225859
Seq. ID
                  LIB3166-044-P1-K1-A4
Method
                  BLASTX
NCBI GI
                   g2146731
BLAST score
                  572
E value
                   3.0e-59
Match length
                  125
% identity
                   29
NCBI Description FK506-binding protein - Arabidopsis thaliana >gi_1354207
                   (U49453) rof1 [Arabidopsis thaliana]
                  225860
Seq. No.
Seq. ID
                  LIB3166-044-P1-K1-A6
Method
                  BLASTX
```

Method BLASTX
NCBI GI g3367578
BLAST score 214
E value 3.0e-17

Match length 75 % identity 53



NCBI Description (AL031135) protein kinase - like protein [Arabidopsis thaliana]

Seq. No. 225861

Seq. ID LIB3166-044-P1-K1-A7

Method BLASTX
NCBI GI g3668089
BLAST score 271
E value 5.0e-24
Match length 83
% identity 60

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 225862

Seq. ID LIB3166-044-P1-K1-B10

Method BLASTX
NCBI GI g1362008
BLAST score 340
E value 5.0e-32
Match length 104
% identity 15

NCBI Description ubiquitin-like protein 12 - Arabidopsis thaliana

Seq. No. 225863

Seq. ID LIB3166-044-P1-K1-B2

Method BLASTX
NCBI GI g3063448
BLAST score 368
E value 3.0e-35
Match length 130
% identity 85

NCBI Description (AC003981) F22013.10 [Arabidopsis thaliana]

Seq. No. 225864

Seq. ID LIB3166-044-P1-K1-B3

Method BLASTX
NCBI GI g3766368
BLAST score 220
E value 6.0e-18
Match length 106
% identity 47

NCBI Description (AL031907) putative trascription factor, ccr4-associated

factor homolog [Schizosaccharomyces pombe]

Seq. No. 225865

Seq. ID LIB3166-044-P1-K1-B6

Method BLASTX
NCBI GI g2129578
BLAST score 569
E value 7.0e-59
Match length 117
% identity 91

NCBI Description dTDP-glucose 4-6-dehydratases homolog - Arabidopsis

thaliana >gi\_928932\_emb\_CAA89205\_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi\_1585435\_prf\_2124427B diamide resistance gene

[Arabidopsis thaliana]



```
225866
Seq. No.
                  LIB3166-044-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1565225
                  284
BLAST score
                  2.0e-25
E value
Match length
                  62
% identity
                  84
NCBI Description (X95572) salt-tolerance protein [Arabidopsis thaliana]
Seq. No.
                  225867
                  LIB3166-044-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3023858
BLAST score
                  637
E value
                  8.0e-67
Match length
                  127
% identity
                  47
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                  PROTEIN >gi 1256608 (U44850) G protein beta subunit
                  [Glycine max]
Seq. No.
                  225868
Seq. ID
                  LIB3166-044-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  q3201554
BLAST score
                  535
E value
                  1.0e-56
Match length
                  126
% identity
                  80
NCBI Description (AJ006501) beta-D-glucosidase [Tropaeolum majus]
Seq. No.
                  225869
Seq. ID
                  LIB3166-044-P1-K1-C11
                  BLASTX
Method
NCBI GI
                  q1545805
BLAST score
                  251
E value
                  3.0e-23
                  95
Match length
                  62
% identity
NCBI Description (D64052) cytochrome P450 like TBP [Nicotiana tabacum]
                  225870
Seq. No.
Seq. ID
                  LIB3166-044-P1-K1-C12
                  BLASTX
Method
NCBI GI
                  g1362103
BLAST score
                  150
E value
                  3.0e-10
Match length
                  42
% identity
                  67
                  ubiquitin conjugating enzyme - tomato
NCBI Description
                  >gi 886679 emb CAA58111 (X82938) ubiquitin conjugating
                  enzyme [Lycopersicon esculentum]
```

Seq. ID LIB3166-044-P1-K1-C2



```
Method
                  BLASTX
NCBI GI
                  q3033400
BLAST score
                  242
E value
                  2.0e-20
Match length
                  81
% identity
                  56
NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  225872
Seq. ID
                  LIB3166-044-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q3043656
BLAST score
                  239
E value
                  4.0e-20
Match length
                  86
                  52
% identity
NCBI Description (AB011138) KIAA0566 protein [Homo sapiens]
Seq. No.
                  225873
Seq. ID
                  LIB3166-044-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  q1657948
BLAST score
                  501
E value
                  7.0e-51
Match length
                  119
                  83
% identity
NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
Seq. No.
                  225874
                  LIB3166-044-P1-K1-D10
Seq. ID
                  BLASTX
                  g3901012
                  322
                  6.0e-30
Match length
                  88
% identity
                  68
```

Method

NCBI GI BLAST score E value

NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus

sylvatica]

225875 Seq. No.

LIB3166-044-P1-K1-D12 Seq. ID

BLASTX Method NCBI GI g2833388 BLAST score 455 E value 2.0e-45 Match length 126 71 % identity

NCBI Description GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR

>qi 629660 pir S43341 ADPqlucose--starch

glucosyltransferase (EC 2.4.1.21) precursor - cassava >gi 437042 emb CAA52273 (X74160) starch (bacterial

glycogen) synthase [Manihot esculenta]

Seq. No. 225876

LIB3166-044-P1-K1-D4 Seq. ID

Method BLASTX



```
NCBI GI
                   g1619321
BLAST score
                   378
E value
                   2.0e-36
Match length
                   123
                   57
% identity
NCBI Description (Y07563) hin1 [Nicotiana tabacum]
Seq. No.
                   225877
Seq. ID
                  LIB3166-044-P1-K1-D7
Method
                  BLASTX
NCBI GI
                   q4538911
BLAST score
                   227
E value
                   3.0e-19
Match length
                   61
                   79
% identity
NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   225878
Seq. ID
                   LIB3166-044-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g3901012
BLAST score
                   506
E value
                   2.0e-51
Match length
                   123
% identity
                   71
NCBI Description (AJ130885) xyloglucan endotransqlycosylase 1 [Fagus
                   sylvatica]
                   225879
Seq. No.
Seq. ID
                   LIB3166-044-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   g169363
BLAST score
                   218
E value
                   6.0e-18
Match length
                  43
% identity
                   81
NCBI Description (M75856) PVPR3 [Phaseolus vulgaris]
Seq. No.
                   225880
Seq. ID
                   LIB3166-044-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   g2982459
BLAST score
                   187
E value
                   4.0e-14
Match length
                   60
% identity
                   67
NCBI Description (AL022223) putative protein [Arabidopsis thaliana]
                   225881
Seq. No.
Seq. ID
                  LIB3166-044-P1-K1-E4
Method
                  BLASTX
NCBI GI
                   g2632252
BLAST score
                   433
E value
                   6.0e-43
Match length
                  119
% identity
```

32170

NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor]



82

% identity

225882

```
Seq. No.
Seq. ID
                  LIB3166-044-P1-K1-E6
Method
                  BLASTX
                  g1174622
NCBI GI
BLAST score
                   332
E value
                   4.0e-31
Match length
                   118
% identity
                   49
                  T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA)
NCBI Description
                   (CCT-THETA) >gi_1078408_pir__S56779 t-complex protein 1
                  homolog YJL008c - yeast (Saccharomyces cerevisiae)
                   >gi_1006721_emb_CAA89300_ (Z49284) ORF YJL008c
                   [Saccharomyces cerevisiae]
                   225883
Seq. No.
Seq. ID
                  LIB3166-044-P1-K1-E7
Method
                  BLASTX
NCBI GI
                   q4262250
BLAST score
                   341
                   4.0e-32
E value
Match length
                   102
% identity
                   74
NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]
                  225884
Seq. No.
Seq. ID
                  LIB3166-044-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q2414650
BLAST score
                   351
E value
                   2.0e-33
Match length
                   107
% identity
                   63
NCBI Description
                  (Z99296) 60s ribosomal protein L32 [Schizosaccharomyces
                  pombe]
Seq. No.
                   225885
Şeq. ID
                  LIB3166-044-P1-K1-E9
Method
                  BLASTX
NCBI GI
                   g2924784
BLAST score
                   405
E value
                   1.0e-39
Match length
                   127
% identity
                   30
NCBI Description
                  (AC002334) similar to jasmonate inducible protein
                   [Arabidopsis thaliana]
Seq. No.
                   225886
Seq. ID
                  LIB3166-044-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  q3775985
BLAST score
                   478
E value
                  3.0e-48
Match length
                  114
```

NCBI Description (AJ010456) RNA helicase [Arabidopsis thaliana]



```
225887
Seq. No.
Seq. ID
                   LIB3166-044-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   q4204575
BLAST score
                   383
                   5.0e-37
E value
                   113
Match length
                   65
% identity
NCBI Description
                  (AF098510) cytochrome b5 DIF-F [Petunia x hybrida]
                   225888
Seq. No.
                   LIB3166-044-P1-K1-F2
Seq. ID
Method
                   BLASTX
                   g3913047
NCBI GI
BLAST score
                   206
E value
                   4.0e-35
Match length
                   116
                   66
% identity
                  FLORAL HOMEOTIC PROTEIN APETALA1 (MADS C)
NCBI Description
                   >gi_1076477_pir__S52236 Saap1 protein - white mustard
                   >gi_609253_emb_CAA57233_ (X81480) Saap1 [Sinapis alba]
                   225889
Seq. No.
Seq. ID
                   LIB3166-044-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   q728744
BLAST score
                   442
                   6.0e-44
E value
                   127
Match length
                   72
% identity
NCBI Description
                   AUXIN-INDUCED PROTEIN PCNT115 >gi 100305 pir S16390
                   auxin-induced protein - common tobacco >gi_19799_emb_CAA39708_ (X56267) auxin-induced protein
                   [Nicotiana tabacum]
Seq. No.
                   225890
Seq. ID
                   LIB3166-044-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   q2282586
BLAST score
                   339
E value
                   7.0e-32
Match length
                   105
% identity
                   65
NCBI Description (U82011) methyltransferase [Prunus armeniaca]
Seq. No.
                   225891
Seq. ID
                   LIB3166-044-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   g3702327
BLAST score
                   177
E value
                   6.0e-13
Match length
                   97
% identity
                   47
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
```

Seq. ID LIB3166-044-P1-K1-G10



```
Method
                  BLASTX
NCBI GI
                  q3885338
BLAST score
                  228
E value
                   7.0e-19
Match length
                  107
                   40
% identity
NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]
Seq. No.
                  225893
                  LIB3166-044-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4335720
BLAST score
                  289
                   5.0e-26
E value
Match length
                  121
                   43
% identity
                  (AC006248) putative reverse transcriptase Tal-1
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   225894
Seq. ID
                  LIB3166-044-P1-K1-G12
Method
                  BLASTX
NCBI GI
                   q4454026
BLAST score
                   315
E value
                   4.0e-29
Match length
                   110
                   58
% identity
NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]
                   225895
Seq. No.
Seq. ID
                   LIB3166-044-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g4115373
BLAST score
                   169
E value
                   6.0e-12
Match length
                   129
% identity
                   6
                  (AC005967) receptor-like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   225896
                   LIB3166-044-P1-K1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4538913
BLAST score
                   381
E value
                   8.0e-37
Match length
                   94
                   78
% identity
NCBI Description (AL049482) putative protein [Arabidopsis thaliana]
Seq. No.
                   225897
                   LIB3166-044-P1-K1-G6
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g166878
BLAST score 178
E value 5.0e-13
Match length 100



% identity 23 (M95796) St12p protein [Arabidopsis thaliana] NCBI Description 225898

Seq. No. Seq. ID LIB3166-044-P1-K1-G8 Method BLASTX

NCBI GI g2505874 BLAST score 561 6.0e-58 E value Match length 118 90 % identity

(Y12776) putative kinase [Arabidopsis thaliana] NCBI Description

225899 Seq. No.

LIB3166-044-P1-K1-G9 Seq. ID

Method BLASTX NCBI GI q2078350 571 BLAST score 4.0e-59 E value 127 Match length 90 % identity

(U95923) transaldolase [Solanum tuberosum] NCBI Description

225900 Seq. No.

LIB3166-044-P1-K1-H1 Seq. ID

Method BLASTX NCBI GI g3024654 543 BLAST score 8.0e-56 E value 129 Match length 82 % identity

NCBI Description HOMEOBOX PROTEIN SHOOTMERISTEMLESS >gi\_2129615\_pir\_\_S68456

homeotic protein shootmeristemless - Arabidopsis thaliana >gi\_1167916 (U32344) class I knotted-like homeodomain containing protein; Method: conceptual translation
supplied by author [Arabidopsis thaliana]

>gi 1586022 prf 2202329A homeo domain protein [Arabidopsis

thaliana]

225901 Seq. No.

LIB3166-044-P1-K1-H10 Seq. ID

Method BLASTX NCBI GI g3355468 BLAST score 313 E value 2.0e-30 Match length 93 % identity

(AC004218) putative ribosomal protein L35 [Arabidopsis NCBI Description

thaliana]

Seq. No. 225902

Seq. ID LIB3166-044-P1-K1-H11

Method BLASTX · NCBI GI g1519241 BLAST score 205 E value 3.0e-25Match length 80

Match length

% identity

127

83



```
% identity
NCBI Description
                 (U65890) 10 kDa chaperonin [Brassica napus]
                  225903
Seq. No.
                  LIB3166-044-P1-K1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3046696
BLAST score
                  421
E value
                  2.0e-41
Match length
                  106
% identity
                  72
                 (AL022224) CTP synthase like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  225904
                  LIB3166-044-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4510422
BLAST score
                  170
E value
                  4.0e-12
Match length
                  73
% identity
                  42
                  (AC006929) putative zinc-finger protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  225905
                  LIB3166-044-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2827559
BLAST score
                  196
E value
                  4.0e-15
                  59
Match length
% identity
                  66
                  (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3292808 emb CAA19798 (AL031018) putative protein
                   [Arabidopsis thaliana]
                 . 225906
Seq. No.
Seq. ID
                  LIB3166-044-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g3914359
BLAST score
                  577
E value
                  8.0e-60
Match length
                  127
% identity
                  88
NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
                   (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                 - >gi 1928979 (U92656) phospholipase D [Vigna unguiculata]
                  225907
Seq. No.
                  LIB3166-044-P1-K1-H9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4567201
BLAST score
                  545
E value
                  5.0e-56
```

32175 '

NCBI Description (AC007168) putative aspartate aminotransferase [Arabidopsis



## thaliana]

```
Seq. No.
                  225908
Seq. ID
                  LIB3166-045-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g1420887
BLAST score
                  147
E value
                  2.0e-09
Match length
                  86
% identity
                  35
NCBI Description (U34334) non-specific lipid transfer-like protein
                  [Phaseolus vulgaris]
Seq. No.
                  225909
Seq. ID
                  LIB3166-045-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g2829880
BLAST score
                  454
E value
                  1.0e-50
Match length
                  120
% identity
NCBI Description (AC002396) glucose-6-phosphate 1-dehydrogenase [Arabidopsis
                  thaliana]
Seq. No.
                  225910
                  LIB3166-045-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3510262
BLAST score
                  134
E value
                  4.0e-15
Match length
                  58
% identity
                  69
NCBI Description (AC005310) NAM like protein [Arabidopsis thaliana]
Seq. No.
                  225911
Seq. ID
                  LIB3166-045-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g1076627
BLAST score
                  428
E value
                  2.0e-42
Match length
                  85
                  98
% identity
NCBI Description inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco
                  >gi_790479_emb_CAA58701_ (X83730) inorganic pyrophosphatase
                  [Nicotiana tabacum]
Seq. No.
                  225912
Seq. ID
                  LIB3166-045-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q729470
BLAST score
                  443
E value
                  4.0e-44
                  111
Match length
                  77
% identity
NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
                  (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
                  >gi 542089 pir JQ2272 formate dehydrogenase (EC 1.2.1.2)
```

Match length

% identity

95

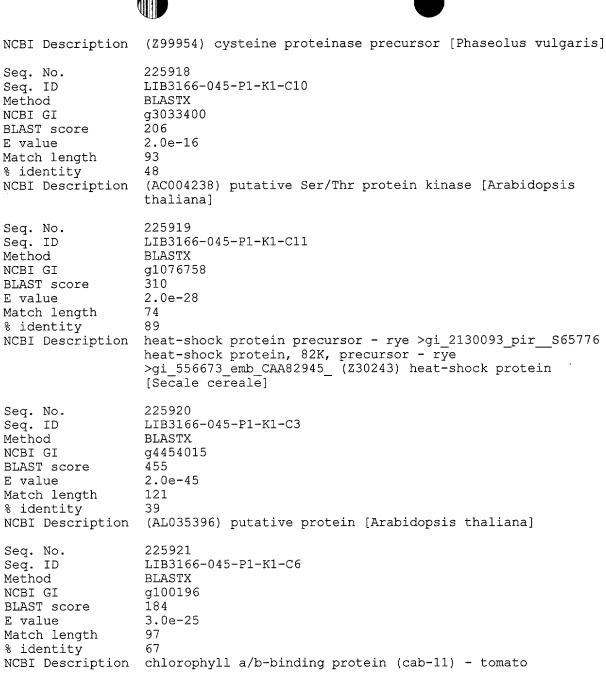
72



precursor, mitochondrial - potato >gi\_297798\_emb\_CAA79702\_
(Z21493) mitochondrial formate dehydrogenase precursor
[Solanum tuberosum]

225913 Seq. No. Seq. ID LIB3166-045-P1-K1-B2 Method BLASTX NCBI GI g2244841 BLAST score 174 E value 1.0e-12 Match length 119 % identity 42 NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana] Seq. No. 225914 Seq. ID LIB3166-045-P1-K1-B3 Method BLASTX NCBI GI g3434973 BLAST score 235 E value 9.0e-20 Match length 85 % identity 60 NCBI Description (AB008106) ethylene responsive element binding factor 4 [Arabidopsis thaliana] Seq. No. 225915 LIB3166-045-P1-K1-B5 Seq. ID Method BLASTX NCBI GI g2982303 BLAST score 216 E value 4.0e-33 Match length 122 % identity 59 NCBI Description (AF051236) hypothetical protein [Picea mariana] Seq. No. 225916 Seq. ID LIB3166-045-P1-K1-B8 Method BLASTX NCBI GI q3334323 BLAST score 512 E value 3.0e-52Match length 124 83 % identity NCBI Description GTP-BINDING PROTEIN SAR1A >gi 1314860 (U56929) Sar1 homolog [Arabidopsis thaliana] >gi 2104532 gb AAC78700.1 (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis thaliana] >gi 2104550 (AF001535) AGAA.4 [Arabidopsis thaliana] Seq. No. 225917 Seq. ID LIB3166-045-P1-K1-C1 Method BLASTX NCBI GI g2511693 BLAST score 300 E value 1.0e-29





Seq. No.

LIB3166-045-P1-K1-D2 Seq. ID

225922

BLASTX Method NCBI GI q3738257 BLAST score 303 E value 1.0e-27 Match length 65 92 % identity

(AB018410) cytosolic phosphoglycerate kinase 1 [Populus NCBI Description

nigra]

BLAST score

E value

352

1.0e-33



```
Seq. No.
                  225923
                  LIB3166-045-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1136298
BLAST score
                  145
                  4.0e-09
E value
Match length
                  32
                  84
% identity
NCBI Description (D61377) WIPK [Nicotiana tabacum]
Seq. No.
                  225924
                  LIB3166-045-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2459429
BLAST score
                  448
                  1.0e-44
E value
Match length
                  113
                  73
% identity
NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]
                  225925
Seq. No.
                  LIB3166-045-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3176707
BLAST score
                  165
E value
                  2.0e-11
Match length
                  54
                   57
% identity
                  (AC002392) putative proline-rich protein APG [Arabidopsis
NCBI Description
                   thaliana]
                   225926
Seq. No.
                  LIB3166-045-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3063471
BLAST score
                   309
                   2.0e-28
E value
                  87
Match length
                   64
% identity
NCBI Description (AC003981) F22013.33 [Arabidopsis thaliana]
                   225927
Seq. No.
                   LIB3166-045-P1-K1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                   g122006
BLAST score
                   246
E value
                   5.0e-21
                   73
Match length
                   67
% identity
NCBI Description HISTONE H2A >gi 81906 pir JQ1183 histone H2A - garden pea
                   225928
Seq. No.
Seq. ID
                   LIB3166-045-P1-K1-E2
                  BLASTX
Method
NCBI GI
                   g3550454
```



Match length 76 % identity (AF085820) alcohol dehydrogenase A [Gossypium barbadense] NCBI Description >gi 3550458 (AF085821) alcohol dehydrogenase A [Gossypium barbadense] >gi\_3551965 (AF085064) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_3551967 (AF085065) alcohol dehydrogenase A [Gossypium hirsutum] >gi 3551971 (AF085067) alcohol dehydrogenase A [Gossypium hirsutum] >gi 3551975 (AF085069) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_3551977 (AF085070) alcohol dehydrogenase A [Gossypium hirsutum] >gi 4140594 (AF090146) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140604 (AF090151) alcohol dehydrogenase A [Gossypium hirsutum] >gi 4140606 (AF090152) alcohol dehydrogenase A [Gossypium hirsutum] >gi 4140608 (AF090153) alcohol dehydrogenase A [Gossypium hirsutum] >qi 4140610 (AF090154) alcohol dehydrogenase A [Gossypium hirsutum] 225929 Seq. No. LIB3166-045-P1-K1-E5 Seq. ID Method BLASTX NCBI GI q3355480 BLAST score 301 2.0e-27 E value Match length 86 65 % identity (AC004218) Medicago nodulin N21-like protein [Arabidopsis NCBI Description thaliana] 225930 Seq. No. Seq. ID LIB3166-045-P1-K1-E6 Method BLASTX g3128215 NCBI GI BLAST score 183 1.0e-13 E value Match length 89 % identity 49 NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana] 225931 Seq. No. Seq. ID LIB3166-045-P1-K1-E9 Method BLASTX NCBI GI g2244749 BLAST score 160 E value 2.0e-14 Match length 98 % identity 51 NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana] 225932 Seq. No. LIB3166-045-P1-K1-F1 Seq. ID Method BLASTX g3047065 NCBI GI

Method BLASTX
NCBI GI g3047065
BLAST score 214
E value 2.0e-17
Match length 72
% identity 58

(AF058825) contains similarity to human OS-9 precurosor NCBI Description (GB:U41635) [Arabidopsis thaliana] 225933 Seq. No. LIB3166-045-P1-K1-F11 Seq. ID BLASTX Method NCBI GI g3694872 BLAST score 409 E value 4.0e-4087 Match length % identity 86 NCBI Description (AF092547) profilin [Ricinus communis] 225934 Seq. No. LIB3166-045-P1-K1-F3 Seq. ID BLASTX Method g2119353 NCBI GI BLAST score 241 2.0e-20 E value Match length 97 31 % identity NCBI Description calmodulin - moss (Physcomitrella patens) 225935 Seq. No. LIB3166-045-P1-K1-F4 Seq. ID BLASTX Method NCBI GI q836954 BLAST score 463

2.0e-46 E value 122 Match length 66 % identity

NCBI Description (U20948) receptor protein kinase [Ipomoea trifida]

225936 Seq. No.

Seq. ID LIB3166-045-P1-K1-F5

BLASTX Method NCBI GI g2129578 BLAST score 475 E value 7.0e-48 106 Match length % identity 84

NCBI Description dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi 928932 emb CAA89205 (Z49239) homolog of

dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi 1585435 prf 2124427B diamide resistance gene

[Arabidopsis thaliana]

225937 Seq. No.

Seq. ID LIB3166-045-P1-K1-F7

BLASTX Method q3033400 NCBI GI BLAST score 200 9.0e-16 E value Match length 66 % identity

(AC004238) putative Ser/Thr protein kinase [Arabidopsis NCBI Description

thaliana]

BLAST score

E value

600

2.0e-62



```
Seq. No.
                  225938
Seq. ID
                  LIB3166-045-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g3395436
BLAST score
                  232
E value
                  2.0e-19
Match length
                  90
% identity
                  49
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                  225939
Seq. No.
Seq. ID
                  LIB3166-045-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q4417286
BLAST score
                  346
E value
                  9.0e - 33
Match length
                  120
                  62
% identity
NCBI Description
                 (AC007019) putative shikimate kinase [Arabidopsis thaliana]
                  225940
Seq. No.
Seq. ID
                  LIB3166-045-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q2462077
BLAST score
                  172
E value
                  2.0e-12
Match length
                  121
% identity
                  31
NCBI Description (Y11871) Oxal protein [Arabidopsis thaliana]
Seq. No.
                  225941
                  LIB3166-045-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1220196
BLAST score
                  555
E value
                  3.0e-57
Match length
                  117
                  89
% identity
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.
                  225942
Seq. ID
                  LIB3166-045-P1-K1-G6
                  BLASTX
Method
NCBI GI
                  q2104446
BLAST score
                  137
                  1.0e-16
E value
                  62
Match length
                   66
% identity
NCBI Description (Z95396) WD-repeat protein [Schizosaccharomyces pombe]
Seq. No.
                  225943
Seq. ID
                  LIB3166-045-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q4062934
```

NCBI Description



```
Match length
% identity
                  90
NCBI Description (D88272) formate dehydrogenase [Hordeum vulgare]
                  225944
Seq. No.
Seq. ID
                  LIB3166-045-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g1220196
BLAST score
                  527
                  6.0e-54
E value
Match length
                  114
                  88
% identity
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.
                  225945
Seq. ID
                  LIB3166-045-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g2244847
BLAST score
                  351
E value
                  2.0e-33
Match length
                  122
                  57
% identity
NCBI Description (Z97337) hydroxyproline-rich glycoprotein homolog
                  [Arabidopsis thaliana]
Seq. No.
                  225946
Seq. ID
                  LIB3166-045-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g441457
BLAST score
                  530
E value
                  3.0e-54
Match length
                  99
                  98
% identity
NCBI Description (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
                  esculentum]
                  225947
Seq. No.
Seq. ID
                  LIB3166-045-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g4490732
BLAST score
                  336
E value
                  1.0e-31
                  125
Match length
                  62
% identity
NCBI Description (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
                  protein [Arabidopsis thaliana]
                  225948
Seq. No.
Seq. ID
                  LIB3166-045-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g4193388
BLAST score
                  354
E value
                  1.0e-33
                  87
Match length
% identity
                  80
```

brasiliensis]

(AF091455) translationally controlled tumor protein [Hevea

Seq. No.

Seq. ID

225954

LIB3166-046-P1-K1-B2



```
Seq. No.
                   225949
Seq. ID
                   LIB3166-045-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   g3913518
BLAST score
                   343
                   2.0e-32
E value
Match length
                   110
% identity
                   66
NCBI Description
                   3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE
                   (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE)
                   (DPNPASE) >gi_1103921 (U40433) 3'(2'),5'-bisphosphate nucleotidase [Arabidopsis thaliana]
Seq. No.
                   225950
                   LIB3166-046-P1-K1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1353352
BLAST score
                   321
E value
                   9.0e-30
Match length
                   85
% identity
                   75
NCBI Description (U31975) alanine aminotransferase [Chlamydomonas
                   reinhardtii]
Seq. No.
                   225951
                   LIB3166-046-P1-K1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1200256
BLAST score
                   423
E value
                   9.0e-42
Match length
                   106
% identity
                   74
NCBI Description (X90990) stpk1 protein kinase [Solanum tuberosum]
                   225952
Seq. No.
Seq. ID
                   LIB3166-046-P1-K1-A8
                   BLASTX
Method
NCBI GI
                   q4204300
BLAST score
                   163
E value
                   3.0e-11
Match length
                   61
                   57
% identity
NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]
                   225953
Seq. No.
                   LIB3166-046-P1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4049346
BLAST score
                   266
                   2.0e-23
E value
Match length
                   112
% identity
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
```



```
Method BLASTX

NCBI GI g543711

BLAST score 157

E value 1.0e-10

Match length 77

% identity 58

NCBI Description 14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3

protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140)

brain specific protein [Oryza sativa]
```

Seq. No. 225955 Seq. ID LIB3166-046-P1-K1-B4

Method BLASTX
NCBI GI g1523800
BLAST score 451
E value 5.0e-45
Match length 110
% identity 77

NCBI Description (Y07694) MAP kinase kinase alpha protein kinase

[Arabidopsis thaliana]

Seq. No. 225956
Seq. ID LIB3166

Seq. ID LIB3166-046-P1-K1-B5

Method BLASTX
NCBI GI g1711512
BLAST score 605
E value 4.0e-63
Match length 128
% identity 91

NCBI Description SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 2 (SRP54)

>gi\_1076577\_pir\_\_S51598 signal recognition particle 54K
protein - tomato (cv. UC82-B) >gi\_556902\_emb\_CAA84288\_
(Z34527) 54-kD signal recognition particle (SRP) specific

protein [Lycopersicon esculentum]

Seq. No. 225957

Seq. ID LIB3166-046-P1-K1-C1

Method BLASTX
NCBI GI g3318611
BLAST score 205
E value 3.0e-16
Match length 94
% identity 50

NCBI Description (AB016063) mitochondrial phosphate transporter [Glycine

max]

Seq. No. 225958

Seq. ID LIB3166-046-P1-K1-C12

Method BLASTX
NCBI GI 94468813
BLAST score 287
E value 8.0e-26
Match length 119
% identity 43

NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 225959

Method

NCBI GI

BLAST score

BLASTX

462

g3063396



```
LIB3166-046-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4490297
BLAST score
                  253
                  8.0e-22
E value
Match length
                  119
                   43
% identity
                  (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                  225960
Seq. No.
                  LIB3166-046-P1-K1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g115492
BLAST score
                  456
                  1.0e-45
E value
Match length
                  89
                   51
% identity
NCBI Description CALMODULIN-RELATED PROTEIN >gi_169205 (M80831)
                  calmodulin-related protein [Petunia hybrida]
Seq. No.
                   225961
                  LIB3166-046-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1617272
BLAST score
                   462
E value
                   2.0e-46
                  127
Match length
% identity
                   71
NCBI Description (Z72151) AMP-binding protein [Brassica napus]
Seq. No.
                   225962
                  LIB3166-046-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3901012
BLAST score
                   247
E value
                   9.0e-44
Match length
                   101
                   79
% identity
NCBI Description
                  (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
                   sylvatica]
Seq. No.
                   225963
Seq. ID
                   LIB3166-046-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   g1931647
BLAST score
                   148
E value
                   1.0e-15
Match length
                   54
                   81
% identity
                  (U95973) endomembrane protein EMP70 precusor isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   225964
Seq. ID
                  LIB3166-046-P1-K1-D9
```



2.0e-46 E value Match length 107 % identity 81 (AB012947) vcCyP [Vicia faba] NCBI Description 225965 Seq. No. Seq. ID LIB3166-046-P1-K1-E12 Method BLASTX NCBI GI q4249385 BLAST score 522 2.0e-53 E value Match length 106 89 % identity NCBI Description (AC005966) T2K10.11 [Arabidopsis thaliana] 225966 Seq. No. LIB3166-046-P1-K1-E4 Seq. ID BLASTX Method NCBI GI g2695711 BLAST score 200 1.0e-15 E value 77 Match length 56 % identity NCBI Description (AJ001370) cytochome b5 [Olea europaea] 225967 Seq. No. LIB3166-046-P1-K1-E5 Seq. ID BLASTX · Method NCBI GI g2440044 BLAST score 328 E value 7.0e-44Match length 107 86 % identity NCBI Description (AJ001293) major intrinsic protein PIPB [Craterostigma plantagineum] 225968 Seq. No. Seq. ID LIB3166-046-P1-K1-E6 Method BLASTX NCBI GI g1209756 BLAST score 247 E value 1.0e-23 Match length 101 % identity 57 NCBI Description (U43629) integral membrane protein [Beta vulgaris] 225969 Seq. No.

Seq. ID LIB3166-046-P1-K1-E8

Method BLASTX NCBI GI g3757514 BLAST score 378 1.0e-36 E value 74 Match length % identity

(AC005167) putative plasma membrane intrinsic protein NCBI Description

[Arabidopsis thaliana]

NCBI Description

tuberosum]



```
Seq. No.
                  225970
                  LIB3166-046-P1-K1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1706323
                  318
BLAST score
                  2.0e-29
E value
                  106
Match length
                  58
% identity
                  ORNITHINE DECARBOXYLASE (ODC) >gi_2118242 pir S64704
NCBI Description
                  ornithine decarboxylase (EC 4.1.1.17) - jimsonweed
                  >gi_871008_emb_CAA61121_ (X87847) ornithine decarboxylase
                   [Datura stramonium]
                  225971
Seq. No.
                  LIB3166-046-P1-K1-F1
Seq. ID
                  BLASTX
Method
                  q3522939
NCBI GI
BLAST score
                  276
                   2.0e-24
E value
                  79
Match length
                   65
% identity
                  (AC004411) putative squamosa-promoter binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   225972
Seq. No.
                   LIB3166-046-P1-K1-F10
Seq. ID
Method
                  BLASTX
                   a4104242
NCBI GI
                   197
BLAST score
                   2.0e-17
E value
Match length
                   68
                   71
% identity
                  (AF034266) palmitoyl-acyl carrier protein thioesterase
NCBI Description
                   [Gossypium hirsutum]
                   225973
Seq. No.
                   LIB3166-046-P1-K1-F12
Seq. ID
                   BLASTX
Method
                   g1669341
NCBI GI
BLAST score
                   334
                   3.0e-31
E value
Match length
                   127
                   52
% identity
NCBI Description (D45066) AOBP (ascorbate oxidase promoter-binding protein)
                   [Cucurbita maxima]
Seq. No.
                   225974
                   LIB3166-046-P1-K1-F5
Seq. ID
                   BLASTX
Method
                   g4103324
NCBI GI
                   316
BLAST score
E value
                   3.0e-29
                   67
Match length
                   96
 % identity
```

(AF022716) GDP-mannose pyrophosphorylase [Solanum

Seq. ID Method



```
Seq. No.
                  225975
Seq. ID
                  LIB3166-046-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q730583
BLAST score
                  235
                  1.0e-19
E value
Match length
                  62
% identity
                  74
NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P2 >gi_551267_emb_CAA55047_
                  (X78213) 60s acidic ribosomal protein P2 [Parthenium
                  argentatum]
                  225976
Seq. No.
                  LIB3166-046-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3258569
BLAST score
                  412
                  2.0e-40
E value
Match length
                  104
% identity
                  82
NCBI Description (U89959) Similar to yeast general negative regulator of
                  transcription subunit 1 [Arabidopsis thaliana]
                  225977
Seq. No.
                  LIB3166-046-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914435
BLAST score
                  164
                  1.0e-14
E value
Match length
                  63
% identity
                  68
NCBI Description PROFILIN 1 >gi_3021375_emb_CAA11756_ (AJ223982) profilin
                  [Glycine max]
                  225978
Seq. No.
                  LIB3166-046-P1-K1-G3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g486784
BLAST score
                  305
                  6.0e-28
E value
                  126
Match length
                  50
% identity
NCBI Description Golgi-associated particle 102K chain - human
Seq. No.
                  225979
                  LIB3166-046-P1-K1-G5
Seq. ID
                  BLASTX
Method
                  q4220537
NCBI GI
BLAST score
                  250
                  2.0e-21
E value
                  70
Match length
% identity
NCBI Description (AL035356) PsRT17-1 like protein [Arabidopsis thaliana]
Seq. No.
                  225980
```

32189

LIB3166-046-P1-K1-G6

BLASTX



```
g1710530
NCBI GI
                  571
BLAST score
                  4.0e-59
E value
                  115
Match length
                  87
% identity
                  60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256
NCBI Description
                  ribosomal protein L27a - Arabidopsis thaliana
                  >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein
                  L27a [Arabidopsis thaliana]
                  225981
Seq. No.
                  LIB3166-046-P1-K1-G7
Seq. ID
                  BLASTX
Method
                  g1235559
NCBI GI
                  216
BLAST score
                  2.0e-17
E value
                  113
Match length
                   43
% identity
                  (X96639) responsible for hereditary multiple exotosis [Mus
NCBI Description
                  musculus]
                   225982
Seq. No.
                  LIB3166-046-P1-K1-H1
Seq. ID
                   BLASTX
Method
                   g3747050
NCBI GI
                   425
BLAST score
                   6.0e-42
E value
                   106
Match length
                   78
% identity
                  (AF093540) ribosomal protein L26 [Zea mays]
NCBI Description
                   225983
Seq. No.
                   LIB3166-046-P1-K1-H5
Seq. ID
                   BLASTX
Method
                   q3759184
NCBI GI
                   131
BLAST score
E value
                   2.0e-10
                   128
Match length
% identity
                   (AB018441) phi-1 [Nicotiana tabacum]
NCBI Description
                   225984
Seq. No.
                   LIB3166-046-P1-K1-H8
Seq. ID
                   BLASTX
Method
                   g3702328
NCBI GI
                   502
BLAST score
E value
                   4.0e-51
Match length
                   115
 % identity
                   78
NCBI Description (AC005397) putative cytochrome b5 [Arabidopsis thaliana]
                   225985
 Seq. No.
                   LIB3166-046-P1-K1-H9
```

Seq. ID

BLASTX Method g1255951 NCBI GI 436 BLAST score 3.0e-43E value



```
105
Match length
                   76
% identity
                  (X96932) PS60 [Nicotiana tabacum]
NCBI Description
                   225986
Seq. No.
                   LIB3166-047-P1-K1-A1
Seq. ID
Method
                   BLASTX
                   g2764941
NCBI GI
BLAST score
                   396
                   1.0e-38
E value
Match length
                   100
                   68
% identity
                  (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                   expressed in meristematic region, and style [Arabidopsis
                   thaliana]
                   225987
Seq. No.
                   LIB3166-047-P1-K1-A2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3152603
                   335
BLAST score
                   2.0e-31
E value
                   128
Match length
                   47
% identity
                  (AC004482) unknown protein [Arabidopsis thaliana]
NCBI Description
                   225988
Seq. No.
                   LIB3166-047-P1-K1-A3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3298502
BLAST score
                   175
                   1.0e-12
E value
Match length
                   113
% identity
                   41
NCBI Description (AB015046) xylulokinase [Homo sapiens]
Seq. No.
                   225989
                   LIB3166-047-P1-K1-A5
Seq. ID
                   BLASTX
Method
                   g4510375
NCBI GI
BLAST score
                   363
                   1.0e-34
E value
Match length
                   114
% identity
                   65
                   (AC007017) putative homeotic protein BEL1 [Arabidopsis
NCBI Description
                   thaliana]
                   225990
Seq. No.
                   LIB3166-047-P1-K1-A7
Seq. ID
                   BLASTX
Method
```

NCBI GI g3738288 223 BLAST score 3.0e-18E value 104 Match length 47 % identity

(AC005309) auxin-responsive GH3-like protein [Arabidopsis NCBI Description

thaliana]

```
225991
Seq. No.
                  LIB3166-047-P1-K1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1946368
                  173
BLAST score
                  2.0e-12
E value
Match length
                  128
                  37
% identity
NCBI Description (U93215) unknown protein [Arabidopsis thaliana]
                  225992
Seq. No.
                  LIB3166-047-P1-K1-B10
Seq. ID
                  BLASTX
Method
                  q1906830
NCBI GI
BLAST score
                  151
                  3.0e-10
E value
                  77
Match length
                  52
% identity
NCBI Description (Y11829) heat shock protein [Arabidopsis thaliana]
                  225993
Seq. No.
                  LIB3166-047-P1-K1-B12
Seq. ID
                BLASTX
Method
                  g1709101
NCBI GI
BLAST score
                  242
E value
                  2.0e-20
                  109
Match length
                  48
% identity
NCBI Description MRP PROTEIN HOMOLOG >gi_1001155 dbj BAA10297 (D64001) put.
                  ATPase [Synechocystis sp.]
                  225994
Seq. No.
                  LIB3166-047-P1-K1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3892057
BLAST score
                   471
                   2.0e-47
E value
Match length
                  120
                   38
% identity
NCBI Description (AC002330) hypothetical protein [Arabidopsis thaliana]
```

Seq. No. 225995

Seq. ID LIB3166-047-P1-K1-B3

Method BLASTX
NCBI GI 94309698
BLAST score 183
E value 1.0e-13
Match length 74
% identity 47

NCBI Description (AC006266) putative glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 225996

Seq. ID LIB3166-047-P1-K1-B4

Method BLASTX NCBI GI 94455184



```
BLAST score
E value
                  7.0e - 38
Match length
                  124
                  62
% identity
                  (AL035521) extra-large G-protein-like [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  225997
                  LIB3166-047-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131399
                  160
BLAST score
                  8.0e-19
E value
Match length
                  90
% identity
                  62
                 PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (LIGHT INDUCIBLE
NCBI Description
                  TISSUE-SPECIFIC ST-LS1 PROTEIN) >gi_82277_pir__S00411
                  photosystem II 10K protein precursor - potato
                  >gi 21489 emb CAA28450 (X04753) ST-LS1 protein [Solanum
                  tuberosum]
Seq. No.
                  225998
                  LIB3166-047-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q731285
BLAST score
                  164
E value
                  2.0e-11
Match length
                  109
% identity
                  38
                 HYPOTHETICAL 27.1 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION
NCBI Description
                  >gi_1077483_pir__S51970 hypothetical protein YAL049c -
                  yeast (Saccharomyces cerevisiae) >gi 595535 (U12980)
                  Yal049cp [Saccharomyces cerevisiae]
Seq. No.
                  225999
Seq. ID
                  LIB3166-047-P1-K1-C10
                  BLASTX
Method
NCBI GI
                  g3367632
BLAST score
                159
                  5.0e-11
E value
                  57
Match length
                  42
% identity
NCBI Description (AJ000539) phosphatidylinositol synthase [Arabidopsis
                  thaliana]
                  226000
Seq. No.
Seq. ID
                  LIB3166-047-P1-K1-C2
```

Method BLASTX NCBI GI g1172664 BLAST score 217 E value 1.0e-17 Match length 47 % identity 91

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)

>gi 419791 pir S31165 photosystem I chain III precursor -Flaveria trinervia >gi 298482 bbs 127083 photosystem I



reaction center subunit III, PSI-RC PsaF [Flaveria trinervia, Peptide, 232 aa] >gi\_168173 (M83119) photosystem I subunit III [Flaveria trinervia]

Seq. No. 226001 Seq. ID LIB3166-047-P1-K1-C3

Method BLASTX
NCBI GI g1076748
BLAST score 219
E value 8.0e-18
Match length 76
% identity 28

NCBI Description major intrinsic protein - rice >gi\_440869\_dbj\_BAA04257\_

(D17443) major intrinsic protein [Oryza sativa]

Seq. No. 226002

Seq. ID LIB3166-047-P1-K1-C4

Method BLASTX
NCBI GI g3885884
BLAST score 398
E value 7.0e-54
Match length 127
% identity 77

NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No. 226003

Seq. ID LIB3166-047-P1-K1-C7

Method BLASTX
NCBI GI g1171866
BLAST score 373
E value 5.0e-36
Match length 105

% identity 69

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR

(COMPLEX I-20KD) (CI-20KD) >gi\_629601\_pir\_\_S48826 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild cabbage >gi\_562282\_emb\_CAA57725\_ (X82274) PSST subunit of

NADH: ubiquinone oxidoreductase [Brassica oleracea]

Seq. No. 226004

Seq. ID LIB3166-047-P1-K1-C8

Method BLASTX
NCBI GI g4481934
BLAST score 163
E value 3.0e-11
Match length 105
% identity 14

NCBI Description (AL035640) CDA peptide synthetase I [Streptomyces

coelicolor]

Seq. No. 226005

Seq. ID LIB3166-047-P1-K1-D1

Method BLASTX
NCBI GI g4099914
BLAST score 296
E value 7.0e-27
Match length 81



% identity (U91857) ethylene-responsive element binding protein NCBI Description homolog [Stylosanthes hamata] 226006 Seq. No. LIB3166-047-P1-K1-D11 Seq. ID Method BLASTX NCBI GI q1531758 BLAST score 408 5.0e-40E value Match length 81 % identity 86 (X98772) AUX1 [Arabidopsis thaliana] >gi\_3335360 (AC003028) NCBI Description unknown protein [Arabidopsis thaliana] 226007 Seq. No. LIB3166-047-P1-K1-D12 Seq. ID Method BLASTX NCBI GI q4558672 BLAST score 185 7.0e-14E value 53 Match length 66 % identity NCBI Description (AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis thaliana] 226008 Seq. No. LIB3166-047-P1-K1-D2 Seq. ID Method BLASTX NCBI GI q3128228 BLAST score 467 E value 6.0e-47Match length 96 90 % identity NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi 3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana] 226009 Seq. No. LIB3166-047-P1-K1-D9 Seq. ID Method BLASTX NCBI GI g3024871 BLAST score 372 E value 8.0e-36 Match length 116 % identity 57 HYPOTHETICAL 77.3 KD PROTEIN SLL0005 NCBI Description >gi 1001579 dbj BAA10206 (D64000) ABC1-like [Synechocystis sp.]

226010 Seq. No.

Seq. ID LIB3166-047-P1-K1-E1

BLASTX Method NCBI GI g1632831 BLAST score 442 E value 5.0e-44100 Match length



```
% identity
                  (Z49698) orf [Ricinus communis]
NCBI Description
                  226011
Seq. No.
                  LIB3166-047-P1-K1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1703375
BLAST score
                  214
                  5.0e-37
E value
                  107
Match length
                  87
% identity
                  ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420)
NCBI Description
                  DcARF1 [Daucus carota]
                  226012
Seq. No.
                  LIB3166-047-P1-K1-E11
Seq. ID
                  BLASTX
Method
                  g2832680
NCBI GI
                  435
BLAST score
                  4.0e-43
E value
                  105
Match length
                  38
% identity
NCBI Description (AL021712) putative protein [Arabidopsis thaliana]
                  226013
Seq. No.
                  LIB3166-047-P1-K1-E3
Seq. ID
                  BLASTX
Method
                  g2213592
NCBI GI
BLAST score
                  281
                  4.0e-25
E value
Match length
                  105
% identity
                  30
NCBI Description (AC000348) T7N9.12 [Arabidopsis thaliana]
                  226014
Seq. No.
Seq. ID
                  LIB3166-047-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  q1827809
                  361
BLAST score
                  1.0e-34
E value
Match length
                  101
% identity
                   75
NCBI Description Chain A, Bovine Mitochondrial F1-Atpase Complexed With
                  Aurovertin B >gi_1827810 pdb 1COW B Chain B, Bovine
                  Mitochondrial F1-Atpase Complexed With Aurovertin B
                   >gi_1827811_pdb_1COW_C Chain C, Bovine Mitochondrial
                   F1-Atpase Complexed With Aurovertin B
                   >gi_1942368_pdb_1EFR_A Chain A, Bovine Mitochondrial
                   F1-Atpase Complexed With The Peptide Antibiotic Efrapeptin
                   >gi_1942369_pdb_1EFR_B Chain B, Bovine Mitochondrial
                   F1-Atpase Complexed With The Peptide Antibiotic Efrapeptin
                   >gi 1942370 pdb 1EFR_C Chain C, Bovine Mitochondrial
                   F1-Atpase Complexed With The Peptide Antibiotic Efrapeptin
```

Seq. No. 226015

Seq. ID LIB3166-047-P1-K1-E8

Method BLASTX



```
q3947735
NCBI GI
                  257
BLAST score
E value
                  2.0e-22
Match length
                  105
% identity
                  49
NCBI Description (AJ009720) NL27 [Solanum tuberosum]
Seq. No.
                  226016
Seq. ID
                  LIB3166-047-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q4335722
BLAST score
                  106
E value
                  5.0e-10
Match length
                  109
% identity
                  47
NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]
                  226017
Seq. No.
Seq. ID
                  LIB3166-047-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  q2462832
BLAST score
                  265
E value
                  3.0e-23
Match length
                  75
% identity
NCBI Description (AF000657) similar to Bacillus CotA [Arabidopsis thaliana]
Seq. No.
                  226018
                  LIB3166-047-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4103324
BLAST score
                  608
E value
                  2.0e-63
Match length
                  127
% identity
                  91
                  (AF022716) GDP-mannose pyrophosphorylase [Solanum
NCBI Description
                  tuberosum]
                  226019
Seq. No.
                  LIB3166-047-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245066
BLAST score
                  336
E value
                  1.0e-31
                  118
Match length
% identity
                   60
NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]
                  226020
Seq. No.
                  LIB3166-047-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2558654
```

Method BLASTX
NCBI GI g2558654
BLAST score 167
E value 9.0e-12
Match length 87
% identity 47

NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]



```
226021
Seq. No.
                  LIB3166-047-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g282881
BLAST score
                  214
                   3.0e-17
E value
                  86
Match length
                   48
% identity
                  receptor-like protein kinase precursor - Arabidopsis
NCBI Description
                   thaliana >gi_166846 (M84658) receptor-like protein kinase
                   [Arabidopsis thaliana]
                   226022
Seq. No.
                  LIB3166-047-P1-K1-G10
Seq. ID
Method
                  BLASTX
                   q4580575
NCBI GI
BLAST score
                   410
                   8.0e-42
E value
Match length
                   125
% identity
                   67
                  (AF082176) auxin response factor 9 [Arabidopsis thaliana]
NCBI Description
                   226023
Seq. No.
                   LIB3166-047-P1-K1-G11
Seq. ID
Method
                   BLASTX
                   a4033469
NCBI GI
                   286
BLAST score
                   9.0e-26
E value
Match length
                   117
% identity
                   53
                   ARGININE/SERINE-RICH SPLICING FACTOR RSP41
NCBI Description
                   >gi 1707370 emb CAA67799 (X99436) splicing factor
                   [Arabidopsis thaliana]
Seq. No.
                   226024
                   LIB3166-047-P1-K1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2351580
BLAST score
                   432
E value
                   7.0e-43
                   93
Match length
% identity
                   86
                  (U82433) thymidine diphospho-glucose 4-6-dehydratase
NCBI Description
                   homolog [Prunus armeniaca]
Seq. No.
                   226025
                   LIB3166-047-P1-K1-G3
Seq. ID
                   BLASTX
Method
                   q1171978
NCBI GI
BLAST score
                   547
                   3.0e-56
E value
Match length
                   126
                   22
% identity
```

(PABP 2) >gi 304109 (L19418) poly(A)-binding protein

[Arabidopsis thaliana] >gi\_2911051\_emb\_CAA17561\_ (AL021961)

NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)



## poly(A)-binding protein [Arabidopsis thaliana]

```
Seq. No.
                  226026
                  LIB3166-047-P1-K1-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g829294
                  273
BLAST score
E value
                  3.0e-24
Match length
                  62
                  84
% identity
                 (X67756) ferritin 5 [Vigna unguiculata]
NCBI Description
                  226027
Seq. No.
                  LIB3166-047-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3522933
BLAST score
                  534
                  9.0e-55
E value
Match length
                  110
% identity
                  92
                  (AC004411) putative anion exchange protein 3 [Arabidopsis
NCBI Description
                  thaliana]
                  226028
Seq. No.
                  LIB3166-047-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267122
BLAST score
                  442
                  6.0e-44
E value
Match length
                  104
                  78
% identity
                  THIOREDOXIN H-TYPE (TRX-H) >gi 478400_pir__JQ2242
NCBI Description
                   thioredoxin h - Arabidopsis thaliana
                   >gi 16552 emb CAA78462 (Z14084) Thioredoxin H [Arabidopsis
                   thaliana] >gi 1388080 (U35827) thioredoxin h [Arabidopsis
                  thaliana]
                   226029
Seq. No.
Seq. ID
                  LIB3166-047-P1-K1-H10
                  BLASTX
Method
                   g3687652
NCBI GI
                   590
BLAST score
                   2.0e-61
E value
                  126
Match length
% identity
NCBI Description (AF047352) rubisco activase precursor [Datisca glomerata]
                   226030
Seq. No.
Seq. ID
                   LIB3166-047-P1-K1-H12
Method
                  BLASTX
NCBI GI
                   g3821280
                   559
BLAST score
                   1.0e-57
E value
Match length
                   116
% identity
                  (AJ009952) asparagine synthetase type II [Phaseolus
NCBI Description
                   vulgaris]
```



```
226031
Seq. No.
                  LIB3166-047-P1-K1-H4
Seq. ID
                  BLASTX
Method
                  g2494264
NCBI GI
BLAST score
                  247
                  4.0e-21
E value
Match length
                  97
% identity
                  52
                  HYPOTHETICAL 66.0 KD GTP-BINDING PROTEIN SLR1105
NCBI Description
                  >gi 1651837 dbj BAA16764_ (D90900) elongation factor EF-G
                  [Synechocystis sp.]
Seq. No.
                  226032
                  LIB3166-047-P1-K1-H5
Sea. ID
                  BLASTX
Method
                  q2832672
NCBI GI
                  450
BLAST score
E value
                  6.0e-45
Match length
                  110
% identity
                  80
NCBI Description (AL021712) nifU-like protein [Arabidopsis thaliana]
Seq. No.
                  226033
Seq. ID
                  LIB3166-047-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q2662415
                  173
BLAST score
                  2.0e-12
E value
Match length
                  56
                  54
% identity
NCBI Description (U97494) metallothionein-like protein [Prunus armeniaca]
                  226034
Seq. No.
                  LIB3166-047-P1-K1-H9
Seq. ID
                  BLASTX
Method
                  q4545262
NCBI GI
BLAST score
                  259
                  2.0e-22
E value
Match length
                  61
                  72
% identity
NCBI Description (AF118230) metallothionein-like protein [Gossypium
                  hirsutum]
Seq. No.
                   226035
Seq. ID
                  LIB3166-048-P1-K1-A11
                  BLASTX
Method
NCBI GI
                  g728905
BLAST score
                  283
                   2.0e-25
E value
Match length
                  128
% identity
                   48
NCBI Description PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC
```

>gi 171114 (L01795) ATPase [Saccharomyces cerevisiae] >gi 595560 (U12980) Drs2p: Membrane spanning

RETICULUM CA2+-ATPASE) >gi 1078206 pir\_\_S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae)



Ca-ATPase(P-type), member of the cation transport(E1-E2)
ATPase [Saccharomyces cerevisiae]

 Seq. No.
 226036

 Seq. ID
 LIB3166-048-P1-K1-A12

 Method
 BLASTX

Method BLASTX
NCBI GI g1531758
BLAST score 455
E value 2.0e-45
Match length 92
% identity 87

NCBI Description (X98772) AUX1 [Arabidopsis thaliana] >gi\_3335360 (AC003028)

unknown protein [Arabidopsis thaliana]

Seq. No. 226037

Seq. ID LIB3166-048-P1-K1-A3

Method BLASTX
NCBI GI g2979688
BLAST score 192
E value 1.0e-14
Match length 43
% identity 93

NCBI Description (AF035619) pyridoxine biosynthesis protein [Cercospora

nicotianae]

Seq. No. 226038

Seq. ID LIB3166-048-P1-K1-A5

Method BLASTX
NCBI GI 94559330
BLAST score 285
E value 1.0e-25
Match length 127
% identity 47

NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 226039

Seq. ID LIB3166-048-P1-K1-A7

Method BLASTX
NCBI GI g3355468
BLAST score 375
E value 3.0e-36
Match length 103
% identity 79

NCBI Description (AC004218) putative ribosomal protein L35 [Arabidopsis

thaliana]

Seq. No. 226040

Seq. ID LIB3166-048-P1-K1-A9

Method BLASTX
NCBI GI g3785986
BLAST score 231
E value 9.0e-20
Match length 52
% identity 83

NCBI Description (AC005560) RGA1 protein [Arabidopsis thaliana]

Seq. No. 226041



Seq. ID LIB3166-048-P1-K1-B10 Method BLASTX NCBI GI g3023858 BLAST score 612 E value 6.0e-64 Match length 120 % identity 50 NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi\_1256608 (U44850) G protein beta subunit [Glycine max] Seq. No. 226042

Seq. ID LIB3166-048-P1-K1-B11 Method BLASTX NCBI GI g3560170 523

BLAST score E value 2.0e-53 Match length 129 % identity 79

NCBI Description (AL031525) 26s protease regulatory subunit S10b

[Schizosaccharomyces pombe]

Seq. No. 226043

Seq. ID LIB3166-048-P1-K1-B4

Method BLASTX NCBI GI g4204265 BLAST score 461 E value 3.0e-46 Match length 123 % identity 69

NCBI Description (AC005223) 45643 [Arabidopsis thaliana]

Seq. No. 226044

Seq. ID LIB3166-048-P1-K1-B8

Method BLASTX NCBI GI g1477428 BLAST score 533 E value 1.0e-54 Match length 119 % identity 84

NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]

Seq. No. 226045

Seq. ID LIB3166-048-P1-K1-C1

Method BLASTX NCBI GI g1498053 BLAST score 459 E value 6.0e-46 Match length 125 % identity 74

NCBI Description (U64436) ribosomal protein S8 [Zea mays]

Seq. No. 226046

Seq. ID LIB3166-048-P1-K1-C11

Method BLASTX NCBI GI q3328122 BLAST score 436

```
E value
                     2.0e-43
  Match length
                     94
  % identity
  NCBI Description (AF073473) phosphoglycerate kinase precursor [Solanum
                    tuberosum]
  Seq. No.
                    226047
                    LIB3166-048-P1-K1-C12
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g1084372
  BLAST score
                    561
  E value
                    6.0e-58
  Match length
                    120
  % identity
                    91
  NCBI Description glyceraldehyde-3-phosphate dehydrogenase (NADP+) (EC
                    1.2.1.9) - garden pea
  Seq. No.
                    226048
  Seq. ID
                    LIB3166-048-P1-K1-C4
  Method
                    BLASTX
  NCBI GI
                    g3201615
  BLAST score
                    306
  E value
                    5.0e-28
  Match length
                    94
  % identity
                    65
  NCBI Description (AC004669) unknown protein [Arabidopsis thaliana]
Seq. No.
                    226049
  Seq. ID
                    LIB3166-048-P1-K1-C9
 Method
                    BLASTX
 NCBI GI
                    g3868758
 BLAST score
                    202
 E value
                    4.0e-16
 Match length
                    92
  % identity
 NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
 Seq. No.
                    226050
 Seq. ID
                    LIB3166-048-P1-K1-D12
 Method
                    BLASTX
 NCBI GI
                    q543650
 BLAST score
                    275
 E value
                    2.0e-24
 Match length
                    69
 % identity
                    68
 NCBI Description P48h-10 protein precursor - Zinnia elegans (cv. Envy)
```

Seq. No. 226051

Seq. ID LIB3166-048-P1-K1-D2

Method BLASTX
NCBI GI 94103635
BLAST score 192
E value 1.0e-14
Match length 97
% identity 45

NCBI Description (AF026538) ABA-responsive protein [Hordeum vulgare]



```
Seq. No.
                   226052
Seq. ID
                  LIB3166-048-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q4263711
BLAST score
                  410
E value
                  3.0e-40
Match length
                  121
% identity
NCBI Description (AC006223) putative CCR4-associated transcription factor
                  [Arabidopsis thaliana]
Seq. No.
                  226053
Seq. ID
                  LIB3166-048-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g2702270
BLAST score
                  309
                  2.0e-28
E value
Match length
                  100
% identity
NCBI Description (AC003033) unknown protein [Arabidopsis thaliana]
Seq. No.
                  226054
Seq. ID
                  LIB3166-048-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g3421087
BLAST score
                  425
E value
                  6.0e-42
Match length
                  87
% identity
                  98
NCBI Description (AF043524) 20S proteasome subunit PAE1 [Arabidopsis
                  thaliana]
Seq. No.
                  226055
Seq. ID
                  LIB3166-048-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g4559382
BLAST score
                  157
E value
                  1.0e-10
Match length
                  70
% identity
                  47
                 (AC006526) putative DNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  226056
Seq. ID
                  LIB3166-048-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g4204265
BLAST score
                  268
E value
                  1.0e-23
Match length
                  99
% identity
                  56
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]
```

Seq. No. 226057

Seq. ID LIB3166-048-P1-K1-F1

Method BLASTX NCBI GI g4539423



. BLAST score 513 E value 3.0e-52 Match length 124 % identity 78

NCBI Description (AL049171) pyrophosphate-dependent phosphofructo-1-kinase

[Arabidopsis thaliana]

Seq. No. 226058

Seq. ID LIB3166-048-P1-K1-F3

Method BLASTX NCBI GI q1702983 BLAST score 237 E value 6.0e-20 Match length 85 % identity 54

NCBI Description AUXIN-REPRESSED 12.5 KD PROTEIN >gi 99855 pir S11850

hypothetical protein - garden strawberry >gi\_22573\_emb\_CAA36676\_ (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi\_927034 (L44142) auxin-repressed protein

[Fragaria ananassa]

Seq. No. 226059

Seq. ID LIB3166-048-P1-K1-G10

Method BLASTX NCBI GI g2213877 BLAST score 545 E value 5.0e-56 Match length 107 95 % identity

NCBI Description (AF003197) glutamine synthetase [Hevea brasiliensis]

Seq. No. 226060

Seq. ID LIB3166-048-P1-K1-G12

Method BLASTX NCBI GI g1621268 BLAST score 489 E value 2.0e-49 Match length 121 % identity 71

NCBI Description (Z81012) unknown [Ricinus communis]

Seq. No. 226061

Seq. ID LIB3166-048-P1-K1-G2

Method BLASTX NCBI GI g3153207 BLAST score 174 E value 1.0e-12 Match length 124 % identity

NCBI Description (AF001949) ATHB-12 [Arabidopsis thaliana]

Seq. No. 226062

Seq. ID LIB3166-048-P1-K1-G3

Method BLASTX q3024871 NCBI GI BLAST score 191 E value 2.0e-14



```
Match length
                    116
% identity
                    36
NCBI Description
                    HYPOTHETICAL 77.3 KD PROTEIN SLL0005
                    >gi_1001579 dbj BAA10206 (D64000) ABC1-like [Synechocystis
                    sp.]
                    226063
Seq. No.
Seq. ID
                    LIB3166-048-P1-K1-G4
Method
                    BLASTX
NCBI GI
                    q1946367
BLAST score
                    110
E value
                    1.0e-10
Match length
                    53
% identity
                    68
NCBI Description (U93215) unknown protein [Arabidopsis thaliana]
Seq. No.
                    226064
Seq. ID
                   LIB3166-048-P1-K1-G5
Method
                   BLASTX
NCBI GI
                    g1838976
BLAST score
                    165
E value
                    2.0e-11
Match length
                   78
% identity
                    54
NCBI Description (X73635) vsf-1 [Lycopersicon esculentum]
Seq. No.
                    226065
Seq. ID
                   LIB3166-048-P1-K1-G9
Method
                   BLASTX
NCBI GI
                    g2494034
BLAST score
                   163
E value
                    6.0e-21
Match length
                   89
% identity
                    58
NCBI Description
                   DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG
                   KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase - Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787)
                   diacylglycerol kinase [Arabidopsis thaliana]
Seq. No.
                   226066
Seq. ID
                   LIB3166-048-P1-K1-H10
Method
                   BLASTX
NCBI GI
                   g4545262
BLAST score
                   239
E value
                   4.0e-20
Match length
                   44
% identity
                   100
NCBI Description
                   (AF118230) metallothionein-like protein [Gossypium
                   hirsutum]
Seq. No.
                   226067
```

Seq. ID LIB3166-048-P1-K1-H11

Method BLASTX NCBI GI g1362009 BLAST score 480 E value 2.0e-48 Match length 119



% identity

NCBI Description ubiquitin-like protein 7 - Arabidopsis thaliana

226068

Seq. ID

LIB3166-048-P1-K1-H2

Method NCBI GI BLASTX

BLAST score

g4128133 274

E value

3.0e-24

Match length

119 45

% identity

NCBI Description (AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]

Seq. No.

226069

Seq. ID

LIB3166-048-P1-K1-H5

Method NCBI GI

BLASTX g1351408

BLAST score

207

E value Match length 2.0e-16

% identity

61 66

NCBI Description

VACUOLAR PROCESSING ENZYME PRECURSOR (VPE)

>gi\_1076563\_pir\_\_S51117 cystein proteinase - sweet orange >gi\_633185\_emb\_CAA87720\_ (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi 1588548 prf 2208463A

vascular processing protease [Citrus sinensis]

Seq. No.

226070

Seq. ID

LIB3166-048-P1-K1-H7

Method NCBI GI

BLASTX g3024148

BLAST score

313

E value

5.0e-29

Match length

77

% identity

79

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE

ADENOSYLTRANSFÈRASE 3) (ADOMET SYNTHETASE 3)

>gi\_1655580\_emb\_CAA95858\_ (Z71273) S-adenosyl-L-methionine

synthetase 3 [Catharanthus roseus]

Seq. No.

226071

Seq. ID Method

LIB3166-049-P1-K1-A10

BLASTX

NCBI GI

g3953471

BLAST score

271

E value

2.0e-24

Match length

74

% identity

NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No.

226072

Seq. ID

LIB3166-049-P1-K1-A12

Method

BLASTX

NCBI GI

g2541876

BLAST score

219

E value

2.0e-18

Match length

110



% identity NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum] Seq. No. 226073 Seq. ID LIB3166-049-P1-K1-A2 Method BLASTX NCBI GI g1943751 BLAST score 458 E value 6.0e-46Match length 103 % identity 85 NCBI Description (U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence >gi 2078292 (U96455) ER-type Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana] Seq. No. 226074 Seq. ID LIB3166-049-P1-K1-A4 Method BLASTX NCBI GI g4056432 BLAST score 432 E value 7.0e-43Match length 113 % identity 68 NCBI Description (AC005990) Similar to gi\_2245014 glucosyltransferase homolog from Arabidopsis thaliana chromosome 4 contig gb\_Z97341. ESTs gb\_T20778 and gb AA586281 come from this gene. [Arabidopsis thaliana] Seq. No. 226075 Seq. ID LIB3166-049-P1-K1-A5 Method BLASTX NCBI GI q3953471 BLAST score 116 E value 6.0e-11 Match length 65 % identity 62 NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana] Seq. No. 226076 Seq. ID LIB3166-049-P1-K1-A7 BLASTX Method NCBI GI g1263291 BLAST score 311 E value 1.0e-28 Match length 60 % identity NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum] Seq. No. 226077 Seq. ID LIB3166-049-P1-K1-A9

Method BLASTX NCBI GI g3184289 BLAST score 189 E value 2.0e-14 Match length 44 % identity 80



```
NCBI Description (AC004136) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  226078
Seq. ID
                  LIB3166-049-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g2245094
BLAST score
                  168
E value
                  5.0e-20
Match length
                 80
% identity
                  65
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  226079
Seq. ID
                 LIB3166-049-P1-K1-B10
Method
                 BLASTX
NCBI GI
                  g220838
BLAST score
                 204
E value
                  4.0e-16
Match length
                 118
% identity
                  40
NCBI Description (D10655) dihydrolipoamide acetyltransferase [Rattus rattus]
Seq. No.
                  226080
Seq. ID
                 LIB3166-049-P1-K1-B11
Method
                 BLASTX
NCBI GI
                 q4538967
BLAST score
                 414
E value
                 9.0e-41
Match length
                 109
                 77
% identity
NCBI Description (AL049488) major intrinsic protein (MIP)-like [Arabidopsis
                 thaliana]
Seq. No.
                 226081
Seq. ID
                 LIB3166-049-P1-K1-B12
Method
                 BLASTX
NCBI GI
                 g2497702
BLAST score
                 173
E value
                 2.0e-12
Match length
                 121
% identity
                 36
NCBI Description OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR
                 Citrobacter freundii >gi_717136 (U21727) lipocalin
                 precursor [Citrobacter freundii]
Seq. No.
                 226082
Seq. ID
                 LIB3166-049-P1-K1-B3
                 BLASTX
                 g3759184
```

Method

NCBI GI BLAST score 300 2.0e-27 E value Match length 97 % identity 59

NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 226083

Method

NCBI GI

BLAST score



```
Seq. ID
                   LIB3166-049-P1-K1-B7
 Method
                   BLASTX
 NCBI GI
                   g2245125
 BLAST score
                   163
 E value
                   2.0e-11
Match length
                   45
 % identity
                   64
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   226084
Seq. ID
                  LIB3166-049-P1-K1-B9
Method
                  BLASTX
NCBI GI
                   g2465012
BLAST score
                   410
E value
                   4.0e-42
Match length
                   107
% identity
                   88
NCBI Description (AJ001447) caffeoyl-CoA 3-O-methyltransferase [Fragaria
                   vesca]
Seq. No.
                   226085
Seq. ID
                  LIB3166-049-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g4098128
BLAST score
                  388
E value
                   2.0e-41
Match length
                  109
% identity
                  83
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
Seq. No.
                  226086
Seq. ID
                  LIB3166-049-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q2500550
BLAST score
                  147
E value
                  2.0e-09
Match length
                  48
% identity
                  62
NCBI Description RIBONUCLEASE III (RNASE III) >gi_2313785_gb_AAD07725.1_
                   (AE000579) ribonuclease III (rnc) [Helicobacter pylori]
                  26695]
Seq. No.
                  226087
Seq. ID
                  LIB3166-049-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  q710308
BLAST score
                  163
E value
                  8.0e-12
Match length
                  47
% identity
                  68
NCBI Description (U11693) victorin binding protein [Avena sativa]
Seq. No.
                  226088
Seq. ID
```

32210

LIB3166-049-P1-K1-C6

BLASTX

418

q4102600



E value 3.0e-41 Match length 117 74

NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.

226089

Seq. ID

LIB3166-049-P1-K1-C7

Method BLASTX
NCBI GI g2462822
BLAST score 447
E value 1.0e-44
Match length 123
% identity 51

NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.

226090

Seq. ID

LIB3166-049-P1-K1-D1

Method BLASTX
NCBI GI g1086252
BLAST score 422
E value 1.0e-41
Match length 104
% identity 73

NCBI Description sucrose cleavage protein - Potato >gi\_707001\_bbs\_157931

(S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa]

[Solanum tuberosum]

Seq. No.

Seq. ID LIB3166-049-P1-K1-D11

226091

Method BLASTX
NCBI GI g1439609
BLAST score 536
E value 5.0e-55
Match length 106
% identity 100

NCBI Description (U62778) delta-tonoplast intrinsic protein [Gossypium

hirsutum]

Seq. No. 226092

Seq. ID LIB3166-049-P1-K1-D12

Method BLASTX
NCBI GI g3377803
BLAST score 235
E value 1.0e-19
Match length 63
% identity 73

NCBI Description (AF075597) Similár to (p)ppGpp synthetase; T2H3.9

[Arabidopsis thaliana]

Seq. No. 226093

Seq. ID LIB3166-049-P1-K1-D3

Method BLASTX
NCBI GI g4056469
BLAST score 631
E value 4.0e-66
Match length 125



```
% identity
NCBI Description
                   (AC005990) Strong similarity to gb_M95166 ADP-ribosylation
                   factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,
                   gb AA712956, gb T46403, gb T46050, gb AI100391 and
                   gb Z25043 come from t
Seq. No.
                   226094
Seq. ID
                   LIB3166-049-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   g2213594
BLAST score
                   337
E value
                   1.0e-31
Match length
                   90
% identity
                   67
NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]
Seq. No.
                   226095
Seq. ID
                   LIB3166-049-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   g584825
BLAST score
                   255
E value
                   3.0e-42
Match length
                   103
% identity
                   81
NCBI Description B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot
                   >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus
                   carota]
Seq. No.
                   226096
                   LIB3166-049-P1-K1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3482977
BLAST score
                   245
E value
                   2.0e-22
Match length
                   102
% identity
                   62
NCBI Description (AL031369) putative protein [Arabidopsis thaliana]
Seq. No.
                   226097
Seq. ID
                   LIB3166-049-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   g99735
BLAST score
                   203
E value
                   3.0e-16
Match length
                   74
% identity
                   53
NCBI Description L-ascorbate peroxidase (EC 1.11.1.11) precursor -
                   Arabidopsis thaliana (fragment)
Seq. No.
                   226098
                   LIB3166-049-P1-K1-E12
Seq. ID
```

Method BLASTX

NCBI GI g3023847
BLAST score 304
E value 2.0e-31
Match length 98



```
% identity
NCBI Description
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                   PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta
                   subunit-like [Medicago sativa]
Seq. No.
                   226099
Seq. ID
                   LIB3166-049-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   g4544443
BLAST score
                   131
E value
                   7.0e-12
Match length
                  53
% identity
                   73
NCBI Description (AC006592) putative mitochondrial uncoupling protein
                   [Arabidopsis thaliana]
Seq. No.
                   226100
Seq. ID
                  LIB3166-049-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g1332579
BLAST score
                   316
E value
                   4.0e-36
Match length
                  98
% identity
                  9
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
Seq. No.
                  226101
Seq. ID
                  LIB3166-049-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g3540181
BLAST score
                  181
E value
                  2.0e-13
Match length
                  80
% identity
                  47
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  226102
Seq. ID
                  LIB3166-049-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g2144271
BLAST score
                  195
E value
                  1.0e-15
Match length
                  68
% identity
                  59
NCBI Description
                  trans-cinnamate 4-monooxygenase (EC 1.14.13.11) C - Populus
                  kitakamiensis (fragment) >gi_1777372_dbj_BAA11578_ (D82814)
                  cinnamic acid 4-hydroxylase [Populus kitakamiensis]
Seq. No.
                  226103
Seq. ID
                  LIB3166-049-P1-K1-F2
Method
                  BLASTX
```

Method BLASTX
NCBI GI 9421855
BLAST score 331
E value 4.0e-31
Match length 107
% identity 68

NCBI Description alanine--tRNA ligase (EC 6.1.1.7) - Arabidopsis thaliana



## (fragment)

Seq. No. 226104 Seq. ID LIB3166-049-P1-K1-F3 Method BLASTX NCBI GI g3158474 BLAST score 392 E value 4.0e-38 Match length 99 % identity 78 NCBI Description (AF067184) aquaporin 1 [Samanea saman] Seq. No. 226105 Seq. ID LIB3166-049-P1-K1-F5 Method BLASTX NCBI GI g136636 BLAST score 216 E value 2.0e-17 Match length 41 % identity 100 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi\_1076424\_pir\_\_S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi\_442594\_pdb\_1AAK\_Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi\_2981894\_pdb\_2AAK\_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi\_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi 431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana] Seq. No. 226106 Seq. ID LIB3166-049-P1-K1-F8 Method BLASTX NCBI GI g399900 BLAST score 230 2.0e-23 E value Match length 91 % identity NCBI Description HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT5 (HD-ZIP PROTEIN 5) (HD-ZIP PROTEIN ATHB-1) >gi\_99659\_pir\_\_S16325 homeotic protein Athb-1 - Arabidopsis thaliana >gi\_16329\_emb\_CAA41625\_ (X58821) Athb-1 protein [Arabidopsis thaliana] Seq. No. 226107 Seq. ID LIB3166-049-P1-K1-G10 Method BLASTX NCBI GI g4538959 BLAST score 384 E value 3.0e - 37Match length 92 % identity 76 NCBI Description (AL049488) putative protein [Arabidopsis thaliana]

Seq. No. 226108

Seq. ID LIB3166-049-P1-K1-G11

Method BLASTX

```
NCBI GI
                   g2230757
BLAST score
                   215
E value
                   1.0e-17
Match length
                  84
% identity
                  55
NCBI Description (Y11969) dnaJ-like protein [Arabidopsis thaliana]
Seq. No.
                  226109
Seq. ID
                  LIB3166-049-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g886116
BLAST score
                  193
E value
                  6.0e-15
Match length
                  42
                  79
% identity
NCBI Description
                  (U27609) TCH4 protein [Arabidopsis thaliana] >gi 2952473
                   (AF051338) xyloglucan endotransglycosylase related protein
                  [Arabidopsis thaliana]
Seq. No.
                  226110
Seq. ID
                  LIB3166-049-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g30,80442
BLAST score
                  408
E value
                  6.0e-40
Match length
                  104
% identity
                  67
NCBI Description (AL022605) putative protein [Arabidopsis thaliana]
Seq. No.
                  226111
Seq. ID
                  LIB3166-049-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g399046
BLAST score
                  147
E value
                  6.0e-10
Match length
                  37
% identity
                  76
NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT)
                  >gi_99657_pir__S20867 adenine phosphoribosyltransferase (EC
```

2.4.2.7) - Arabidopsis thaliana >gi\_16164\_emb\_CAA41497\_(X58640) adenine phosphoribosyltransferase [Arabidopsis

thaliana] >gi\_433050 (L19637) adenine

phosphoribosyltransferase [Arabidopsis thaliana]

>gi\_3935182 (AC004557) F17L21.25 [Arabidopsis thaliana]

Seq. No. 226112

Seq. ID LIB3166-049-P1-K1-H11

Method BLASTX
NCBI GI g2494034
BLAST score 636
E value 1.0e-66
Match length 129
% identity 88

NCBI Description DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG KINASE 1) >gi\_2129573\_pir S71467 diacylglycerol kinase -

Arabidopsis thaliana >gi\_1374772\_dbj\_BAA09856\_ (D63787)

diacylglycerol kinase [Arabidopsis thaliana]



```
Seq. No.
                   226113
Seq. ID
                   LIB3166-049-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   q3901012
BLAST score
                   304
E value
                   4.0e-35
Match length
                   112
% identity
                   71
NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
                  sylvatica]
Seq. No.
                   226114
Seq. ID
                  LIB3166-049-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g4454484
BLAST score
                  270
E value
                   8.0e-24
Match length
                  88
% identity
                   61
NCBI Description (AC006234) putative diacylglycerol kinase [Arabidopsis
                  thaliana
Seq. No.
                  226115
Seq. ID
                  LIB3166-049-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q2832625
BLAST score
                  208
E value
                  1.0e-16
Match length
                  54
                  72
% identity
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                  226116
Seq. ID
                  LIB3166-050-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q1352821
BLAST score
                  466
E value
                  8.0e-47
Match length
                  90
                  98
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                  (RUBISCO SMALL SUBUNIT) >gi_279581_pir__RKCNSU
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - upland cotton >gi_450505_emb_CAA38026_ (X54091)
                  ribulose bisphosphate carboxylase [Gossypium hirsutum]
Seq. No.
                  226117
Seq. ID
                  LIB3166-050-P1-K1-A2
                  BLASTX
Method
NCBI GI
                  g1172571
BLAST score
                  530
                  2.0e-54
E value
Match length
                  99
% identity
                  97
```

>gi\_1076277\_pir\_\_S52637 phosphoenolpyruvate carboxykinase

NCBI Description PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP)



(ATP) (EC 4.1.1.49) - cucumber >gi\_567102 (L31899) phosphoenolpyruvate carboxykinase [Cucumis sativus]

Seq. No. 226118

Seq. ID LIB3166-050-P1-K1-A3

Method BLASTX
NCBI GI g1086989
BLAST score 583
E value 2.0e-60
Match length 123
% identity 95

NCBI Description (S79323) plasma membrane H(+)-ATPase [Vicia faba, Otafuku,

abaxial epidermis, guard cell protoplasts, Peptide, 963 aa]

[Vicia faba]

Seq. No. 226119

Seq. ID LIB3166-050-P1-K1-A5

Method BLASTX
NCBI GI g1345787
BLAST score 464
E value 1.0e-46
Match length 92
% identity 93

NCBI Description CHALCONE SYNTHASE 2 (NARINGENIN-CHALCONE SYNTHASE 2)

>gi\_567937\_dbj\_BAA05641\_ (D26594) chalcone synthase

[Camellia sinensis]

Seq. No. 226120

Seq. ID LIB3166-050-P1-K1-A9

Method BLASTX
NCBI GI g1703375
BLAST score 270
E value 6.0e-24
Match length 80
% identity 75

NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi\_965483\_dbj\_BAA08259 (D45420)

DcARF1 [Daucus carota]

Seq. No. 226121

Seq. ID LIB3166-050-P1-K1-B2

Method BLASTX
NCBI GI g4033467
BLAST score 389
E value 8.0e-38
Match length 121
% identity 43

NCBI Description ARGININE/SERINE-RICH SPLICING FACTOR RSP31

>gi\_1707366\_emb\_CAA67798\_ (X99435) splicing factor

[Arabidopsis thaliana]

Seq. No. 226122

Seq. ID LIB3166-050-P1-K1-B3

Method BLASTX
NCBI GI g416664
BLAST score 572
E value 3.0e-59
Match length 121



% identity 89

NCBI Description PLASMA MEMBRANE ATPASE 4 (PROTON PUMP)

>gi\_485504\_pir\_\_S33548 H+-transporting ATPase (EC 3.6.1.35)

type 4, plasma membrane - curled-leaved tobacco

>gi\_19704\_emb\_CAA47275\_ (X66737) plasma membrane H+-ATPase

[Nicotiana plumbaginifolia]

Seq. No. 226123

Seq. ID LIB3166-050-P1-K1-C10

Method BLASTX
NCBI GI g2244732
BLAST score 595
E value 6.0e-62
Match length 120
% identity 92

NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No. 226124

Seq. ID LIB3166-050-P1-K1-C11

Method BLASTX
NCBI GI g3766368
BLAST score 122
E value 1.0e-13
Match length 73
% identity 53

NCBI Description (AL031907) putative trascription factor, ccr4-associated

factor homolog [Schizosaccharomyces pombe]

Seq. No. 226125

Seq. ID LIB3166-050-P1-K1-C2

Method BLASTX
NCBI GI g1200256
BLAST score 454
E value 2.0e-45
Match length 96
% identity 89

NCBI Description (X90990) stpk1 protein kinase [Solanum tuberosum]

Seq. No. 226126

Seq. ID LIB3166-050-P1-K1-C6

Method BLASTX
NCBI GI g3193284
BLAST score 533
E value 1.0e-54
Match length 122
% identity 87

NCBI Description (AF069298) No definition line found [Arabidopsis thaliana]

Seq. No. 226127

Seq. ID LIB3166-050-P1-K1-C7

Method BLASTX
NCBI GI g4432857
BLAST score 189
E value 3.0e-17
Match length 96
% identity 50

NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No.

Seq. ID

226133

LIB3166-050-P1-K1-E5

```
Seq. No.
                     226128
  Seq. ID
                     LIB3166-050-P1-K1-D1.
  Method
                     BLASTX
  NCBI GI
                     g3980393
  BLAST score
                     371
  E value
                     1.0e-35
 Match length
                     104
  % identity
                     65
 NCBI Description (AC004561) putative glutathione S-transferase [Arabidopsis
                     thaliana]
  Seq. No.
                     226129
  Seq. ID
                     LIB3166-050-P1-K1-D10
 Method
                     BLASTX
 NCBI GI
                     g2262100
 BLAST score
                     465
 E value
                     9.0e-47
 Match length
                     97
 % identity
                     89
 NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
 Seq. No.
                     226130
 Seq. ID
                     LIB3166-050-P1-K1-D12
 Method
                     BLASTX
 NCBI GI
                     g4539351
 BLAST score
                     407
 E value
                     6.0e-40
 Match length
                     113
 % identity
                     61
 NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
 Seq. No.
                     226131
 Seq. ID
                    LIB3166-050-P1-K1-D2
 Method
                    BLASTX
 NCBI GI
                    g416651
 BLAST score
                    191
 E value
                     9.0e-15
 Match length
                    74
 % identity
                     51
 NCBI Description
                    PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN
                    PCNT103) >gi_100301_pir__S16269 auxin-induced protein (clone pCNT103) - common tobacco >gi_19791_emb_CAA39704_
                     (X56263) auxin-induced protein [Nicotiana tabacum]
 Seq. No.
                    226132
 Seq. ID
                    LIB3166-050-P1-K1-E12
 Method
                    BLASTX
 NCBI GI
                    g2739381
 BLAST score
                    375
                    4.0e-36
 E value
 Match length
                    120
 % identity
NCBI Description
                    (AC002505) putative patatin [Arabidopsis thaliana]
```



```
Method
                    BLASTX
NCBI GI
                    g1616616
BLAST score
                    261
E value
                    8.0e-23
Match length
                    50
                    98
% identity
NCBI Description (Y08424) small GTP-binding protein [Nicotiana
                   plumbaginifolia]
Seq. No.
                    226134
Seq. ID
                   LIB3166-050-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   q2335104
BLAST score
                   234
E value
                    7.0e-20
Match length
                   85
% identity
                   56
NCBI Description (AC002339) putative villin [Arabidopsis thaliana]
Seq. No.
                   226135
Seq. ID
                   LIB3166-050-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   g2792240
BLAST score
                   179
E value
                   3.0e-13
Match length
                   78
% identity
                   47
NCBI Description (AF032698) NBS-LRR type resistance protein [Oryza sativa]
Seq. No.
                   226136
Seq. ID
                   LIB3166-050-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   g114335
BLAST score
                   549
E value
                   1.0e-56
Match length
                   113
                   94
% identity
NCBI Description PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)
                   >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35)
type 2, plasma membrane - Arabidopsis thaliana >gi_166629
                   (J05570) H+-ATPase [Arabidopsis thaliana]
Seq. No.
                   226137
Seq. ID
                   LIB3166-050-P1-K1-F7
                   BLASTX
                   q120669
                   399
                   6.0e-39
                   89
```

Method NCBI GI BLAST score E value Match length % identity

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 226138



```
Seq. ID
                   LIB3166-050-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   g2961375
BLAST score
                   159
E value
                   8.0e-11
Match length
                   51
% identity
NCBI Description (AL022141) NAM like protein [Arabidopsis thaliana]
Seq. No.
                   226139
Seq. ID
                   LIB3166-050-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   g3236254
BLAST score
                   224
E value
                   2.0e-18
Match length
                   118
% identity
                   40
NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]
Seq. No.
                   226140
Seq. ID
                   LIB3166-050-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   g124224
BLAST score
                   468
E value
                   4.0e-47
Match length
                   113
% identity
                   82
NCBI Description
                  INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)
                   >gi_100345_pir__S21060 translation initiation factor eIF-5A
                   - common tobacco >gi_19887_emb_CAA45105_ (X63543)
                   eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]
Seq. No.
                   226141
Seq. ID
                  LIB3166-050-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g123580
BLAST score
                  351
E value
                  2.0e-33
Match length
                  109
% identity
                   67
NCBI Description
                  17.9 KD CLASS II HEAT SHOCK PROTEIN >gi_81787_pir__S01859
                  heat shock protein 17.9-D - soybean >gi_18652_emb_CAA30153_
                  (X07159) hsp17.9-D protein (AA 1 - 159) [Glycine max]
Seq. No.
                  226142
Seq. ID
                  LIB3166-050-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g1703446
BLAST score
                  305
E value
                  5.0e-28
Match length
                  96
% identity
                  67
```

NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)

>gi\_1076292\_pir\_\_S53127 asparaginase - Arabidopsis thaliana >gi\_735918\_emb\_CAA84367\_ (Z34884) asparaginase [Arabidopsis thaliana]

```
226143
LIB3166-05
```

```
Seq. No.
Seq. ID
                   LIB3166-050-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   g3236254
BLAST score
                   289
E value
                   4.0e-26
Match length
                  120
% identity
                  48
NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]
Seq. No.
                   226144
Seq. ID
                  LIB3166-050-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g1169382
BLAST score
                  394
E value
                  2.0e-42
Match length
                  105
% identity
                  81
NCBI Description DNAJ PROTEIN HOMOLOG 2 >gi 542196 pir S42031 LDJ2 protein
                  - leek >gi_454303 emb_CAA54720 (X77632) LDJ2 [Allium
                  porrum]
Seq. No.
                  226145
Seq. ID
                  LIB3166-050-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g2706450
BLAST score
                  507
E value
                  1.0e-51
Match length
                  116
% identity
                  84
NCBI Description (AJ225172) magnesium dependent soluble inorganic
                  pyrophosphatase [Solanum tuberosum]
Seq. No.
                  226146
Seq. ID
                  LIB3166-050-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q3914442
BLAST score
                  463
E value
                  2.0e-46
Match length
                  107
% identity
                  83
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
                  (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                  >gi 1916350 (U92504) PSI-H subunit [Brassica rapa]
Seq. No.
                  226147
Seq. ID
                  LIB3166-050-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g3702339
BLAST score
                  184
E value
                  9.0e-14
Match length
                  77
% identity
                  48
NCBI Description
                 (AC005397) unknown protein [Arabidopsis thaliana]
```

Seq. No. 226148

Seq. ID LIB3166-050-P1-K1-H7

```
Method
                  BLASTX
NCBI GI
                  q3702339
BLAST score
                  184
E value
                  9.0e-14
Match length
                 70
                  54
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.
                  226149
Seq. ID
                  LIB3166-050-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g3549680
                  152
```

BLAST score 152
E value 3.0e-10
Match length 51
% identity 59
NCBL Description (ALCO100)

NCBI Description (AL031394) putative protein [Arabidopsis thaliana]

Seq. ID LIB3166-051-P1-K1-A1 Method BLASTX NCBI GI g2832359 BLAST score 268 E value 1.0e-23 Match length % identity 51

226150

Seq. No.

NCBI Description (Y14072) HMG protein [Arabidopsis thaliana]

Seq. No. 226151 Seq. ID LIB3166-051-P1-K1-A11 Method BLASTX NCBI GI g1297359 BLAST score 497 E value 2.0e-50 Match length 129 % identity 72

NCBI Description (U53701) alcohol dehydrogenase 2d [Gossypium hirsutum]

Seq. No. 226152

Seq. ID LIB3166-051-P1-K1-A8

Method BLASTX
NCBI GI g2462745
BLAST score 199
E value 3.0e-20
Match length 93
% identity 53

NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 226153

Seq. ID LIB3166-051-P1-K1-A9

Method BLASTX
NCBI GI g1172872
BLAST score 256
E value 2.0e-22
Match length 87
% identity 63

NCBI Description CYSTEINE PROTEINASE RD19A PRECURSOR >gi\_541856\_pir\_\_JN0718

drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi\_435618\_dbj\_BAA02373\_ (D13042) thiol protease [Arabidopsis thaliana] >gi\_4539328\_emb\_CAB38829.1\_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No. 226154 Seq. ID LIB3166-051-P1-K1-B10 Method BLASTX NCBI GI g1263291 BLAST score 595 E value 7.0e-62 Match length 130 % identity 83

91

NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No. 226155 Seq. ID LIB3166-051-P1-K1-B11 Method BLASTX NCBI GI g2529229 BLAST score 308 E value 1.0e-42 Match length 101 % identity

NCBI Description (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]

Seq. No. 226156 Seq. ID LIB3166-051-P1-K1-B2

Method BLASTX NCBI GI g2267153 BLAST score 277 E value 6.0e-25 Match length 65 % identity 80

NCBI Description (AF009050) alcohol dehydrogenase 1A [Paeonia lactiflora]

Seq. No. 226157

Seq. ID LIB3166-051-P1-K1-B3

Method BLASTX NCBI GI g1049255 BLAST score 146 2.0e-18 E value Match length 71 % identity

NCBI Description (U36437) H+-pyrophosphatase [Zea mays]

Seq. No. 226158

Seq. ID LIB3166-051-P1-K1-B8

Method BLASTX NCBI GI g2769642 BLAST score 230 E value 4.0e-19 Match length 55 % identity

NCBI Description (Z97215) nine-cis-epoxycarotenoid dioxygenase [Lycopersicon

esculentum]



```
Seq. No.
                   226159
Seq. ID
                   LIB3166-051-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   q3335341
BLAST score
                   348
E value
                   6.0e-33
Match length
                   118
% identity
NCBI Description (AC004512) T8F5.10 [Arabidopsis thaliana]
Seq. No.
                   226160
                   LIB3166-051-P1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3834304
BLAST score
                   330
E value
                   8.0e-31
Match length
                   85
% identity
                   78
NCBI Description
```

(AC005679) Contains similarity to gi 1786244 hypothetical 24.9 kD protein in surA-hepA intergenic region yab0 from Escherichia coli genome gb\_AE000116, and to hypothetical

YABO family PF\_00849. [Arabidopsis thaliana]

Seq. No. 226161 Seq. ID

LIB3166-051-P1-K1-C12

Method BLASTX NCBI GI g2131525 BLAST score 146 E value 3.0e-09 Match length 95 % identity 34

hypothetical protein YDR489w - yeast (Saccharomyces NCBI Description

cerevisiae) >gi\_927735 (U33050) Ydr489wp; CAI: 0.16

[Saccharomyces cerevisiae]

Seq. No. 226162

Seq. ID LIB3166-051-P1-K1-C2

Method BLASTX NCBI GI g3551983 BLAST score 508 E value 8.0e-52 Match length 107

% identity 91

NCBI Description (AF085073) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_3551985 (AF085074) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_3551987 (AF085075) alcohol dehydrogenase A

[Gossypium hirsutum] >gi\_3551989 (AF085076) alcohol

dehydrogenase A [Gossypium hirsutum] >gi\_4140602 (AF090150) alcohol dehydrogenase A [Gossypium hirsutum] >gi 4140612 (AF090155) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140614 (AF090156) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140616 (AF090157) alcohol dehydrogenase A

[Gossypium hirsutum]

Seq. No. 226163

LIB3166-051-P1-K1-C3 Seq. ID

Method BLASTX

```
NCBI GI
                   q4098129
 BLAST score
                   592
E value
                   1.0e-61
Match length
                   126
 % identity
                   90
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
Seq. No.
                   226164
Seq. ID
                   LIB3166-051-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g2833381
BLAST score
                   619
E value
                   1.0e-64
Match length
                   125
% identity
                   90
                   GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR
NCBI Description
                   >gi_1172159 (U44126) starch synthase [Ipomoea batatas]
Seq. No.
                   226165
Seq. ID
                   LIB3166-051-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   g1934730
BLAST score
                   139
E value
                   1.0e-08
Match length
                   39
% identity
                   62
NCBI Description (U95036) germin-like protein [Arabidopsis thaliana]
Seq. No.
                   226166
Seq. ID
                   LIB3166-051-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   g2104681
BLAST score
                   316
E value
                   3.0e-29
Match length
                   126
% identity
                   56
-NCBI Description (X97907) transcription factor [Vicia faba]
Seq. No.
                   226167
Seq. ID
                   LIB3166-051-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   g505482
BLAST score
                   460
E value
                   4.0e-46
Match length
                  117
% identity
                   80
NCBI Description (X64349) 33 kDa polypeptide of water-oxidizing complex of
                  photosystem II [Nicotiana tabacum]
Seq. No.
                   226168
Seq. ID
                  LIB3166-051-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g1220196
BLAST score
                  436
E value
                  3.0e-43
Match length
                  105
% identity
                   76
```

Match length

NCBI Description

% identity

101

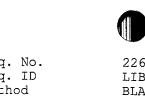


```
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
 Seq. No.
                    226169
Seq. ID
                    LIB3166-051-P1-K1-D1
Method
                    BLASTX
NCBI GI
                    q2829862
BLAST score
                    209
E value
                    1.0e-16
Match length
                    118
% identity
                    41
NCBI Description (AC002396) Similar to glucosyltransferases [Arabidopsis
                    thaliana]
Seq. No.
                    226170
Seq. ID
                    LIB3166-051-P1-K1-D12
Method
                    BLASTX
NCBI GI
                    g1928981
BLAST score
                    145
E value
                    9.0e-21
Match length
                   76
% identity
                    74
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                   oleracea var. botrytis]
Seq. No.
                   226171
Seq. ID
                   LIB3166-051-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   g2708624
BLAST score
                   589
E value
                   3.0e-61
Match length
                   110
% identity
                   93
NCBI Description (AF036618) acetyl-CoA synthetase [Arabidopsis thaliana]
Seq. No.
                   226172
Seq. ID
                   LIB3166-051-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   g115834
BLAST score
                   212
E value
                   5.0e-24
Match length
                   85
% identity
                   71
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN CP24 10B PRECURSOR
                   (CAB-10B) (LHCP) >gi_100202_pir__S11878 chlorophyll a/b-binding protein Cab10B - tomato >gi_170400 (M32606)
                   chlorophyll b-binding protein [Lycopersicon esculentum]
Seq. No.
                   226173
Seq. ID
                   LIB3166-051-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g4262226
BLAST score
                   298
E value
                   4.0e-27
```

(AC006200) putative protein kinase [Arabidopsis thaliana]

% identity

NCBI Description



```
Seq. No.
 Seq. ID
                   LIB3166-051-P1-K1-E7
 Method
                   BLASTX
 NCBI GI
                   g3122785
 BLAST score
                   242
 E value
                   8.0e-21
Match length
                   68
 % identity
                   74
 NCBI Description 40S RIBOSOMAL PROTEIN S14 >gi 2565340 (AF026079) ribosomal
                   protein S14 [Lupinus luteus]
 Seq. No.
                   226175
 Seq. ID
                   LIB3166-051-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   q479413
BLAST score
                   386
E value
                   2.0e-37
Match length
                   128
% identity
                   66
NCBI Description myosin-like protein - Arabidopsis thaliana
Seq. No.
                   226176
Seq. ID
                   LIB3166-051-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   q2130051
BLAST score
                   157
E value
                   9.0e-11
Match length
                   61
% identity
                   54
NCBI Description
                   xylose isomerase (EC 5.3.1.5) - barley
                   >gi_1296807_emb_CAA64544_ (X95256) xylose isomerase
                   [Hordeum vulgare] >gi_1588664_prf__2209268A xylose
                   isomerase [Hordeum vulgare]
Seq. No.
                   226177
Seq. ID
                   LIB3166-051-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   q1771160
BLAST score
                   531
E value
                   2.0e-54
Match length
                   128
                   79
% identity
NCBI Description
                  (X98929) SBT1 [Lycopersicon esculentum]
                   >gi_3687305_emb_CAA06999 (AJ006378) subtilisin-like
                   protease [Lycopersicon esculentum]
Seq. No.
                   226178
Seq. ID
                  LIB3166-051-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g3377941
BLAST score
                  160
E value
                  3.0e-11
Match length
                  86
```

(AL021960) putative protein (fragment) [Arabidopsis

32228

43

thaliana]



```
Seq. No.
                   226179
Seq. ID
                   LIB3166-051-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   g2244998
BLAST score
                  483
E value
                   9.0e-49
Match length
                  121
% identity
                   72
NCBI Description (Z97341) similarity to probable transcriptional adaptor
                  ADA2 [Arabidopsis thaliana]
Seq. No.
                  226180
Seq. ID
                  LIB3166-051-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g4544409
BLAST score
                  471
E value
                  2.0e-47
Match length
                  125
% identity
                  63
NCBI Description (AC006955) putative transcription factor [Arabidopsis
                  thaliana]
Seq. No.
                  226181
Seq. ID
                  LIB3166-051-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g2191187
BLAST score
                  190
E value
                  2.0e-14
Match length
                  76
% identity
                  49
NCBI Description (AF007271) contains similarity to a DNAJ-like domain
                  [Arabidopsis thaliana]
Seq. No.
                  226182
Seq. ID
                  LIB3166-051-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g4150963
BLAST score
                  225
E value
                  1.0e-18
Match length
                  97
% identity
NCBI Description (Y18620) DsPTP1 protein [Arabidopsis thaliana]
Seq. No.
                  226183
Seq. ID
                  LIB3166-051-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q113362
BLAST score
                  228
E value
                  5.0e-23
Match length
                  69
% identity
                  68
NCBI Description
                 ALCOHOL DEHYDROGENASE 1 (SLOW-ALLELE) >gi 65901_pir__DEILSP
                  alcohol dehydrogenase (EC 1.1.1.1) 1-S - pearl millet
```

Seq. No. 226184

1-379) [Pennisetum americanum]

>gi\_20409\_emb\_CAA34547\_ (X16547) alcohol dehydrogenase (AA



```
Seq. ID
                   LIB3166-051-P1-K1-H1
 Method
                   BLASTX
 NCBI GI
                   g3062801
 BLAST score
                   525
 E value
                   9.0e-54
 Match length
                   119
 % identity
 NCBI Description (AB012873) arginine decarboxylase [Nicotiana sylvestris]
 Seq. No.
                   226185
 Seq. ID
                   LIB3166-051-P1-K1-H12
Method
                   BLASTX
 NCBI GI
                   g3153902
BLAST score
                   364
E value
                   7.0e-35
Match length
                   95
 % identity
                   79
NCBI Description (AF066076) 14-3-3-like protein [Helianthus annuus]
Seq. No.
                   226186
Seq. ID
                   LIB3166-051-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   g134101
BLAST score
                   507
E value
                   1.0e-51
Match length
                   125
% identity
NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT (60 KD
                   CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA)
                   >gi_72958_pir__HHCSBA ribulose-bisphosphate carboxylase
                   subunit-binding protein alpha chain - castor bean
                   (fragment)
Seq. No.
                   226187
Seq. ID
                   LIB3166-051-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   q2661422
BLAST score
                   261
E value
                   9.0e-23
Match length
                   66
% identity
NCBI Description
                   (AJ001342) Putative S-phase-specific ribosomal protein
                   [Arabidopsis thaliana] >gi_3096936 emb CAA18846.1
                   (AL023094) Putative S-phase-specific ribosomal protein
                   [Arabidopsis thaliana]
Seq. No.
                   226188
Seq. ID
                   LIB3166-052-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g1174592
BLAST score
                   278
                   4.0e-25
E value
Match length
                   72
% identity
                   79
NCBI Description
```

32230

sativum]

TUBULIN ALPHA-1 CHAIN >gi\_2119270\_pir\_\_S60233 alpha-tubulin - garden pea >gi\_525332 (U12589) alpha-tubulin [Pisum



```
Seq. No.
                    226189
 Seq. ID
                   LIB3166-052-P1-K1-A12
 Method
                   BLASTX
 NCBI GI
                    g3158474
 BLAST score
                   295
 E value
                    9.0e-27
 Match length
                   75
 % identity
                   80
 NCBI Description (AF067184) aquaporin 1 [Samanea saman]
 Seq. No.
                   226190
 Seq. ID
                   LIB3166-052-P1-K1-A4
 Method
                   BLASTX
 NCBI GI
                   q2245136
 BLAST score
                   297
 E value
                    5.0e-33
 Match length
                   112
 % identity
                    66
                   (Z97344) trehalose-6-phosphate synthase homolog
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                   226191
 Seq. ID
                   LIB3166-052-P1-K1-A7
 Method
                   BLASTX
 NCBI GI
                   q4164408
 BLAST score
                   602
 E value
                   9.0e-63
 Match length
                   123
 % identity
                   88
 NCBI Description (AJ132228) amino acid carrier [Ricinus communis]
 Seq. No.
                   226192
 Seq. ID
                   LIB3166-052-P1-K1-A8
Method
                   BLASTX
 NCBI GI
                   g1346524
BLAST score
                   489
 E value
                   1.0e-49
Match length
                   103
 % identity
                   92
 NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
                   ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi 497900
                   (M73430) S-adenosyl methionine synthetase [Populus
                   deltoides]
 Seq. No.
                   226193
 Seq. ID
                   LIB3166-052-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   g1354849
BLAST score
                   184
E value
                   8.0e-14
Match length
                   59
 % identity
                   64
NCBI Description (U57350) epoxide hydrolase [Nicotiana tabacum]
```

LIB3166-052-P1-K1-B10

226194

Seq. No.

Seq. ID



```
Method
                   BLASTX ...
NCBI GI
                   g445612
BLAST score
                   492
E value
                   7.0e-50
Match length
                   104
% identity
                   91
NCBI Description ribosomal protein S19 [Solanum tuberosum]
Seq. No.
                   226195
Seq. ID
                   LIB3166-052-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   q2072626
BLAST score
                   293
E value
                   2.0e-26
Match length
                   79
% identity
                   71
NCBI Description
                  (Y12904) hypothetical protein [Arabidopsis thaliana]
                   >gi_3281856_emb_CAA19751_ (AL031004) Transcription factor
                   II homolog [Arabidopsis thaliana]
Seq. No.
                   226196
Seq. ID
                   LIB3166-052-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   g2129944
BLAST score
                   326
E value
                  2.0e-30
Match length
                   84
% identity
                   73
NCBI Description RNA-binding protein RZ-1 - wood tobacco
                   >gi_1395193_dbj_BAA12064_ (D83696) RNA-binding protein RZ-1
                   [Nicotiana sylvestris] >gi_1435062_dbj_BAA06012_ (D28861)
                   RNA binding protein, RZ-1 [Nicotiana sylvestris]
Seq. No.
                   226197
Seq. ID
                  LIB3166-052-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g2708744
BLAST score
                  245
E value
                  6.0e-24
Match length
                  121
% identity
                  52
NCBI Description
                  (AC003952) putative Bop-like zinc finger protein
                   [Arabidopsis thaliana]
Seq. No.
                  226198
Seq. ID
                  LIB3166-052-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g4457221
BLAST score
                  167
E value
                  9.0e-12
Match length
                  45
% identity
                  89
NCBI Description
                  (AF127797) putative bZIP DNA-binding protein [Capsicum
                  chinense]
```

Seq. No. 226199 Seq. ID LIB3166

LIB3166-052-P1-K1-B7

```
Method
                    BLASTX
NCBI GI
                    g4105696
BLAST score
                    449
E value
                    8.0e-45
Match length
                    116
% identity
                    78
NCBI Description (AF049870) beta tubulin 1 [Arabidopsis thaliana]
Seq. No.
                    226200
Seq. ID
                    LIB3166-052-P1-K1-B8
Method
                    BLASTX
NCBI GI
                    g2511574
BLAST score
                    414
E value
                    9.0e-41
Match length
                    90
% identity
                    94
NCBI Description
                    (Y13176) multicatalytic endopeptidase [Arabidopsis
                    thaliana] >gi_3421075 (AF043520) 20S proteasome subunit
                    PAB1 [Arabidopsis thaliana]
Seq. No.
                    226201
Seq. ID
                    LIB3166-052-P1-K1-B9
Method
                   BLASTX
NCBI GI
                    g116923
BLAST score
                    421
E value
                    1.0e-41
Match length
                   123
% identity
                    66
NCBI Description
                   COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
                   >gi_111414_pir__S13520 beta-COP protein - rat
>gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus
                   norvegicus]
Seq. No.
                   226202
Seq. ID
                   LIB3166-052-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   g2088662
BLAST score
                   145
E value
                   3.0e-09
Match length
                   48
% identity
NCBI Description (AF002109) unknown protein [Arabidopsis thaliana]
Seq. No.
                   226203
Seq. ID
                   LIB3166-052-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g4164408
BLAST score
                   450
E value
                   6.0e-45
Match length
                   99
% identity
NCBI Description (AJ132228) amino acid carrier [Ricinus communis]
```

Seq. No. 226204

Seq. ID LIB3166-052-P1-K1-C12

Method BLASTX NCBI GI g3850111



```
BLAST score
E value
                   3.0e-11
Match length
                   51
                   55
% identity
NCBI Description (AL033388) hypothetical integral membrane protein, putative
                   involvement in lipid metabolism [Schizosaccharomyces pombe]
Seq. No.
                   226205
Seq. ID
                  LIB3166-052-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q1843527
BLAST score
                  167
E value
                   9.0e-12
Match length
                  36
                  89
% identity
NCBI Description (U73747) annexin [Gossypium hirsutum]
Seq. No.
                  226206
Seq. ID
                  LIB3166-052-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g2832677
BLAST score
                  278
E value
                  9.0e-25
Match length
                  103
% identity
                  50
NCBI Description (AL021712) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  226207
Seq. ID
                  LIB3166-052-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g1843527
BLAST score
                  517
E value
                  5.0e-55
Match length
                  115
% identity
                  57
NCBI Description (U73747) annexin [Gossypium hirsutum]
Seq. No.
                  226208
Seq. ID
                  LIB3166-052-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g4580460
BLAST score
                  215
E value
                  1.0e-30
Match length
                  81
% identity
                  (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  226209
Seq. ID
                  LIB3166-052-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g3434973
BLAST score
                  253
```

E value 8.0e-22 Match length 76 % identity 71

NCBI Description (AB008106) ethylene responsive element binding factor 4

Method

NCBI GI

BLASTX

g832876



## [Arabidopsis thaliana]

```
Seq. No.
                   226210
Seq. ID
                   LIB3166-052-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   g3885338
BLAST score
                   202
E value
                   5.0e-16
Match length
                   61
% identity
                   57
NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]
Seq. No.
                   226211
Seq. ID
                   LIB3166-052-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   g4510363
BLAST score
                   434
E value
                   5.0e-43
Match length
                  92
                   90
% identity
NCBI Description (AC007017) putative DNA-binding protein [Arabidopsis
                   thaliana]
Seq. No.
                   226212
Seq. ID
                  LIB3166-052-P1-K1-D3
Method
                  BLASTX
NCBI GI
                   g1403024
BLAST score
                  215
E value
                   2.0e-17
Match length
                  82
% identity
                  55
NCBI Description (Z54163) hnRNP protein [Chironomus tentans]
Seq. No.
                  226213
Seq. ID
                  LIB3166-052-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q4165323
BLAST score
                  600
E value
                  2.0e-62
Match length
                  125
% identity
NCBI Description (AB022442) p-type H+-ATPase [Vicia faba]
Seq. No.
                  226214
Seq. ID
                  LIB3166-052-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g2764574
BLAST score
                  347
E value
                  8.0e-33
Match length
                  102
% identity
NCBI Description (AJ001009) pore protein of 24 kD (OEP24) [Pisum sativum]
Seq. No.
                  226215
Seq. ID
                  LIB3166-052-P1-K1-D8
```



```
BLAST score
E value
                   8.0e-49
Match length
                   100
% identity
                   94
NCBI Description
                  (L41345) ascorbate free radical reductase [Solanum
                   lycopersicum] >gi_1097368_prf__2113407A ascorbate free
                  radical reductase [Lycopersicon esculentum]
Seq. No.
                   226216
Seq. ID
                  LIB3166-052-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q3695384
BLAST score
                  203
E value
                  5.0e-16
Match length
                  60
% identity
                   62
NCBI Description
                  (AF096370) contains similarity to the helix-loop-helix
                  DNA-binding domain (Pfam: PF00010 HLH, E-value: 0.0046)
                   [Arabidopsis thaliana]
Seq. No.
                  226217
Seq. ID
                  LIB3166-052-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g2493146
BLAST score
                  355
E value
                  8.0e-34
Match length
                  89
% identity
                  53
NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi 755148
                   (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit
                  [Gossypium hirsutum] >gi_4519415_dbj_BAA75542.1_ (AB024275)
                  vacuolar H+-ATPase c subunit [Citrus unshiu]
Seq. No.
                  226218
Seq. ID
                  LIB3166-052-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g2129715
BLAST score
                  225
E value
                  2.0e-18
Match length
                  99
% identity
                  42
NCBI Description reverse transcriptase - Arabidopsis thaliana
                  retrotransposon Ta25 (fragment)
Seq. No.
                  226219
Seq. ID
                  LIB3166-052-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g3661603
```

NCBI GI g3661603
BLAST score 124
E value 1.0e-10
Match length 74
% identity 57

NCBI Description (AF092841) ribonucleoside-diphosphate reductase large

subunit [Arabidopsis thaliana]

Seq. No. 226220

Seq. ID LIB3166-052-P1-K1-E5

BLAST score

Match length

E value

529

126

3.0e-54



```
Method
                   BLASTX
NCBI GI
                   g4102727
BLAST score
                   144
E value
                   5.0e-09
Match length
                   75
% identity
                   43
NCBI Description (AF015782) blight-associated protein p12 precursor [Citrus
                   jambhiri]
Seq. No.
                   226221
Seq. ID
                  LIB3166-052-P1-K1-E6
Method
                  BLASTX
NCBI GI
                   q349379
BLAST score
                  421
E value
                  2.0e-41
Match length
                  128
                  75
% identity
NCBI Description (L22847) HAHB-1 [Helianthus annuus]
Seq. No.
                  226222
Seq. ID
                  LIB3166-052-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q3063396
BLAST score
                  444
E value
                 3.0e-44
Match length
                  103
% identity
                  81
NCBI Description (AB012947) vcCyP [Vicia faba]
Seq. No.
                  226223
Seq. ID
                  LIB3166-052-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g3281846
BLAST score
                  144
E value
                  4.0e-09
Match length
                  112
% identity
                  32
NCBI Description (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]
Seq. No.
                  226224
Seq. ID
                  LIB3166-052-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g1363325
BLAST score
                  328
E value
                  7.0e-31
Match length
                  83
% identity
                  72
NCBI Description RNA helicase HEL117 - rat >gi_897915 (U25746) RNA helicase
                  [Rattus norvegicus]
Seq. No.
                  226225
Seq. ID
                  LIB3166-052-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g4538905
```

```
% identity
NCBI Description (AL049482) putative protein [Arabidopsis thaliana]
                   226226
Seq. ID
                   LIB3166-052-P1-K1-F12 '
Method
                   BLASTX
NCBI GI
                   g2764941
BLAST score
                   369
E value
                   2.0e-35
Match length
                   93
% identity
                   69
                   (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                   expressed in meristematic region, and style [Arabidopsis
                   thaliana]
Seq. No.
                   226227
Seq. ID
                   LIB3166-052-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   q3702332
BLAST score
                   270
E value
                   8.0e-24
Match length
                   90
% identity
                   62
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.
                   226228
Seq. ID
                   LIB3166-052-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   g3341685
BLAST score
                   270
E value
                   8.0e-24
Match length
                   86
% identity
                   67
NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]
Seq. No.
                   226229
Seq. ID
                   LIB3166-052-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   g2213867
BLAST score
                   261
E value
                   1.0e-45
Match length
                  127
% identity
                   77
NCBI Description
                  (AF003124) fructose-biphosphate aldolase [Mesembryanthemum
                  crystallinum]
Seq. No.
                  226230
Seq. ID
                  LIB3166-052-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g3334322
BLAST score
                  429
E value
                  2.0e-42
Match length
                  83
% identity
```

GTP-binding protein Bsarlb [Brassica rapa]

NCBI Description GTP-BINDING PROTEIN SAR1B >gi 2108347 (U55036) small



```
Seq. No.
                       226231
    Seq. ID
                       LIB3166-052-P1-K1-F9
    Method
                       BLASTX
    NCBI GI
                       g399046
    BLAST score
                       284
    E value
                       1.0e-25
    Match length
                       106
    % identity
                       54
    NCBI Description ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT)
                       >gi_99657_pir__S20867 adenine phosphoribosyltransferase (EC
                       2.4.2.7) - Arabidopsis thaliana >gi_16164_emb_CAA41497_
                       (X58640) adenine phosphoribosyltransferase [Arabidopsis
                       thaliana] >gi_433050 (L19637) adenine
                       phosphoribosy\overline{1}transferase [Arabidopsis thaliana]
                       >gi_3935182 (AC004557) F17L21.25 [Arabidopsis thaliana]
    Seq. No.
                      226232
    Seq. ID
                      LIB3166-052-P1-K1-G1
    Method
                      BLASTX
    NCBI GI
                      g3281858
    BLAST score
                      222
E value
                      3.0e-18
   Match length
                      50
    % identity
                      86
   NCBI Description (AL031004) ribosomal protein S6 - like [Arabidopsis
                      thalianal
                      226233
    Seq. No.
    Seq. ID
                      LIB3166-052-P1-K1-G11
   Method
                      BLASTX
   NCBI GI
                      g1763063
   BLAST score
                      221
   E value
                      5.0e-18
   Match length
                      101
    % identity
                      49
   NCBI Description (U68763) SCOF-1 [Glycine max]
   Seq. No.
                      226234
   Seq. ID
                      LIB3166-052-P1-K1-G12
   Method
                      BLASTX
   NCBI GI
                      g951427
   BLAST score
                      559
   E value
                      1.0e-57
   Match length
                      120
   % identity
   NCBI Description (M59857) stearoyl-acyl-carrier protein desaturase [Ricinus
                      communis]
   Seq. No.
                      226235
   Seq. ID
                      LIB3166-052-P1-K1-G2
   Method
                      BLASTX
   NCBI GI
                      g4574320
   BLAST score
                      239
   E value .
                      3.0e-20
   Match length
                      74
   % identity
```

NCBI Description (AF117224) wound-induced protein WI12 [Mesembryanthemum



## crystallinum]

```
Seq. No.
                   226236
                   LIB3166-052-P1-K1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                  q3643603
BLAST score
                  245
E value
                   4.0e-26
Match length
                  116
% identity
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
                  226237
Seq. ID
                  LIB3166-052-P1-K1-G4
Method
                  BLASTX
                  q3831444
NCBI GI
BLAST score
                  398
E value
                  8.0e-39
Match length
                  109
% identity
                  72
NCBI Description (AC005819) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  226238
Seq. ID
                  LIB3166-052-P1-K1-G6
Method
                  BLASTX
                  g3283072
NCBI GI
BLAST score
                  374
E value
                  5.0e-36
Match length
                  124
% identity
NCBI Description (AF056022) p60 katanin [Homo sapiens]
Seq. No.
                   226239
Seq. ID
                  LIB3166-052-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g2245005
BLAST score
                  298
E value
                  3.0e-27
                  77
Match length
% identity
                  81
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  226240
Seq. ID
                  LIB3166-052-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g3868758
BLAST score
                  465
E value
                  1.0e-46
Match length
                  122
% identity
                  70
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
Seq. No.
                  226241
Seq. ID
                  LIB3166-052-P1-K1-H1
```

Method BLASTX NCBI GI g3882081 BLAST score 613



E value 5.0e-64Match length 124 % identity 33

NCBI Description (AJ012552) polyubiquitin [Vicia faba]

Seq. No. 226242

Seq. ID LIB3166-052-P1-K1-H10

Method BLASTX NCBI GI g3183088 BLAST score 240 E value 2.0e-20 Match length 70 % identity

NCBI Description PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR

(LTP)  $\geq gi_629658_pir_S47084$  lipid transfer like protein cowpea  $gi_499034$ \_emb\_CAA56113\_ (X79604) lipid transfer

like protein [Vigna unguiculata]

Seq. No. 226243

Seq. ID LIB3166-052-P1-K1-H12

Method BLASTX NCBI GI g136636 BLAST score 568 E value 9.0e-59 Match length 107 % identity 97

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN NCBI Description

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi\_1076424\_pir\_\_S43781 ubiquitin-conjugating enzyme UBC1 -

Arabidopsis thaliana >gi 442594 pdb 1AAK Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi 2981894 pdb 2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi\_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi\_431260 (L19351) ubiquitin conjugating enzyme

[Arabidopsis thaliana]

Seq. No. 226244

Seq. ID LIB3166-052-P1-K1-H2

Method BLASTX NCBI GI g3095075 BLAST score 179 E value 4.0e-13 Match length 113 % identity 37

NCBI Description (AF031471) pollen allergen [Juniperus oxycedrus]

Seq. No. 226245

Seq. ID LIB3166-052-P1-K1-H4

Method BLASTX g1330399 NCBI GI BLAST score 169 E value 6.0e-12 Match length 77

% identity 44

NCBI Description (U58762) coded for by C. elegans cDNA yk27e9.5; coded for

by C. elegans cDNA yk27e9.3 [Caenorhabditis elegans]

Method

NCBI GI

BLAST score

BLASTX

175

q144985



```
Seq. No.
                   226246
Seq. ID
                  LIB3166-052-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g3426043
BLAST score
                  368
E value
                  3.0e-35
Match length
                  120
% identity
                  62
NCBI Description (AC005168) putative choline kinase [Arabidopsis thaliana]
Seq. No.
                  226247
Seq. ID
                  LIB3166-052-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  q3540181
BLAST score
                  187
E value
                  3.0e-14
Match length
                  59
% identity
                  56
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  226248
Seq. ID
                  LIB3166-053-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g3785989
BLAST score
                  462
E value
                  2.0e-46
Match length
                  104
% identity
                  86
NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]
Seq. No.
                  226249
Seq. ID
                  LIB3166-053-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q4415931
BLAST score
                  222
E value
                  4.0e-18
Match length
                  99
% identity
                  51
NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]
                  >gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  226250
Seq. ID
                  LIB3166-053-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g3540181
BLAST score
                  148
E value
                  1.0e-09
Match length
                  91
% identity
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  226251
Seq. ID
                  LIB3166-053-P1-K1-A6
```

NCBI GI

E value

BLAST score

Match length

g3549666

6.0e-33

348

83



```
E value
                   1.0e-12
Match length
                   120
% identity
                   29
NCBI Description
                   (M25819) phosphoenolpyruvate carboxylase [Corynebacterium
                   glutamicum]
                   226252
Seq. No.
Seq. ID
                   LIB3166-053-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   g441457
BLAST score
                   277
E value
                   7.0e-25
Match length
                   66
                   79
% identity
NCBI Description
                  (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
                   esculentum]
                   226253
Seq. No.
                   LIB3166-053-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2662341
BLAST score
                   565
E value
                   2.0e-58
Match length
                   120
% identity
                   92
NCBI Description
                   (D63580) EF-1 alpha [Oryza sativa]
                   >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza
                   sativa] >gi_2662347_dbj BAA23660 (D63583) EF-1 alpha
                   [Oryza sativa]
Seq. No.
                   226254
Seq. ID
                   LIB3166-053-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   q4490341
BLAST score
                   327
E value
                   2.0e-30
Match length
                  72
% identity
NCBI Description (AL035656) putative protein [Arabidopsis thaliana]
Seq. No.
                   226255
Seq. ID
                   LIB3166-053-P1-K1-B8
Method
                  BLASTX
NCBI GI
                   g2894606
BLAST score
                  133
E value
                  1.0e-11
Match length
                  102
% identity
                   40
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                   226256
Seq. ID
                  LIB3166-053-P1-K1-C10
Method
                  BLASTX
```

% identity

NCBI Description



```
% identity
NCBI Description (AL031394) putative protein [Arabidopsis thaliana]
Seq. No.
                   226257
Seq. ID
                  LIB3166-053-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g3288883
BLAST score
                  372
E value
                   8.0e-36
Match length
                  102
% identity
NCBI Description (AB015431) SAR DNA binding protein [Oryza sativa]
Seq. No.
                  226258
Seq. ID
                  LIB3166-053-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g1168191
BLAST score
                  377
E value
                  9.0e-42
Match length
                  108
% identity
                  87
NCBI Description 14-3-3-LIKE PROTEIN 4 (PBLT4) >gi 1362089_pir S57272
                  14-3-3 brain protein homolog (clone pBLT4) - tomato
                  >gi 466336 (L29150) 14-3-3 protein homologue [Solanum
                  lycopersicum] >gi_1090847_prf__2019487B 14-3-3 protein
                   [Lycopersicon esculentum]
Seq. No.
                  226259
Seq. ID
                  LIB3166-053-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2465434
BLAST score
                  323
E value
                  4.0e-30
Match length
                  71
% identity
NCBI Description (AF022142) flavanone 3beta-hydroxylase [Petunia x hybrida]
Seq. No.
                  226260
Seq. ID
                  LIB3166-053-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q2464855
BLAST score
                  139
E value
                  1.0e-08
Match length
                  37
% identity
NCBI Description (Z99707) myb-related protein [Arabidopsis thaliana]
Seq. No.
                  226261
Seq. ID
                  LIB3166-053-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q2465925
BLAST score
                  334
E value
                  3.0e-31
Match length
                  128
```

32244

[Arabidopsis thaliana]

(AF024649) receptor-like serine/threonine kinase

Seq. No.

Seq. ID

Method

226267

BLASTX

LIB3166-053-P1-K1-E2



```
226262
Seq. No.
Seq. ID
                  LIB3166-053-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g4454484
BLAST score
                  508
E value
                  1.0e-51
Match length
                  127
% identity
                  80
NCBI Description
                 (AC006234) putative diacylglycerol kinase [Arabidopsis
                  thaliana]
Seq. No.
                  226263
Seq. ID
                  LIB3166-053-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g3650028
BLAST score
                  196
E value
                  4.0e-15
Match length
                  63
                  59
% identity
NCBI Description (AC005396) putative 22 kDa peroxisomal membrane protein
                  [Arabidopsis thaliana]
Seq. No.
                  226264
Seq. ID
                  LIB3166-053-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g2829869
BLAST score
                  266
E value
                  2.0e-23
Match length
                  83
% identity
                  65
NCBI Description (AC002396) pyruvate dehydrogenase E1 alpha subunit
                  [Arabidopsis thaliana]
Seq. No.
                  226265
Seq. ID
                  LIB3166-053-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g1850968
BLAST score
                  439
E value
                  1.0e-43
Match length
                  125
% identity
                  65
NCBI Description (U79733) Hs1pro-1 [Beta procumbens]
Seq. No.
                  226266
Seq. ID
                  LIB3166-053-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q3158474
BLAST score
                  413
E value
                  1.0e-40
Match length
                  105
% identity
NCBI Description (AF067184) aquaporin 1 [Samanea saman]
```



```
NCBI GI
                   q131397
BLAST score
                   254
E value
                   6.0e-22
Match length
                  116
% identity
                   52
NCBI Description
                  OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD
                  SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
                  >gi_81480_pir__S00008 photosystem II oxygen-evolving
                  complex protein 3 precursor - spinach
                  >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the
                  photosynthetic oxygen- evolving protein (OEC) [Spinacia
                  oleracea] >gi_225597_prf__1307179B luminal protein 16kD
                   [Spinacia oleracea]
Seq. No.
                  226268
Seq. ID
                  LIB3166-053-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g1362152
BLAST score
                  550
E value
                  1.0e-56
Match length
                  120
% identity
                  88
NCBI Description
                  ribosomal protein S6 kinase homolog (clone Aspkl1) - oat
                  >gi_871986_emb_CAA56313_ (X79992) putative pp70 ribosomal
                  protein S6 kinase [Avena sativa]
                  226269
Seq. No.
Seq. ID
                  LIB3166-053-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  q3193316
BLAST score
                  150
E value
                  5.0e-10
Match length
                  87
% identity
NCBI Description (AF069299) contains similarity to nucleotide sugar
                  epimerases [Arabidopsis thaliana]
Seq. No.
                  226270 -
Seq. ID
                  LIB3166-053-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g4490705
BLAST score
                  496
E value
                  3.0e-50
Match length
                  116
% identity
                  86
NCBI Description
                  (AL035680) ribosomal protein L14-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  226271
Seq. ID
                  LIB3166-053-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g541847
BLAST score
                  301
```

E value 2.0e-27

Match length 99 % identity 63

NCBI Description alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana

NCBI Description



```
Seq. No.
                   226272
Seq. ID
                   LIB3166-053-P1-K1-F10
Method
                   BLASTX
                   q3786314
NCBI GI
BLAST score
                   250
E value
                   1.0e-21
Match length
                   86
% identity
                   57
NCBI Description
                   (AB012141) translation elongation factor3 [Candida
                   glabrata]
Seq. No.
                   226273
Seq. ID
                   LIB3166-053-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   q4539301
BLAST score
                   423
E value
                   1.0e-41
Match length
                   110
% identity
                   73
NCBI Description
                  (AL049480) putative mitochondrial protein [Arabidopsis
                   thaliana]
Seq. No.
                   226274
Seq. ID
                   LIB3166-053-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   g4321762
BLAST score
                   177
E value
                   3.0e-13
Match length
                   81
% identity
                   48
NCBI Description (AF061107) transcription factor MYC7E [Zea mays]
Seq. No.
                   226275
Seq. ID
                   LIB3166-053-P1-K1-F7
Method
                  BLASTX
NCBI GI
                   q2500115
BLAST score
                   387
E value
                   1.0e-37
Match length
                   90
% identity
                   82
NCBI Description
                  GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE)
                   >gi_529375_dbj_BAA07108_ (D37870) Glutathione Reductase
                  precursor [Spinacia oleracea]
Seq. No.
                   226276
Seq. ID
                  LIB3166-053-P1-K1-F8
Method
                  BLASTX
NCBI GI
                   g1362067
BLAST score
                  598
E value
                   3.0e-62
Match length
                  124
% identity
                  94
```

>gi\_871508\_emb\_CAA90082\_ (Z49902) small GTP-binding protein

small GTP-binding protein - garden pea

[Pisum sativum]



Seq. No. 226277

Seq. ID LIB3166-053-P1-K1-F9

Method BLASTX NCBI GI g1055130 BLAST score 163 E value 1.0e-11 Match length 76 % identity

NCBI Description (U39998) coded for by C. elegans cDNA yk92b11.3; coded for by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by

C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA

yk78c2.3

Seq. No. 226278

Seq. ID LIB3166-053-P1-K1-G10

Method BLASTX NCBI GI q1345919 BLAST score 603 E value 7.0e-63 Match length 124 % identity

NCBI Description APOCYTOCHROME F PRECURSOR >gi 984315 (U26948) cytochrome f

precursor [Glycine max]

Seq. No. 226279

Seq. ID LIB3166-053-P1-K1-G11

Method BLASTX NCBI GI q3550454 BLAST score 195 E value 1.0e-15 Match length 44 % identity

(AF085820) alcohol dehydrogenase A [Gossypium barbadense] NCBI Description

>gi\_3550458 (AF085821) alcohol dehydrogenase A [Gossypium barbadense] >gi\_3551965 (AF085064) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_3551967 (AF085065) alcohol

dehydrogenase A [Ğossypium hirsutum] >gi\_3551971 (AF085067) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_3551975 (AF085069) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_3551977 (AF085070) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140594 (AF090146) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140604 (AF090151) alcohol

dehydrogenase A [Gossypium hirsutum] >gi 4140606 (AF090152) alcohol dehydrogenase A [Gossypium hirsutum] >gi 4140608 (AF090153) alcohol dehydrogenase A [Gossypium hirsutum]

>gi\_4140610 (AF090154) alcohol dehydrogenase A [Gossypium

hirsutum]

Seq. No. 226280

Seq. ID LIB3166-053-P1-K1-G12

Method BLASTX NCBI GI g70642 BLAST score 421 E value 1.0e-41 Match length 103 % identity 18



NCBI Description ubiquitin precursor - Arabidopsis thaliana >gi\_17678\_emb\_CAA31331\_ (X12853) polyubiquitin (AA 1 - 382) [Arabidopsis thaliana] >gi\_987519 (U33014) polyubiquitin [Arabidopsis thaliana] >gi\_226499\_prf\_1515347A poly-ubiquitin [Arabidopsis thaliana]

Seq. No. 226281 Seq. ID LIB3166-053-P1-K1-G2 Method BLASTX NCBI GI g68200 BLAST score 487 E value 3.0e-49Match length 124 % identity 81

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) precursor, chloroplast - spinach >gi\_22633\_emb\_CAA47293\_ (X66814) fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No. 226282 Seq. ID LIB3166-053-P1-K1-G3 Method BLASTX NCBI GI q3868758 BLAST score 405 E value 1.0e-39 Match length 101

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 226283 Seq. ID

% identity

LIB3166-053-P1-K1-G5

74

Method BLASTX NCBI GI g2462762 BLAST score 185 E value 6.0e-14 Match length 64 % identity 55

NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 226284

Seq. ID LIB3166-053-P1-K1-G6

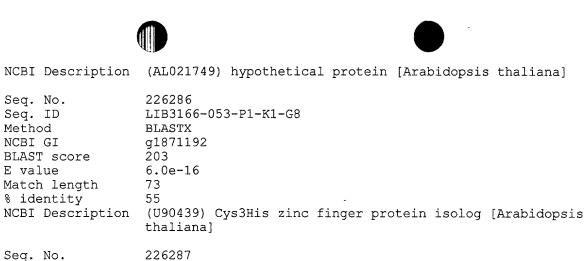
Method BLASTX NCBI GI g1944216 BLAST score 386 E value 1.0e-37 Match length 84 % identity

NCBI Description (D84246) alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No. 226285

LIB3166-053-P1-K1-G7 Seq. ID

Method BLASTX NCBI GI g2842485 BLAST score 152 E value 4.0e-10 Match length 80 % identity 41



 Seq. No.
 226287

 Seq. ID
 LIB3166-053-P1-K1-H11

 Method
 BLASTX

 NCBI GI
 g3334259

 BLAST score
 461

 E value
 3.0e-46

BLAST score 461 E value 3.0e-46 Match length 116 % identity 79

NCBI Description WD-40 REPEAT PROTEIN MSI4 >gi\_2599092 (AF028711) WD-40

repeat protein MSI4 [Arabidopsis thaliana]

Seq. No. 226288

Seq. ID LIB3166-053-P1-K1-H12

Method BLASTX
NCBI GI g2832625
BLAST score 362
E value 1.0e-34
Match length 127
% identity 50

NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 226289

Seq. ID LIB3166-053-P1-K1-H3

Method BLASTX
NCBI GI g3367515
BLAST score 381
E value 8.0e-37
Match length 97
% identity 72

NCBI Description (AC004392) Similar to

glucose-6-phosphate/phosphate-translocator (GPT) gb AF020814 from Pisum sativum. [Arabidopsis thaliana]

Seq. No. 226290

Seq. ID LIB3166-053-P1-K1-H6

Method BLASTX
NCBI GI g4249385
BLAST score 434
E value 3.0e-43
Match length 79
% identity. 96

NCBI Description (AC005966) T2K10.11 [Arabidopsis thaliana]

Seq. No. 226291

Method

NCBI GI

BLASTX

q1934730



```
Seq. ID
                  LIB3166-054-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g2879811
BLAST score
                  339
E value
                  4.0e-32
                  71
Match length
% identity
                  94
NCBI Description (AJ223316) ribosomal protein L30 [Lupinus luteus]
                  226292
Seq. No.
Seq. ID
                  LIB3166-054-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  q3068717
BLAST score
                  432
E value
                  9.0e-43
Match length
                  116
                  72
% identity
NCBI Description (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                  226293
Seq. ID
                  LIB3166-054-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g3023190
BLAST score
                  288
E value
                  3.0e-26
Match length
                  69
                  84
% identity
NCBI Description 14-3-3-LIKE PROTEIN 16R >qi 1888459 emb CAA72381 (Y11685)
                  14-3-3 protein [Solanum tuberosum]
Seq. No.
                  226294
Seq. ID
                  LIB3166-054-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g417154
BLAST score
                  230
E value
                  3.0e-19
Match length
                  80
% identity
                  65
NCBI Description HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
                  protein 82 - rice (strain Taichung Native One)
                  >gi 20256_emb_CAA77978_ (Z11920) heat shock protein 82
                  (HSP82) [Oryza sativa]
Seq. No.
                  226295
Seq. ID
                  LIB3166-054-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g3894385
BLAST score
                  169
E value
                  5.0e-12
Match length
                  112
% identity
NCBI Description (AF053994) Hcr2-OA [Lycopersicon esculentum]
Seq. No.
                  226296
Seq. ID
                  LIB3166-054-P1-K1-B3
```



% identity

```
BLAST score
E value
                   2.0e-16
Match length
                  73
% identity
                  52
NCBI Description (U95036) germin-like protein [Arabidopsis thaliana]
Seq. No.
                  226297
                  LIB3166-054-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4455278
BLAST score
                  202
E value
                  5.0e-16
                  90
Match length
% identity
                  41
NCBI Description (AL035527) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  226298
                  LIB3166-054-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3935148
BLAST score
                  282
E value
                  3.0e-25
Match length
                  72
                  71
% identity
NCBI Description (AC005106) T25N20.12 [Arabidopsis thaliana]
                  226299
Seq. No.
                  LIB3166-054-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  523
E value
                  1.0e-53
Match length
                  103
% identity
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
Seq. No.
                  226300
Seq. ID
                  LIB3166-054-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g3860323
BLAST score
                  210
E value
                  6.0e-17
Match length
                  63
% identity
NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]
Seq. No.
                  226301
Seq. ID
                  LIB3166-054-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  q4580513
BLAST score
                  385
E value
                  2.0e-37
Match length
                  104
```

NCBI Description (AF036300) scarecrow-like 1 [Arabidopsis thaliana]



Seq. No. 226302

Seq. ID LIB3166-054-P1-K1-C9

Method BLASTX
NCBI GI g3212869
BLAST score 490
E value 1.0e-49
Match length 106
% identity 86

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 226303

Seq. ID LIB3166-054-P1-K1-D10

Method BLASTX
NCBI GI g100616
BLAST score 367
E value 2.0e-35
Match length 82
% identity 82

NCBI Description ribulose-bisphosphate carboxylase activase B precursor -

barley >gi\_167093 (M55448) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare] >gi\_167095 (M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum

vulgare]

Seq. No. 226304

Seq. ID LIB3166-054-P1-K1-D11

Method BLASTX
NCBI GI g4539301
BLAST score 226
E value 4.0e-19
Match length 60
% identity 68

NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis

thaliana]

Seq. No. 226305

Seq. ID LIB3166-054-P1-K1-D2

Method BLASTX
NCBI GI 93552003
BLAST score 601
E value 1.0e-62
Match length 113
% identity 99

NCBI Description (AF085083) alcohol dehydrogenase A [Gossypium hirsutum]

>gi\_3552005 (AF085084) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_3552007 (AF085085) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140632 (AF090165) alcohol

dehydrogenase A [Gossypium hirsutum] >gi\_4140634 (AF090166) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140636 (AF090167) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140638 (AF090168) alcohol dehydrogenase A [Gossypium

hirsutum]

Seq. No. 226306

Seq. ID LIB3166-054-P1-K1-D8

Method BLASTX NCBI GI g439489

BLAST score

Match length

E value

139

48

1.0e-08



```
BLAST score
                   1.0e-13
E value
Match length
                   84
% identity
                   54
NCBI Description
                  (D26084) zinc-finger DNA binding protein [Petunia x
                   hybrida]
Seq. No.
                   226307
Seq. ID
                   LIB3166-054-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   g2924792
BLAST score
                   446
E value
                   1.0e-44
Match length
                   101
                   79
% identity
NCBI Description (AC002334) similar to synaptobrevin [Arabidopsis thaliana]
                   226308
Seq. No.
Seq. ID
                   LIB3166-054-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g1928981
BLAST score
                   325
E value
                   1.0e-30
Match length
                   72
% identity
                   90
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                  oleracea var. botrytis]
Seq. No.
                   226309
Seq. ID
                   LIB3166-054-P1-K1-E2
Method
                  BLASTX
NCBI GI
                   g3901012
BLAST score
                   369
E value
                   2.0e-35
Match length
                  93
% identity
                   72
NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus
                  sylvatica]
Seq. No.
                   226310
Seq. ID
                  LIB3166-054-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g4102859
BLAST score
                  505
E value
                   3.0e-56
Match length
                  128
                   80
% identity
NCBI Description
                  (AF016892) cytoplasmic superoxide dismutase 1 [Populus
                  tremuloides]
Seq. No.
                  226311
Seq. ID
                  LIB3166-054-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g4544460
```



```
% identity
NCBI Description
                   (AC006592) putative reverse transcriptase [Arabidopsis
                   thaliana]
Seq. No.
                   226312
Seq. ID
                   LIB3166-054-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   q1076715
BLAST score
                   187
E value
                   3.0e-14
Match length
                   63
                   54
% identity
NCBI Description abscisic acid-induced protein HVA22 - barley >gi_404589
                   (L19119) A22 [Hordeum vulgare]
Seq. No.
                   226313
Seq. ID
                  LIB3166-054-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  q1706958
BLAST score
                  507
E value
                   9.0e-52
Match length
                  97
% identity
NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]
Seq. No.
                  226314
Seq. ID
                  LIB3166-054-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g2961346
BLAST score
                   358
E value
                   2.0e-34
Match length
                  98
% identity
                   67
NCBI Description
                  (AL022140) pectinesterase like protein [Arabidopsis
                  thaliana]
Seq. No.
                   226315
Seq. ID
                  LIB3166-054-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q4539344
BLAST score
                  267
E value
                  9.0e-24
Match length
                  80
% identity
                  68
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
Seq. No.
                  226316
Seq. ID
                  LIB3166-054-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g1353352
BLAST score
                  335
E value
                  1.0e-31
Match length
                  98
% identity
                  61
```

NCBI Description (U31975) alanine aminotransferase [Chlamydomonas

reinhardtii]



```
Seq. No.
                   226317
                  LIB3166-054-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1353352
BLAST score
                  247
E value
                   3.0e-21
Match length
                  77
                  58
% identity
NCBI Description
                  (U31975) alanine aminotransferase [Chlamydomonas
                  reinhardtii]
Seq. No.
                  226318
Seq. ID
                  LIB3166-054-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q4539452
BLAST score
                  336
E value
                   8.0e-32
Match length
                  84
                  76
% identity
                  (AL049500) putative phosphoribosylanthranilate transferase
NCBI Description
                   [Arabidopsis thaliana]
                  226319
Seq. No.
                  LIB3166-054-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220482
BLAST score
                  182
E value
                  1.0e-13
Match length
                  70
                   53
% identity
NCBI Description (AC006069) hypothetical protein [Arabidopsis thaliana]
                   226320
Seq. No.
Seq. ID
                  LIB3166-054-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q1527191
BLAST score
                   301
E value
                   1.0e-27
Match length
                   67
% identity
NCBI Description
                   (U67861) 1-aminocyclopropane-1-carboxylate oxidase
                   [Pelargonium x hortorum]
Seq. No.
                   226321
Seq. ID
                  LIB3166-054-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g3550440
BLAST score
                  262
E value
                   3.0e-23
Match length
                  79
% identity
                   71
NCBI Description (AF085816) alcohol dehydrogenase A [Gossypium barbadense]
                  226322
Seq. No.
```

Seq. ID LIB3166-054-P1-K1-H1 Method BLASTX

Method BLASTX NCBI GI g2129915



BLAST score 150 E value 6.0e-10 Match length 59 % identity 54

NCBI Description ferredoxin precursor - sweet orange

>gi\_1360725\_emb\_CAA87068\_ (Z46944) non-photosynthetic

ferredoxin [Citrus sinensis]

Seq. No. 226323

Seq. ID LIB3166-054-P1-K1-H10

Method BLASTX
NCBI GI g4538929
BLAST score 257
E value 2.0e-22
Match length 110
% identity 55

NCBI Description (AL049483) putative nucleic acid binding protein

[Arabidopsis thaliana]

Seq. No. 226324

Seq. ID LIB3166-054-P1-K1-H11

Method BLASTX
NCBI GI g4455364
BLAST score 356
E value 5.0e-34
Match length 89
% identity 74

NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis

thaliana]

Seq. No. 226325

Seq. ID LIB3166-054-P1-K1-H2

Method BLASTX
NCBI GI g3183088
BLAST score 176
E value 5.0e-13
Match length 51
% identity 63

NCBI Description PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR

(LTP) >gi\_629658\_pir\_\_S47084 lipid transfer like protein -cowpea >gi\_499034\_emb\_CAA56113\_ (X79604) lipid transfer

like protein [Vigna unguiculata]

Seq. No. 226326

Seq. ID LIB3166-054-P1-K1-H4

Method BLASTX
NCBI GI g119150
BLAST score 295
E value 4.0e-31
Match length 82
% identity 88

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi\_82081\_pir\_\_S10507 translation elongation factor eEF-1
alpha chain - tomato >gi\_19273\_emb\_CAA32618\_ (X14449) EF

1-alpha (AA 1-448) [Lycopersicon esculentum]

>gi\_295810\_emb\_CAA37212\_ (X53043) elongation factor 1-alpha

[Lycopersicon esculentum]

BLAST score

E value

416

7.0e-41



```
Seq. No.
                   226327
Seq. ID
                   LIB3166-054-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g4455208
BLAST score
                   461
E value
                   2.0e-46
Match length
                  101
% identity
                   86
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                   226328
Seq. ID
                  LIB3166-054-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  q4220477
BLAST score
                  166
E value
                   7.0e-12
                  77
Match length
% identity
                  52
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.
                   226329
Seq. ID
                  LIB3166-054-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g2444178
BLAST score
                  271
E value
                  3.0e-24
Match length
                  91
% identity
                  67
NCBI Description (U94784) unconventional myosin [Helianthus annuus]
Seq. No.
                  226330
Seq. ID
                  LIB3166-055-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g3337350
BLAST score
                  428
E value
                  2.0e-42
Match length
                  102
% identity
                  80
NCBI Description (AC004481) putative permease [Arabidopsis thaliana]
Seq. No.
                  226331
Seq. ID
                  LIB3166-055-P1-K1-A3
Method
                  BLASTX
                  g2995384
NCBI GI
BLAST score
                  186
E value
                  4.0e-14
Match length
                  65
% identity
NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]
Seq. No.
                  226332
Seq. ID
                  LIB3166-055-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g4204294
```

Match length

% identity

116



```
Match length
                   123
% identity
                   73
NCBI Description
                   (AC003027) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                   226333
Seq. ID
                   LIB3166-055-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   q1220196
BLAST score
                   475
E value
                   8.0e-48
Match length
                   117
% identity
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.
                   226334
Seq. ID
                   LIB3166-055-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   q1732511
BLAST score
                   463
E value
                   2.0e-46
Match length
                   100
% identity
                   85
NCBI Description
                   (U62742) Ran binding protein 1 homolog [Arabidopsis
                  thaliana]
Seq. No.
                   226335
Seq. ID
                   LIB3166-055-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   g2129471
BLAST score
                   524
E value
                   1.0e-53
Match length
                   128
% identity
NCBI Description glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
                   precursor - Scotch pine >gi_1100223 (L32560)
                  glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
Seq. No.
                   226336
Seq. ID
                  LIB3166-055-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g1850546
BLAST score
                  329
E value
                   9.0e-31
Match length
                  86
                  79
% identity
NCBI Description
                  (U88045) syntaxin related protein AtVam3p [Arabidopsis
                  thaliana]
                  226337
Seq. No.
Seq. ID
                  LIB3166-055-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g4544409
BLAST score
                  430
E value
                  1.0e-42
```



```
NCBI Description
                  (AC006955) putative transcription factor [Arabidopsis
                  thaliana]
Seq. No.
                   226338
Seq. ID
                  LIB3166-055-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q3249066
BLAST score
                   436
E value
                   3.0e-43
Match length
                   120
% identity
                   72
NCBI Description
                   (AC004473) Similar to S. cerevisiae SIK1P protein
                  gb 984964. ESTs gb_F15433 and gb AA395158 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  226339
Seq. ID
                  LIB3166-055-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q1220196
BLAST score
                  152
E value
                   3.0e-10
Match length
                  80
% identity
                   46
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.
                  226340
Seq. ID
                  LIB3166-055-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g3068717
BLAST score
                  427
E value
                   3.0e-42
Match length
                  131
% identity
                   60
NCBI Description (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                  226341
Seq. ID
                  LIB3166-055-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g228210
BLAST score
                  396
E value
                  1.0e-38
Match length
                  113
% identity
                  68
NCBI Description granule-bound starch synthase [Solanum tuberosum]
Seq. No.
                  226342
Seq. ID
                  LIB3166-055-P1-K1-C10
                  BLASTX
```

Method NCBI GI g2791834 BLAST score 385 E value 3.0e-43 94 Match length 97 % identity

NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No. 226343

LIB3166-055-P1-K1-C11 Seq. ID



```
Method
                  BLASTX
NCBI GI
                  q4432866
BLAST score
                  142
E value
                  9.0e-09
Match length
                  121
% identity
NCBI Description
                  (AC006300) putative reverse transcriptase [Arabidopsis
                  thaliana]
Seq. No.
                  226344
Seq. ID
                  LIB3166-055-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q2370232
BLAST score
                  225
E value
                  6.0e-36
Match length
                  112
% identity
                  71
NCBI Description (AJ001341) putative acyl-CoA oxidase [Hordeum vulgare]
Seq. No.
                  226345
Seq. ID
                  LIB3166-055-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q1946369
BLAST score
                  197
E value
                  3.0e-15
Match length
                  78
% identity
                  50
NCBI Description (U93215) unknown protein [Arabidopsis thaliana]
Seq. No.
                  226346
Seq. ID
                  LIB3166-055-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g1174149
BLAST score
                  143
E value
                  6.0e-09
Match length
                  51
% identity
                  82
NCBI Description (U44104) small GTP binding protein Rab7 [Homo sapiens]
Seq. No.
                  226347
Seq. ID
                  LIB3166-055-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g3551983
BLAST score
                  704
E value
                  1.0e-74
Match length
                  129
                  98
% identity
NCBI Description
                  (AF085073) alcohol dehydrogenase A [Gossypium hirsutum]
                  >gi_3551985 (AF085074) alcohol dehydrogenase A [Gossypium
                  hirsutum] >gi 3551987 (AF085075) alcohol dehydrogenase A
                  [Gossypium hirsutum] >gi 3551989 (AF085076) alcohol
                  dehydrogenase A [Gossypium hirsutum] >gi 4140602 (AF090150)
                  alcohol dehydrogenase A [Gossypium hirsutum] >gi 4140612
```

(AF090155) alcohol dehydrogenase A [Gossypium hirsutum] >gi\_4140614 (AF090156) alcohol dehydrogenase A [Gossypium hirsutum] >gi 4140616 (AF090157) alcohol dehydrogenase A [Gossypium hirsutum]



Seq. No. 226348

Seq. ID LIB3166-055-P1-K1-C7

Method BLASTX
NCBI GI g464707
BLAST score 574
E value 2.0e-59
Match length 117
% identity 96

NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal

protein S18.A - Arabidopsis thaliana

>gi\_405613\_emb\_CAA80684\_ (Z23165) ribosomal protein S18A
[Arabidopsis thaliana] >gi\_434343\_emb\_CAA82273\_ (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi\_434345\_emb\_CAA82274\_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi\_434906\_emb\_CAA82275\_ (Z28962)

S18 ribosomal protein [Arabidopsis thaliana]

>gi\_2505871\_emb\_CAA72909\_ (Y12227) ribosomal protein S18A
[Arabidopsis thaliana] >gi\_3287678 (AC003979) Match to
ribosomal S18 gene mRNA gb\_Z28701, DNA gb\_Z23165 from A.
thaliana. ESTs gb\_T21121, gb\_Z17755, gb\_R64776 and
gb\_R30430 come from this gene. [Arabidopsis thaliana]
>gi\_4538910\_emb\_CAB39647.1\_ (AL049482) S18.A ribosomal

protein [Arabidopsis thaliana]

Seq. No. 226349

Seq. ID LIB3166-055-P1-K1-C9

Method BLASTX
NCBI GI g120669
BLAST score 245
E value 2.0e-21
Match length 69
% identity 70

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde
'3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 226350

Seq. ID LIB3166-055-P1-K1-D10

Method BLASTX
NCBI GI g3776559
BLAST score 303
E value 1.0e-27
Match length 114
% identity 55

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi\_3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb AC003970. ESTs gb\_Z35332 and gb\_F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No. 226351

Seq. ID LIB3166-055-P1-K1-D11

Method BLASTX NCBI GI g3402684 BLAST score 572



```
E value
                   3.0e-59
Match length
                  130
% identity
                  79
NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  226352
Seq. ID
                  LIB3166-055-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g2769642
BLAST score
                  405
E value
                  9.0e-40
Match length
                  101
                  76
% identity
NCBI Description (Z97215) nine-cis-epoxycarotenoid dioxygenase [Lycopersicon
                  esculentum]
Seq. No.
                  226353
                  LIB3166-055-P1-K1-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3355467
BLAST score
                  275
E value
                  2.0e-24
Match length
                  129
                  40
% identity
NCBI Description (AC004218) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  226354
Seq. ID
                  LIB3166-055-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g2961357
BLAST score
                  574
E value
                  2.0e-59
Match length
                  128
% identity
                  82
NCBI Description (AL022140) putative protein [Arabidopsis thaliana]
              - 226355
Seq. No.
Seq. ID
                  LIB3166-055-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g3402750
BLAST score
                  212
E value
                  5.0e-17
Match length
                  102
% identity
                  46
NCBI Description (AL031187) putative protein [Arabidopsis thaliana]
Seq. No.
                  226356
Seq. ID
                  LIB3166-055-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q586004
BLAST score
                  570
E value
                  6.0e-59
Match length
                  116
% identity
                  90
NCBI Description SUPEROXIDE DISMUTASE [CU-ZN] >gi 421962 pir S34267
```

superoxide dismutase (EC  $1.15.1.\overline{1}$ ) (Cu- $\overline{Z}n$ ) - sweet potato >gi\_542090\_pir\_\_S40404 superoxide dismutase (EC 1.15.1.1)





(Cu-Zn) - sweet potato >gi\_311971\_emb\_CAA51654\_ (X73139) superoxide dismutase [Ipomoea batatas]

 Seq. No.
 226357

 Seq. ID
 LIB3166-055-P1-K1-E2

 Method
 BLASTX

 NCBI GI
 g132168

 BLAST score
 463

 E value
 2.0e-46

Match length 115 % identity 74

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi\_81488\_pir\_\_A31082

ribulose-bisphosphate carboxylase activase precursor - spinach >gi\_170129 (J03610) rubisco activase precursor

[Spinacia oleracea]

Seq. No. 226358

Seq. ID LIB3166-055-P1-K1-E4

Method BLASTX
NCBI GI g4376815
BLAST score 236
E value 8.0e-20
Match length 123
% identity 37

NCBI Description (AE001637) GutQ/KpsF Family Sugar-P Isomerase [Chlamydia

pneumoniae]

Seq. No. 226359

Seq. ID LIB3166-055-P1-K1-E5

Method BLASTX
NCBI GI g1321661
BLAST score 351
E value 3.0e-33
Match length 111
% identity 64

NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

Seq. No. 226360

Seq. ID LIB3166-055-P1-K1-E6

Method BLASTX
NCBI GI g860932
BLAST score 175
E value 3.0e-13
Match length 67
% identity 52

NCBI Description (Z49856) alpha-tubulin [Epidinium sp.]

Seq. No. 226361

Seq. ID LIB3166-055-P1-K1-F1

Method BLASTX
NCBI GI g4539330
BLAST score 377
E value 1.0e-37
Match length 123
% identity 67

NCBI Description (AL035679) putative receptor-like protein kinase (fragment)



## [Arabidopsis thaliana]

```
Seq. No.
                  226362
Seq. ID
                  LIB3166-055-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  q2149955
BLAST score
                  178
E value
                  8.0e-27
Match length
                  97
% identity
NCBI Description (U97023) putative aquaporin-1 [Phaseolus vulgaris]
Seq. No.
                  226363
Seq. ID
                  LIB3166-055-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  q4220455
BLAST score
                  315
E value
                  4.0e-29
Match length
                  124
% identity
                  59
NCBI Description (AC006216) Identical to gene gb D88746 AR791 from
                  Arabidopsis thaliana. [Arabidopsis thaliana]
Seq. No.
                  226364
Seq. ID
                  LIB3166-055-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  q1944216
BLAST score
                  394
E value
                  1.0e-38
Match length
                  82
% identity
                  89
NCBI Description (D84246) alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.
                  226365
                  LIB3166-055-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827630
BLAST score
                  398
E value
                  8.0e-39
Match length
                  114
% identity
                  69
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]
                  226366
Seq. No.
                  LIB3166-055-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g130600
BLAST score
                  417
E value
                  5.0e-41
Match length
                  129
% identity
                  63
NCBI Description ENZYMATIC POLYPROTEIN [CONTAINS: ASPARTIC PROTEASE;
                  ENDONUCLEASE; REVERSE TRANSCRIPTASE ] >qi 76782 pir S01283
```

mosaic virus]

hypothetical protein 5 - figwort mosaic virus

>gi\_58813\_emb\_CAA29527\_ (X06166) ORF V (AA 1-666) [Figwort



```
Seq. No.
                   226367
Seq. ID
                   LIB3166-055-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   g2623297
BLAST score
                   468
E value
                   2.0e-48
Match length
                  122
% identity
                   75
                  (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3790583 (AF079180) RING-H2 finger protein RHCla
                   [Arabidopsis thaliana]
Seq. No.
                  226368
Seq. ID
                  LIB3166-055-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2760830
BLAST score
                  629
E value
                  7.0e-66
Match length
                  128
% identity
                  86
NCBI Description (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
                  thaliana]
Seq. No.
                  226369
Seq. ID
                  LIB3166-055-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  q3318611
BLAST score
                  144
E value
                  1.0e-10
Match length
                  74
% identity
NCBI Description (AB016063) mitochondrial phosphate transporter [Glycine
                  max]
Seq. No.
                  226370
Seq. ID
                  LIB3166-055-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g2194142
BLAST score
                  552
E value
                  7.0e-57
Match length
                  131
% identity
                  73
NCBI Description
                  (AC002062) ESTs gb_N38288,gb_T43486,gb_AA395242 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  226371
Seq. ID
                  LIB3166-055-P1-K1-G2
Method
                  BLASTX
                  g4056506
NCBI GI
BLAST score
                  347
E value
                  8.0e-33
```

Match length 107 % identity

NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]

Seq. No. 226372

Seq. ID LIB3166-055-P1-K1-G4



```
Method
                  BLASTX
NCBI GI
                  g1709825
BLAST score
                  197
E value
                  3.0e-15
Match length
                  118
                  42
% identity
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
                  (PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana]
Seq. No.
                  226373
Seq. ID
                  LIB3166-055-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  q3860264
BLAST score
                  558
E value
                  1.0e-57
Match length
                  119
                  87
% identity
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
                  226374
Seq. No.
Seq. ID
                  LIB3166-055-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q1263291
BLAST score
                  589
E value
                  3.0e-61
Match length
                  129
% identity
                  81
NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]
Seq. No.
                  226375
Seq. ID
                  LIB3166-055-P1-K1-H5
                  BLASTX
Method
NCBI GI
                  g2129832
BLAST score
                  561
                  7.0e-58
E value
Match length
                  110
                  93
% identity
NCBI Description heat shock transcription factor 5 - soybean
                  >gi 671868 emb CAA87080 (Z46956) heat shock transcription
                  factor 5 [Glycine max]
                  226376
Seq. No.
Seq. ID
                  LIB3166-055-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g4539348
BLAST score
                  252
E value
                  1.0e-21
Match length
                  92
% identity
                  51
NCBI Description (AL035539) putative pollen allergen [Arabidopsis thaliana]
Seq. No.
                  226377
```

Seq. ID LIB3166-056-P1-K1-A11

Method BLASTX NCBI GI g3608171 BLAST score 174 E value 6.0e-13



```
Match length
% identity
NCBI Description
                  (D86306) proton-translocating inorganic pyrophosphatase
                  [Cucurbita moschata]
Seq. No.
                  226378
Seq. ID
                  LIB3166-056-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q4467128
BLAST score
                  163
E value
                  8.0e-12
Match length
                  58
% identity
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]
                  226379
Seq. No.
Seq. ID
                  LIB3166-056-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g1345674
BLAST score
                  285
E value
                  8.0e-26
Match length
                  95
                  62
% identity
NCBI Description
                  CATALASE ISOZYME 1 >gi 99598 pir S10770 catalase (EC
                  1.11.1.6) - upland cotton >gi 18484 emb CAA36380 (X52135)
                  catalase subunit 1 (AA 1-492) [Gossypium hirsutum]
Seq. No.
                  226380
Seq. ID
                  LIB3166-056-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g2493046
BLAST score
                  178
E value
                  5.0e-13
Match length
                  66
% identity
                  55
NCBI Description ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR
                  >gi_82297 pir A41740 H+-transporting ATP synthase (EC
                  3.6.1.34) delta' chain precursor - sweet potato
                  >gi 217938 dbj BAA01511 (D10660) mitochondrial F1-ATPase
                  delta subunit [Ipomoea batatas]
Seq. No.
                  226381
Seq. ID
                  LIB3166-056-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  q2827699
BLAST score
                  173
E value
                  1.0e-12
Match length
                  66
% identity
NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]
```

Seq. No. 226382

Seq. ID LIB3166-056-P1-K1-C11

Method BLASTX g1888357 NCBI GI BLAST score 262 E value 4.0e-23



Match length % identity 54 NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana] >gi\_1890154\_emb\_CAA72432\_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana] Seq. No. 226383 Seq. ID LIB3166-056-P1-K1-D3 Method BLASTX NCBI GI q2996202 BLAST score 184 E value 3.0e-14 Match length 48 % identity 67 NCBI Description (AF053725) myristoyl-CoA: protein N-myristoyl transferase [Drosophila melanogaster] Seq. No. 226384 Seq. ID LIB3166-056-P1-K1-D7 Method BLASTX NCBI GI g3367593 BLAST score 178 E value 2.0e-13 Match length 60 % identity 68 NCBI Description (AL031135) putative protein [Arabidopsis thaliana] >gi 3805841 emb CAA21461 (AL031986) putative protein [Arabidopsis thaliana] Seq. No. 226385 LIB3166-056-P1-K1-E1 Seq. ID Method BLASTX NCBI GI g3688600 BLAST score 188 1.0e-14 E value Match length 61 % identity NCBI Description (AB009030) beta-Amyrin Synthase [Panax ginseng] 226386 Seq. No. Seq. ID LIB3166-056-P1-K1-E10 Method BLASTX NCBI GI g4406780 BLAST score 263 E value 3.0e-23 Match length 86

% identity

NCBI Description (AC006532) putative multispanning membrane protein

[Arabidopsis thaliana]

Seq. No. 226387

Seq. ID LIB3166-056-P1-K1-E11

Method BLASTX NCBI GI g1076511 BLAST score 440 E value 7.0e-44Match length 103



```
% identity
NCBI Description H+-transporting ATPase (EC 3.6.1.35) - kidney bean
                   >gi_758250_emb_CAA59799 (X85804) H(+)-transporting ATPase
                   [Phaseolus vulgaris]
Seq. No.
                   226388
Seq. ID
                   LIB3166-056-P1-K1-G9
Method
                  BLASTX
NCBI GI
                   a198884
BLAST score
                  142
E value
                  2.0e-09
Match length
                  47
% identity
                   51
NCBI Description (M63848) leukotriene A-4 hydrolase [Mus musculus]
Seq. No.
                  226389
                  LIB3166-057-P1-K1-A1
Seq. ID
Method
                  BLASTX
                  g1362051
NCBI GI
BLAST score
                  514
E value
                  2.0e-52
Match length
                  118
% identity
                  69
NCBI Description protein kinase 3 - soybean >gi_310582 (L19361) protein
                  kinase 3 [Glycine max]
Seq. No.
                  226390
Seq. ID
                  LIB3166-057-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g3204108
BLAST score
                  301
E value
                  1.0e-27
Match length
                  72
% identity
                  76
NCBI Description (AJ006764) putative deoxycytidylate deaminase [Cicer
                  arietinum]
Seq. No.
                  226391
Seq. ID
                  LIB3166-057-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g1255951
BLAST score
                  128
E value
                  4.0e-17
Match length
                  51
% identity
                  73
NCBI Description (X96932) PS60 [Nicotiana tabacum]
Seq. No.
                  226392
Seq. ID
                  LIB3166-057-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g1346180
BLAST score
                  193
E value
                  1.0e-19
Match length
                  95
% identity
                  58
NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN GRP1A >gi_496233 (L31374)
```

homology with RNA-binding proteins in meristematic tissue

Match length

% identity

69

83



## [Sinapis alba]

```
Seq. No.
                   226393
Seq. ID
                   LIB3166-057-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   q123650
BLAST score
                   416
E value
                   5.0e-41
Match length
                   79
% identity
                   100
NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN >gi 82245 pir $03250 heat
                   shock protein 70 (clone pMON9743) - garden petunia
                   >gi_20557_emb_CAA30018_ (X06932) heat shock protein 70
                   [Petunia \bar{x} hybrida]
Seq. No.
                   226394
Seq. ID
                   LIB3166-057-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   q541816
BLAST score
                   236
E value
                   7.0e-20
Match length
                   80
% identity
                   62
NCBI Description protein kinase - common ice plant >gi_457689_emb_CAA82990_
                   (Z30329) protein kinase [Mesembryanthemum crystallinum]
Seq. No.
                   226395
Seq. ID
                   LIB3166-057-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   g2864625
BLAST score
                   280
E value
                   6.0e-25
Match length
                   62
% identity
                  77
NCBI Description (AL021811) putative protein [Arabidopsis thaliana]
Seq. No.
                   226396
Seq. ID
                  LIB3166-057-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g1170747
BLAST score
                   309
E value
                  2.0e-28
Match length
                  63
% identity
                  100
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
                   (M88324) late embryogenesis-abundant protein [\overline{G}ossypium]
                  hirsutum] >gi 167347 (M37697) Lea5-A late
                  embryogenesis-abundant protein [Gossypium hirsutum]
Seq. No.
                  226397
Seq. ID
                  LIB3166-057-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g2982303
BLAST score
                  305
E value
                  6.0e-28
```





```
NCBI Description (AF051236) hypothetical protein [Picea mariana]
                  226398
Seq. No.
Seq. ID
                  LIB3166-057-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g2664200
BLAST score
                  182
E value
                  1.0e-13
                  103
Match length
                  32
% identity
NCBI Description (AJ003216) GTL2 [Arabidopsis thaliana]
Seq. No.
                  226399
Seq. ID
                  LIB3166-057-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g4039155
BLAST score
                  432
E value
                  7.0e-43
Match length
                  116
% identity
                  66
NCBI Description (AF104258) putative copper-inducible 35.6 kDa protein
                  [Festuca rubra]
                  226400
Seq. No.
Seq. ID
                  LIB3166-057-P1-K1-C11
                  BLASTX
Method
NCBI GI
                  g3047114
BLAST score
                  435
E value
                  3.0e-43
Match length
                  118
% identity
                  63
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.
                  226401
                  LIB3166-057-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3024127
BLAST score
                  490
E value
                  8.0e-51
Match length
                  117
                  79
% identity
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
                  ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)
                  >gi 1655578 emb CAA95857\_ (Z71272) S-adenosyl-L-methionine
                  synthetase 2 [Catharanthus roseus]
Seq. No.
                  226402
Seq. ID
                  LIB3166-057-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q4415931
BLAST score
                  425
E value
                  5.0e-42
Match length
                  114
% identity
                  71
NCBI Description
                  (AC006418) unknown protein [Arabidopsis thaliana]
```

protein [Arabidopsis thaliana]

>gi 4559393 gb AAD23053.1 AC006526 18 (AC006526) unknown



```
226403
Seq. No.
Seq. ID
                  LIB3166-057-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g1173198
BLAST score
                  337
E value
                  6.0e-32
Match length
                  76
                  88
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S13 >gi 480095 pir S36423 ribosomal
                  protein S13.e - garden pea >qi 396639 emb CAA80974
                  (Z25509) ribosomal protein S13 [Pisum sativum]
                  226404
Seq. No.
Seq. ID
                  LIB3166-057-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g2160756
BLAST score
                  188
E value
                  1.0e-23
Match length
                  112
% identity
                  54
NCBI Description (U96879) CLV1 receptor kinase [Arabidopsis thaliana]
Seq. No.
                  226405
                  LIB3166-057-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539543
BLAST score
                  561
E value
                  5.0e-58
Match length
                  116
% identity
                  95
NCBI Description (AJ133422) glyceraldehyde-3-phosphate dehydrogenase
                  [Nicotiana tabacum]
Seq. No.
                  226406
                  LIB3166-057-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1723125
BLAST score
                  197
E value
                  3.0e-15
Match length
                  71
% identity
                  55
NCBI Description HYPOTHETICAL 27.8 KD PROTEIN SLL0194
                  >gi_1001604_dbj_BAA10232 (D64000) hypothetical protein
                  [Synechocystis sp.]
Seq. No.
                  226407
Seq. ID
                  LIB3166-057-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g2495365
BLAST score
                  344
E value
                  2.0e-32
Match length
                  86
% identity
                  78
```

heat shock protein HSP81-2 [Arabidopsis thaliana]

NCBI Description HEAT SHOCK PROTEIN 81-2 (HSP81-2) >qi 445127 prf 1908431B

Seq. ID

Method

NCBI GI



```
Seq. No.
                  226408
Seq. ID
                  LIB3166-057-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g2462758
BLAST score
                  341
E value
                   3.0e - 32
Match length
                  90
% identity
                  73
                  (AC002292) putative RNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  226409
Seq. No.
Seq. ID
                  LIB3166-057-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g3600040
BLAST score
                  241
E value
                  2.0e-20
Match length
                  118
% identity
                  47
NCBI Description (AF080119) similar to Arabidopsis thaliana disease
                  resistance protein RPS2 (GB:U14158) [Arabidopsis thaliana]
Seq. No.
                  226410
Seq. ID
                  LIB3166-057-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g3334320
BLAST score
                  434
E value
                  4.0e-43
Match length
                  94
                  95
% identity
NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553)
                  ribosome-associated protein p40 [Glycine max]
Seq. No.
                  226411
Seq. ID
                  LIB3166-057-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g2583108
BLAST score
                  251
E value
                  1.0e-21
Match length
                  95
% identity
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]
Seq. No.
                  226412
Seq. ID
                  LIB3166-057-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g2204077
BLAST score
                  190
E value
                  2.0e-14
Match length
                  86
% identity
NCBI Description (D85623) extracellular insoluble cystatin [Daucus carota]
Seq. No.
                  226413
```

32274

LIB3166-057-P1-K1-E3

BLASTX

q231574



```
BLAST score
E value
                   4.0e-15
Match length
                  64
% identity
                  61
NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
                  >gi 81837 pir __S22523 asparaginase (EC 3.5.1.1) - tree
                  lupine (fragment) >gi_19137_emb_CAA36824 (X52588)
                  asparaginase [Lupinus arboreus]
Seq. No.
                  226414
Seq. ID
                  LIB3166-057-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g3549626
BLAST score
                  476
E value
                  5.0e-48
Match length
                  120
% identity
NCBI Description (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
Seq. No.
                  226415
Seq. ID
                  LIB3166-057-P1-K1-E6
Method
                  BLASTX
                  q100490
NCBI GI
BLAST score
                  556
E value
                  2.0e-57
Match length
                  112
% identity
                  25
NCBI Description polyubiquitin - garden snapdragon (fragment)
                  >gi_16071 emb_CAA48140_ (X67957) ubiquitin [Antirrhinum
                  majus]
Seq. No.
                  226416
Seq. ID
                  LIB3166-057-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g3193326
BLAST score
                  150
E value
                  1.0e-12
Match length
                  88
% identity
                  57
NCBI Description
                  (AF069299) contains similarity to transcriptional
                  activators such as Ra-like and myc-like regulatory R
                  proteins [Arabidopsis thaliana]
Seq. No.
                  226417
Seq. ID
                  LIB3166-057-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g3560264
BLAST score
                  195
E value
                  4.0e-15
Match length
                  103
% identity
                  48
NCBI Description (AL031535) soll family protein [Schizosaccharomyces pombe]
```

Seq. No. 226418

Seq. ID LIB3166-057-P1-K1-F12

Method BLASTX NCBI GI g2662415

Match length

% identity

91



```
BLAST score
E value
                   1.0e-08
Match length
                   48
                   56
% identity
NCBI Description (U97494) metallothionein-like protein [Prunus armeniaca]
Seq. No.
                   226419
Seq. ID
                  LIB3166-057-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g3832528
BLAST score
                  355
E value
                  8.0e-34
Match length
                  100
                   71
% identity
NCBI Description (AF100167) unknown [Glycine max]
Seq. No.
                   226420
Seq. ID
                  LIB3166-057-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g967125
BLAST score
                  543
E value
                  1.0e-56
Match length
                  120
% identity
                   93
NCBI Description (U08140) calcium dependent protein kinase [Vigna radiata]
Seq. No.
                   226421
Seq. ID
                  LIB3166-057-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g3482967
BLAST score
                  129
E value
                   4.0e-17
Match length
                  56
% identity
                  82
                  (AL031369) Protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                  thaliana] >gi_4559345 gb AAD23006.1 AC006585 1 (AC006585)
                  protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.
                  226422
Seq. ID
                  LIB3166-057-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q4490937
BLAST score
                  226
                  1.0e-18
E value
Match length
                  121
% identity
                  33
NCBI Description
                  (AJ132261) hypothetical helicase K12H4.8-like protein [Homo
                  sapiens]
Seq. No.
                  226423
Seq. ID
                  LIB3166-057-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g3176681
BLAST score
                  160
E value
                  6.0e-11
```



```
NCBI Description (AC003671) F1707.11 [Arabidopsis thaliana]
Seq. No.
                  226424
Seq. ID
                  LIB3166-057-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  q100226
BLAST score
                  490
E value
                  1.0e-49
Match length
                  115
% identity
                  83
NCBI Description hypothetical protein - tomato >gi_19275_emb_CAA78112
                  (Z12127) protein of unknown function [Lycopersicon
                  esculentum] >gi_445619_prf__1909366A Leu zipper protein
                  [Lycopersicon esculentum]
                  226425
Seq. No.
Seq. ID
                  LIB3166-057-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g2981169
                  226
BLAST score
E value
                  1.0e-18
Match length
                  96
% identity
                  60
NCBI Description (AF053077) osmotic stress-induced zinc-finger protein
                  [Nicotiana tabacum]
Seq. No.
                  226426
Seq. ID
                  LIB3166-057-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q2454182
BLAST score
                  306
E value
                  4.0e-28
Match length
                  79
% identity
                  72
NCBI Description (U80185) pyruvate dehydrogenase E1 alpha subunit
                  [Arabidopsis thaliana]
Seq. No.
                  226427
Seq. ID
                  LIB3166-057-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  q2583130
BLAST score
                  155
E value
                  2.0e-10
Match length
                  114
% identity
NCBI Description
                 (AC002387) putative reverse transcriptase [Arabidopsis
                  thalianal
Seq. No.
                  226428
Seq. ID
                  LIB3166-057-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g4309742
```

BLAST score 141 E value 1.0e-08 53 Match length % identity 45

NCBI Description (AC006439) putative Rerl protein [Arabidopsis thaliana]

% identity



```
Seq. No.
                   226429
Seq. ID
                   LIB3166-057-P1-K1-H9
Method
                  BLASTX
NCBI GI
                   g1076764
BLAST score
                   274
E value
                   3.0e-24
Match length
                   105
% identity
                   18
NCBI Description AWJL236 protein - wheat >gi_551214_emb_CAA57135_ (X81370)
                  AWJL236 [Triticum aestivum]
                   226430
Seq. No.
Seq. ID
                   LIB3166-058-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g1345970
BLAST score
                   532
E value
                   1.0e-54
Match length
                   112
% identity
                   83
NCBI Description OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR
                   >gi 870784 (U25817) omega-3 fatty acid desaturase [Sesamum
                   indicum]
Seq. No.
                   226431
Seq. ID
                   LIB3166-058-P1-K1-A2
                   BLASTX
Method
                   g2982459
NCBI GI
BLAST score
                   373
E value
                   6.0e-36
                  99
Match length
                   73
% identity
NCBI Description (AL022223) putative protein [Arabidopsis thaliana]
                   226432
Seq. No.
Seq. ID
                   LIB3166-058-P1-K1-A5
                   BLASTX
Method
NCBI GI
                   g2108252
BLAST score
                   283
E value
                   2.0e-25
Match length
                   117
                   23
% identity
NCBI Description (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]
                   >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
[Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_
                   (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
                   226433
Seq. No.
Seq. ID
                   LIB3166-058-P1-K1-A6
Method
                   BLASTX
                   g3766377
NCBI GI
BLAST score
                  148
E value
                   2.0e-09
Match length
                  95
```

NCBI Description (AL031907) hypothetical protein [Schizosaccharomyces pombe]



```
Seq. No.
                   226434
Seq. ID
                   LIB3166-058-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   q2245066
BLAST score
                   182
E value
                   1.0e-13
Match length
                   111
% identity
                   42
NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]
Seq. No.
                   226435
Seq. ID
                   LIB3166-058-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   q4432835
                   175
BLAST score
                   7.0e-13
E value
Match length
                   52
% identity
                   58
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                   226436
Seq. ID
                   LIB3166-058-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   q3885329
BLAST score
                   366
E value
                   4.0e-35
Match length
                   76
% identity
                   88
NCBI Description (AC005623) alien-like protein [Arabidopsis thaliana]
Seq. No.
                   226437
Seq. ID
                   LIB3166-058-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   g3047125
BLAST score
                   362
E value
                   1.0e-34
Match length
                   116
% identity
                   65
NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.
                   226438
Seq. ID
                   LIB3166-058-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g4559339
BLAST score
                  185
E value
                   6.0e-14
Match length
                  76
% identity
                   (AC007087) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  226439
Seq. ID
                  LIB3166-058-P1-K1-B6
Method
                  BLASTX
NCBI GI
```

g602076

1.0e-58

567

BLAST score

E value

Match length

% identity

116



```
Match length
                   118
% identity
                   22
NCBI Description (X77456) pentameric polyubiquitin [Nicotiana tabacum]
                   226440
Seq. No.
Seq. ID
                   LIB3166-058-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   g3434971
BLAST score
                   201
E value
                   9.0e-16
                   40
Match length
                   88
% identity
NCBI Description (AB008105) ethylene responsive element binding factor 3
                   [Arabidopsis thaliana]
Seq. No.
                   226441
Seq. ID
                   LIB3166-058-P1-K1-C10
                   {\tt BLASTX}
Method
NCBI GI
                   g122007
BLAST score
                   256
E value
                   3.0e-22
                   74
Match length
                   70
% identity
NCBI Description HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley
                   >gi 20448 emb \overline{\text{CAA}37828} (X\overline{53}831) H2A histone protein (AA 1
                   - 149) [Petroselinum crispum]
Seq. No.
                   226442
Seq. ID
                   LIB3166-058-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g3790554
BLAST score
                   140
E value
                   1.0e-08
Match length
                   98
% identity
                   33
NCBI Description (AF078683) RING-H2 finger protein RHA1a [Arabidopsis
                   thaliana]
                   226443
Seq. No.
Seq. ID
                   LIB3166-058-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   q3023605
BLAST score
                   233
E value
                   3.0e-37
Match length
                   104
                   77
% identity
NCBI Description CYTOCHROME B6 >gi 2224430 dbj BAA57914 (AB001684)
                   cytochrome b6 [Chlorella vulgaris]
Seq. No.
                   226444
Seq. ID
                   LIB3166-058-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   g3668089
BLAST score
                   308
E value
                   2.0e-28
```



```
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.
                   226445
Seq. ID
                   LIB3166-058-P1-K1-C9
Method
                   BLASTX
NCBI GI
                  q1076755
BLAST score
                  194
E value
                   6.0e-15
Match length
                   112
% identity
                   36
NCBI Description protein kinase - rice >gi 450300 (L27821) protein kinase
                  [Oryza sativa]
Seq. No.
                   226446
Seq. ID
                  LIB3166-058-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g100226
BLAST score
                   309
                  2.0e-28
E value
Match length
                  117
% identity
                   45
NCBI Description
                  hypothetical protein - tomato >gi_19275_emb CAA78112
                   (Z12127) protein of unknown function [Lycopersicon
                  esculentum] >gi_445619_prf__1909366A Leu zipper protein
                   [Lycopersicon esculentum]
Seq. No.
                  226447
Seq. ID
                  LIB3166-058-P1-K1-D11
Method
                  BLASTX
                  q3763916
NCBI GI
BLAST score
                  249
E value
                  2.0e-21
Match length
                  116
% identity
NCBI Description
                  (AC004450) unknown protein [Arabidopsis thaliana]
                  >gi 4531439 gb AAD22124.1 AC006224 6 (AC006224) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  226448
                  LIB3166-058-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3924596
BLAST score
                  327
E value
                  1.0e-51
Match length
                  118
% identity
                  86
                  (AF069442) putative phospho-ser/thr phosphatase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  226449
                  LIB3166-058-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827143
BLAST score
                  576
E value
                  9.0e-60
Match length
```

91

% identity

NCBI Description

thaliana]



```
NCBI Description
                   (AF027174) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
                   226450
Seq. No.
                  LIB3166-058-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2275217
BLAST score
                  194
E value
                   6.0e-15
Match length
                  75
% identity
                   45
NCBI Description
                  (AC002337) chloroplast protein CP12 isolog [Arabidopsis
                  thaliana]
Seq. No.
                  226451
Seq. ID
                  LIB3166-058-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g1362093
BLAST score
                  241
E value
                  2.0e-20
Match length
                  85
% identity
                  62
                  hypothetical protein (clone TPP15) - tomato (fragment)
NCBI Description
                  >gi_924632 (U20595) unknown [Solanum lycopersicum]
Seq. No.
                  226452
Seq. ID
                  LIB3166-058-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g4190952
BLAST score
                  429
E value
                  2.0e-42
Match length
                  110
                  71
% identity
NCBI Description
                 (AB022689) similar to hsr203J [Lycopersicon esculentum]
Seq. No.
                  226453
Seq. ID
                  LIB3166-058-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g4263712
BLAST score
                  294
E value
                  1.0e-26
Match length
                  77
                  70
% identity
NCBI Description
                  (AC006223) putative ribosomal protein S12 [Arabidopsis
                  thaliana]
Seq. No.
                  226454
Seq. ID
                  LIB3166-058-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g3033400
BLAST score
                  556
E value
                  2.0e-57
Match length
                  127
% identity
                  85
```

32282

(AC004238) putative Ser/Thr protein kinase [Arabidopsis



```
Seq. No.
                   226455
Seq. ID
                   LIB3166-058-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   g3549667
BLAST score
                   219
E value
                   8.0e-18
Match length
                   69
% identity
                   62
NCBI Description
                  (AL031394) Arabidopsis dynamin-like protein ADL2
                   [Arabidopsis thaliana]
Seq. No.
                   226456
Seq. ID
                  LIB3166-058-P1-K1-F12
Method
                  BLASTX
NCBI GI
                   g2245005
BLAST score
                  170
E value
                   4.0e-12
Match length
                  58
% identity
                   59
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  226457
Seq. ID
                  LIB3166-058-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  q2981169
BLAST score
                  271
E value
                   5.0e-24
Match length
                  104
% identity
                   52
NCBI Description (AF053077) osmotic stress-induced zinc-finger protein
                   [Nicotiana tabacum]
Seq. No.
                  226458
Seq. ID
                  LIB3166-058-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g1008904
BLAST score
                  524
E value
                  1.0e-57
Match length
                  116
% identity
                  88
NCBI Description (L43094) xyloglucan endotransglycosylase [Tropaeolum majus]
Seq. No.
                  226459
Seq. ID
                  LIB3166-058-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q2462762
BLAST score
                  291
E value
                  2.0e-26
Match length
                  109
% identity
                  56
                 (AC002292) Highly similar to auxin-induced protein
NCBI Description
                  (aldo/keto reductase family) [Arabidopsis thaliana]
```

Seq. No. 226460

Seq. ID LIB3166-058-P1-K1-G12

Method BLASTX NCBI GI g1076633



```
BLAST score
E value
                  1.0e-42
Match length
                  101
% identity
                  85
NCBI Description
                  protein kinase NPK5 (EC 2.7.1.-) - common tobacco
                  >gi_496385_dbj_BAA05649_ (D26602) protein kinase [Nicotiana
                  tabacum]
Seq. No.
                  226461
Seq. ID
                  LIB3166-058-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q4544443
BLAST score
                  343
E value
                  2.0e-32
Match length
                  119
% identity
                  62
                  (AC006592) putative mitochondrial uncoupling protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  226462
Seq. ID
                  LIB3166-058-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q3850816
BLAST score
                  327
E value
                  2.0e-30
Match length
                  61
% identity
                  93
NCBI Description
                  (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza
                  sativa]
Seq. No.
                  226463
Seq. ID
                  LIB3166-058-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q1730566
BLAST score
                  440
E value
                  8.0e-44
Match length
                  119
% identity
                  45
NCBI Description PHYTOCHROME E >gi 1145714 (U39787) phytochrome E [Ipomoea
                  nil]
Seq. No.
                  226464
Seq. ID
                  LIB3166-058-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g1871192
BLAST score
                  145
E value
                  3.0e-09
Match length
                  64
% identity
                  45
NCBI Description
                  (U90439) Cys3His zinc finger protein isolog [Arabidopsis
                  thaliana]
Seq. No.
                  226465
Seq. ID
                  LIB3166-058-P1-K1-H10
```

Method BLASTX NCBI GI q1871192 BLAST score 180



```
E value
                   3.0e-13
Match length
                   115
% identity
                   (U90439) Cys3His zinc finger protein isolog [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   226466
Seq. ID
                  LIB3166-058-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q3281848
BLAST score
                   334
E value
                   3.0e - 31
Match length
                  107
                   72
% identity
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]
                  226467
Seq. No.
Seq. ID
                  LIB3166-058-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g4455364
BLAST score
                  326
E value
                   2.0e-30
Match length
                  94
% identity
                   66
NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis
                  thaliana]
Seq. No.
                  226468
Seq. ID
                  LIB3166-058-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  q3759184
BLAST score
                   462
E value
                   2.0e-46
Match length
                  104
% identity
                  82
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
                  226469
Seq. ID
                  LIB3166-059-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g4337025
BLAST score
                  370
E value
                  1.0e-35
Match length
                  88
% identity
                  77
NCBI Description (AF123253) AIM1 protein [Arabidopsis thaliana]
Seq. No.
                  226470
Seq. ID
                  LIB3166-059-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q2495179
BLAST score
                  437
E value
                  1.0e-43
                  99
Match length
% identity
                  84
```

(HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN

NCBI Description PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG)



SYNTHASE) >gi\_1084340\_pir\_\_S50762 hydroxymethylbilane synthase (EC 4.3.1.8) precursor - Arabidopsis thaliana >gi\_313150\_emb\_CAA51941\_ (X73535) hydroxymethylbilane synthase [Arabidopsis thaliana] >gi\_313838\_emb\_CAA52061\_ (X73839) hydroxymethylbilane synthase [Arabidopsis thaliana]

```
Seq. No.
                   226471
Seq. ID
                  LIB3166-059-P1-K1-C1
Method
                  BLASTX
NCBI GI
                   q434759
BLAST score
                   378
E value
                   1.0e-36
Match length
                   96
% identity
                   72
NCBI Description
                   (D21163) similar to human elongation factor 2 mRNA (HSEF2).
                   [Homo sapiens]
Seq. No.
                   226472
Seq. ID
                  LIB3166-059-P1-K1-C2
Method
                  BLASTX
                   g4008441
                   204
                   3.0e-16-
```

NCBI GI BLAST score E value Match length 72 % identity 56 NCBI Description

(AL034488) predicted using Genefinder; cDNA EST yk433c6.3 comes from this gene; cDNA EST EMBL:D72601 comes from this gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST yk433c6.5 comes from this gene [Caenorhabditis elegans]

Seq. No. 226473 Seq. ID LIB3166-059-P1-K1-C3 Method BLASTX NCBI GI g1914685 BLAST score 279 E value 5.0e-25

Match length 60 % identity 87

NCBI Description (Y12014) RAD23 protein, isoform II [Daucus carota]

Seq. No. 226474 Seq. ID LIB3166-059-P1-K1-D1 Method BLASTX

NCBI GI g2347199 BLAST score 360 E value 2.0e-34 Match length 107 % identity

NCBI Description (AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No. 226475

Seq. ID LIB3166-059-P1-K1-D3

Method BLASTX NCBĪ·GI g2980760 BLAST score 221 E value 4.0e-18



```
Match length
                  75
% identity
                  59
                  (AL022198) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  226476
Seq. ID
                  LIB3166-059-P1-K1-E1
                  BLASTX
Method
NCBI GI
                  q1170507
BLAST score
                  337
                  1.0e-31
E value
                  66
Match length
                  100
% identity
                  EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3)
NCBI Description
                  >gi 100276 pir S22579 translation initiation factor eIF-4A
                  - curled-leaved tobacco >gi 19699 emb CAA43514 (X61206)
                  nicotiana eukaryotic translation initiation factor 4A
                  [Nicotiana plumbaginifolia]
Seq. No.
                  226477
                  LIB3166-059-P1-K1-F10
Seq. ID
                  BLASTX
Method
                  q4539359
NCBI GI
BLAST score
                  161
E value
                  5.0e-11
                  67
Match length
% identity
NCBI Description (AL049525) putative protein [Arabidopsis thaliana]
Seq. No.
                  226478
                  LIB3166-059-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1946220
BLAST score
                  241
E value
                  2.0e-20
Match length
                  120
% identity
                  62
NCBI Description (Z71979) kn1-like protein [Malus domestica]
Seq. No.
                  226479
Seq. ID
                  LIB3166-059-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g3914002
BLAST score
                  198
                   3.0e-19
E value
                  73
Match length
                  77
% identity
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 2935279
                   (AF033862) Lon protease [Arabidopsis thaliana]
                   226480
Seq. No.
                  LIB3189-001-P1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3513727
BLAST score
                   397
```

8.0e-39

99

81

E value

Match length

% identity



```
(AF080118) contains similarity to TPR domains (Pfam:
NCBI Description
                  TPR.hmm: score: 11.15) and kinesin motor domains (Pfam:
                  kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis
                  thaliana] >qi 4539358 emb CAB40052.1 (AL049525) putative
                  protein [Arabidopsis thaliana]
Seq. No.
                  226481
Seq. ID
                  LIB3189-001-P1-K1-A2
                  BLASTX
Method
                  q3319353
NCBI GI
                  148
BLAST score
E value
                  1.0e-09
Match length
                  48
                  58
% identity
                  (AF077407) contains similarity to copper-binding proteins
NCBI Description
                  [Arabidopsis thaliana]
                  226482
Seq. No.
Seq. ID
                  LIB3189-001-P1-K1-A3
                  BLASTX
Method
                  q3063467
NCBI GI
BLAST score
                  331
                  4.0e-31
E value
Match length
                  85
                  74
% identity
NCBI Description (AC003981) F22013.29 [Arabidopsis thaliana]
                  226483
Seq. No.
Seq. ID
                  LIB3189-001-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  q3176725
BLAST score
                  189
                  3.0e-14
E value
Match length
                  64
                  48
% identity
NCBI Description (AC002392) unknown protein [Arabidopsis thaliana]
                  226484
Seq. No.
                  LIB3189-001-P1-K1-A8
Seq. ID
                  BLASTX
Method
                  q2370595
NCBI GI
                  196
BLAST score
                  4.0e-15
E value
                  79
Match length
                  48
% identity
NCBI Description (AJ001414) GTPase activating protein [Yarrowia lipolytica]
                  226485
Seq. No.
                  LIB3189-001-P1-K1-B1
Seq. ID
                  BLASTX
Method
                  g1173055
NCBI GI
                  577
BLAST score
E value
                  8.0e-60
Match length
                  116
```

ribosomal protein L11.e - alfalfa >gi\_1076504 pir\_\_S51819

NCBI Description 60S RIBOSOMAL PROTEIN L11 (L5) >gi 541961 pir S42497

99

% identity



RL5 ribosomal protein - alfalfa >gi\_463252\_emb\_CAA55090\_ (X78284) RL5 ribosomal protein [Medicago sativa]

 Seq. No.
 226486

 Seq. ID
 LIB3189-001-P1-K1-B10

 Method
 BLASTX

 NCBI GI
 g4539292

NCBI GI g4539292 BLAST score 502 E value 5.0e-51 Match length 108 % identity 86

NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis

thaliana]

Seq. No. 226487

Seq. ID LIB3189-001-P1-K1-B3

Method BLASTX
NCBI GI g1619297
BLAST score 546
E value 4.0e-56
Match length 103
% identity 98

NCBI Description (Y08490) alpha-tubulin 2 [Hordeum vulgare]

Seq. No. 226488

Seq. ID LIB3189-001-P1-K1-B5

Method BLASTX
NCBI GI g4544399
BLAST score 439
E value 1.0e-43
Match length 128
% identity 65

NCBI Description (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana]

Seq. No. 226489

Seq. ID LIB3189-001-P1-K1-B6

Method BLASTX
NCBI GI g3643609
BLAST score 100
E value 1.0e-10
Match length 89

% identity 45
NCBI Description (AC005395) putative Cys3His zinc finger protein

[Arabidopsis thaliana]

Seq. No. 226490

Seq. ID LIB3189-001-P1-K1-C10

Method BLASTX
NCBI GI g3335355
BLAST score 575
E value 1.0e-59
Match length 118
% identity 27

NCBI Description (AC004512) Match to polyubiquitin DNA gb\_L05401 from A.

thaliana. Contains insertion of mitochondrial NADH

dehydrogenase gb\_X82618 and gb\_X98301. May be a pseudogene



with an expressed insert. EST gb AA586248 comes from this region. [Arabi

Seq. No. 226491 Seq. ID

LIB3189-001-P1-K1-C11

Method BLASTX NCBI GI g4126401 BLAST score 392 E value 4.0e-38 Match length 88 % identity

NCBI Description (AB011795) flavanone 3-hydroxylase [Citrus sinensis]

Seq. No. 226492

Seq. ID LIB3189-001-P1-K1-C12

Method BLASTX NCBI GI g2677830 BLAST score 544 E value 6.0e-56 Match length 115 % identity 93

NCBI Description (U93168) ribosomal protein L12 [Prunus armeniaca]

Seq. No. 226493

Seq. ID LIB3189-001-P1-K1-C5

Method BLASTX NCBI GI q1169534 BLAST score 362 E value 1.0e-34 Match length 104 70 % identity

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

> (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi\_542019\_pir\_\_\$39203 phosphopyruvate hydratase (EC 4.2.1.11) - castor bean

>gi 433609 emb CAA82232 (Z28386) enolase [Ricinus

communis]

Seq. No. 226494

Seq. ID LIB3189-001-P1-K1-C6

Method BLASTX NCBI GI g629641 BLAST score 299 E value 9.0e-34 Match length 106 % identity 68

NCBI Description PsHSC71.0 protein - garden pea >gi 1076530 pir S53500

HSC71.0 protein - garden pea >gi 473217 emb CAA83548

(Z32537) PsHSC71.0 [Pisum sativum]

Seq. No. 226495

Seq. ID LIB3189-001-P1-K1-D10

Method BLASTX NCBI GI g586004 BLAST score 547 E value 3.0e-56 Match length 111 % identity 89

```
NCBI Description SUPEROXIDE DISMUTASE [CU-ZN] >gi 421962 pir S34267
                   superoxide dismutase (EC 1.15.\overline{1.1}) (Cu-\overline{Zn}) - sweet potato
                   >gi_542090_pir__S40404 superoxide dismutase (EC 1.15.1.1)
(Cu-Zn) - sweet potato >gi_311971_emb_CAA51654_ (X73139)
                   superoxide dismutase [Ipomoea batatas]
Seq. No.
                   226496
Seq. ID
                   LIB3189-001-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   g320552
BLAST score
                   213
E value
                    4.0e-17
Match length
                   93
% identity
                   51
                   anthranilate synthase (EC 4.1.3.27) alpha-1 chain -
NCBI Description
                   Arabidopsis thaliana
Seq. No.
                   226497
Seq. ID
                   LIB3189-001-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   g3334115
BLAST score
                   513
E value
                    3.0e-52
Match length
                   103
% identity
                    97
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                    (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664
                    (AF006489) adenine nucleotide translocator 1 [Gossypium
                   hirsutum]
                   226498
Seq. No.
                   LIB3189-001-P1-K1-D3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2827548
BLAST score
                   397
E value
                   1.0e-38
                   127
Match length
                   55
% identity
                  (AL021635) cytochrome P450 - like protein [Arabidopsis
NCBI Description
                   thaliana]
                    226499
Seq. No.
Seq. ID
                   LIB3189-001-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   g2811278
BLAST score
                   238
E value
                   1.0e-20
```

46 Match length % identity 93

NCBI Description (AF043284) expansin [Gossypium hirsutum]

Seq. No. 226500

LIB3189-001-P1-K1-D7 Seq. ID

Method BLASTX NCBI GI q4469015 BLAST score 608 E value 2.0e-63

```
Match length
                  131
% identity
                  92
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                  226501
Seq. ID
                  LIB3189-001-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q2088651
BLAST score
                  179
E value
                  4.0e-13
Match length
                  82
% identity
                  38
NCBI Description
                  (AF002109) hypersensitivity-related gene 201 isolog
                  [Arabidopsis thaliana]
                  226502
Seq. No.
Seq. ID
                  LIB3189-001-P1-K1-E1
                  BLASTX
                  g1076660
                  231
                  3.0e-19
```

Method NCBI GI BLAST score E value 47 Match length 89 % identity

NCBI Description D13F(MYBST1) protein - potato >gi 786426 bbs 159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes,

leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No. 226503 Seq. ID LIB3189-001-P1-K1-E10 Method BLASTX NCBI GI g1314711 BLAST score 586 E value 7.0e-61 131 Match length 87 % identity

NCBI Description (U54615) calcium-dependent protein kinase [Arabidopsis thaliana] >gi 3068712 (AF049236) calcium dependent protein

kinase [Arabidopsis thaliana]

Seq. No. 226504

Seq. ID LIB3189-001-P1-K1-E11

Method BLASTX NCBI GI q3882185 BLAST score 194 7.0e-15 E value 98 Match length % identity 41

NCBI Description (AB018275) KIAA0732 protein [Homo sapiens]

Seq. No. 226505

Seq. ID LIB3189-001-P1-K1-E12

Method BLASTX NCBI GI q2058282 BLAST score 288 E value 7.0e-26 Match length 82

```
% identity
NCBI Description (X97377) atranbpla [Arabidopsis thaliana]
Seq. No.
                  226506
                  LIB3189-001-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076746
BLAST score
                   463
E value
                   2.0e-46
Match length
                   122
% identity
                   76
                  heat shock protein 70 - rice (fragment)
NCBI Description
                  >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
Seq. No.
                   226507
Seq. ID
                  LIB3189-001-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g4455170
BLAST score
                  145
E value
                   1.0e-09
Match length
                  57
% identity
                   47
NCBI Description
                  (AL035521) fatty acid elongase-like protein [Arabidopsis
                  thaliana]
Seq. No.
                   226508
                  LIB3189-001-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128175
                  174
BLAST score
                   2.0e-12
E value
Match length
                  126
% identity
                   33
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                   226509
Seq. ID
                  LIB3189-001-P1-K1-E8
Method
                  {\tt BLASTX}
NCBI GI
                   g1001622
BLAST score
                   298
E value
                   4.0e-27
                  94
Match length
                   65
% identity
NCBI Description (D64002) hypothetical protein [Synechocystis sp.]
Seq. No.
                   226510
Seq. ID
                  LIB3189-001-P1-K1-E9
Method
                  BLASTX
NCBI GI
                   g1350795
BLAST score
                  186
E value
                   6.0e-14
Match length
                  99
% identity
                   44
NCBI Description MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L24 PRECURSOR (YML24)
```

>gi\_1078342\_pir\_\_S50921 ribosomal protein YmL24, mitochondrial - yeast (Saccharomyces cerevisiae)



>gi\_642285\_emb\_CAA87814\_ (Z47815) ribosomal protein [Saccharomyces cerevisiae]

Seq. No. 226511 LIB3189-001-P1-K1-F12 Seq. ID Method BLASTX NCBI GI g285741 BLAST score 199 E value 2.0e-15 Match length 123 % identity 40

NCBI Description (D14550) EDGP precursor [Daucus carota]

Seq. No. 226512

Seq. ID LIB3189-001-P1-K1-F2

Method BLASTX
NCBI GI g3122785
BLAST score 384
E value 8.0e-46
Match length 109
% identity 91

NCBI Description 40S RIBOSOMAL PROTEIN S14 >gi\_2565340 (AF026079) ribosomal

protein S14 [Lupinus luteus]

Seq. No. 226513

Seq. ID LIB3189-001-P1-K1-F7

Method BLASTX
NCBI GI g4490316
BLAST score 298
E value 4.0e-27
Match length 58
% identity 81

NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana]

Seq. No. 226514

Seq. ID LIB3189-001-P1-K1-F8

Method BLASTX 91706325 BLAST score 237 E value 5.0e-20 Match length 46 % identity 96

NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC) >gi 476286 (U07339)

pyruvate decarboxylase 1 [Oryza sativa] >gi 1098559

(U26660) pyruvate decarboxylase [Oryza sativa]

Seq. No. 226515

Seq. ID LIB3189-001-P1-K1-G11

Method BLASTX
NCBI GI g3243234
BLAST score 271
E value 7.0e-24
Match length 123
% identity 44

NCBI Description (AF071477) isoflavone reductase related protein [Pyrus

communis]



```
Seq. No.
                  226516
Seq. ID
                  LIB3189-001-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g2832625
BLAST score
                  401
E value
                  4.0e-39
Match length
                  94
% identity
                  73
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                  226517
Seq. ID
                  LIB3189-001-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  q3023190
BLAST score
                  449
E value
                  8.0e-45
Match length
                  110
                  81
% identity
NCBI Description 14-3-3-LIKE PROTEIN 16R >gi_1888459_emb_CAA72381_ (Y11685)
                  14-3-3 protein [Solanum tuberosum]
                  226518
Seq. No.
Seq. ID
                  LIB3189-001-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q2811278
BLAST score
                  457
E value
                  1.0e-45
Match length
                  126
% identity
                  70
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                  226519
Seq. ID
                  LIB3189-002-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g3319882
BLAST score
                  611
E value
                  8.0e-64
Match length
                  121
                  96
% identity
NCBI Description
                 (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
                  arietinum]
                  226520
Seq. No.
Seq. ID
                  LIB3189-002-P1-K1-A11
                  BLASTX
Method
NCBI GI
                  g2431769
BLAST score
                  234
E value
                  1.0e-19
                  57
Match length
                  81
% identity
NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]
                  226521
Seq. No.
```

Seq. ID LIB3189-002-P1-K1-A12

Method BLASTX NCBI GI q3176098 BLAST score 314



E value 5.0e-29 Match length 117 % identity 58

NCBI Description (Y15036) annexin [Medicago truncatula]

Seq. No. 226522

Seq. ID LIB3189-002-P1-K1-A2

Method BLASTX
NCBI GI g2244732
BLAST score 531
E value 2.0e-54
Match length 105
% identity 99

NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]

Seq. No. 226523

Seq. ID LIB3189-002-P1-K1-A3

Method BLASTX
NCBI GI g127112
BLAST score 311
E value 1.0e-28
Match length 93
% identity 61

NCBI Description MAK16 PROTEIN >gi\_73269\_pir\_\_BVBYK6 MAK16 protein - yeast

(Saccharomyces cerevisiae) >gi\_171880 (J03852) MAK16 protein [Saccharomyces cerevisiae] >gi\_595561 (U12980) Mak16p: putative nuclear protein [Saccharomyces cerevisiae]

Seq. No. 226524

Seq. ID LIB3189-002-P1-K1-A4

Method BLASTX
NCBI GI g2829204
BLAST score 330
E value 6.0e-31
Match length 83
% identity 80

NCBI Description (AF044204) lipid transfer protein precursor [Gossypium

hirsutum]

Seq. No. 226525

Seq. ID LIB3189-002-P1-K1-A5

Method BLASTX
NCBI GI g3876865
BLAST score 161
E value 5.0e-11
Match length 73
% identity 40

NCBI Description (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177

comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No. 226526

Seq. ID LIB3189-002-P1-K1-A6

Method BLASTX NCBI GI g4469015 BLAST score 484



```
1.0e-54
E value
Match length
                  124
                  85
% identity
                   (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
                  226527
Seq. No.
                  LIB3189-002-P1-K1-A9
Seq. ID
                  BLASTX
Method
                   g1657855
NCBI GI
                   370
BLAST score
                   2.0e-35
E value
                   104
Match length
                   65
% identity
                   (U73216) cold acclimation protein WCOR413 [Triticum
NCBI Description
                   aestivum]
                   226528
Seq. No.
                   LIB3189-002-P1-K1-B1
Seq. ID
                   BLASTX
Method
                   g115765
NCBI GI
                   395
BLAST score
                   2.0e-38
E value
                   90
Match length
                   77
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR
NCBI Description
                   (CAB-7) >gi 100201_pir _S07408 chlorophyll a/b-binding
                   protein type II (cab-7) - tomato >gi_19180_emb_CAA32197_
                   (X14036) chlorophyll a/b-binding protein [Lycopersicon
                   esculentum] >gi_170431 (M20241) chlorophyll a/b-binding
                   protein [Lycopersicon esculentum] >gi_226546 prf 1601518A
                   chlorophyll a/b binding protein II [Lycopersicon
                   esculentum]
                   226529
Seq. No.
                   LIB3189-002-P1-K1-B11
Seq. ID
                   BLASTX
Method
                   g4490316
NCBI GI
BLAST score
                   245
                   6.0e-21
E value
                   48
Match length
% identity
                   (AL035678) nucellin-like protein [Arabidopsis thaliana]
NCBI Description
                   226530
Seq. No.
                   LIB3189-002-P1-K1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4371290
BLAST score
                   232
E value
                   2.0e-19
                   98
Match length
 % identity
NCBI Description
                   (AC006260) unknown protein [Arabidopsis thaliana]
```

Seq. No. 226531

Seq. ID LIB3189-002-P1-K1-B6

Method BLASTX NCBI GI g4490310



```
BLAST score
                  2.0e-36
E value
Match length
                  123
                  63
% identity
                  (AL035678) somatic embryogenesis receptor-like kinase-like
NCBI Description
                  protein [Arabidopsis thaliana]
                  226532
Seq. No.
                  LIB3189-002-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129879
BLAST score
                  245
                   6.0e-21
E value
                  59
Match length
                   71
% identity
                  chlorophyll a/b-binding protein type II precursor,
NCBI Description
                  photosystem I - garden pea >gi 602359 emb CAA57492
                   (X81962) Type II chlorophyll a/b binding protein from
                  photosystem I [Pisum sativum]
Seq. No.
                   226533
                  LIB3189-002-P1-K1-C12
Seq. ID
                   BLASTX
Method
                   q4539308
NCBI GI
BLAST score
                   158
                   1.0e-10
E value
                   39
Match length
                   74
% identity
                  (AL049480) possible apospory-associated like protein
NCBI Description
                   [Arabidopsis thaliana]
                   226534
Seq. No.
                   LIB3189-002-P1-K1-C2
Seq. ID
                   BLASTX
Method
                   q4457219
NCBI GI
BLAST score
                   281
E value
                   4.0e-25
                   99
Match length
% identity
NCBI Description (AF127796) acyl carrier protein [Capsicum chinense]
Seq. No.
                   226535
                   LIB3189-002-P1-K1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1703375
BLAST score
                   432
E value
                   8.0e-43
                   89
Match length
                   97
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259 (D45420)
                   DcARF1 [Daucus carota]
                   226536
Seq. No.
                   LIB3189-002-P1-K1-C6
Seq. ID
```

BLASTX

406

g2827755

Method

NCBI GI

BLAST score

```
9.0e - 40
E value
Match length
                  103
                  74
% identity
                  INORGANIC PYROPHOSPHATASE, VACUOLAR (PYROPHOSPHATE
NCBI Description
                  PHOSPHOHYDROLASE) (PPASE) >gi_951323 (U31467)
                  pyrophosphatase [Vigna radiata]
                  226537
Seq. No.
Seq. ID
                  LIB3189-002-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q1055368
BLAST score
                  678
E value
                  1.0e-71
Match length
                  124
                  99
% identity
                  (U39567) ribulose-1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Glycine max]
Seq. No.
                  226538
Seq. ID
                  LIB3189-002-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  q4406814
BLAST score
                  254
                   5.0e-22
E value
                   65
Match length
% identity
                   74
                  (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis
NCBI Description
                   thaliana]
                   226539
Seq. No.
                   LIB3189-002-P1-K1-D12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2832783
BLAST score
                   481
E value
                   1.0e-48
Match length
                   95
% identity
                   92
NCBI Description (AJ225806) potassium channel beta subunit [Egeria densa]
                   226540
Seq. No.
                   LIB3189-002-P1-K1-D4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1049293
BLAST score
                   341
E value
                   4.0e-44
Match length
                   122
% identity
                   80
                  (U37247) SecY homolog; targetted to the thylakoid membrane;
NCBI Description
                   the protein has a chloroplast targetting signal, but the
                   processing site is not known [Arabidopsis thaliana]
```

Seq. No. 226541

Seq. ID LIB3189-002-P1-K1-D5

Method BLASTX
NCBI GI g4539292
BLAST score 483
E value 8.0e-49



```
Match length
                   103
% identity
                   (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                   thaliana]
                   226542
Seq. No.
                   LIB3189-002-P1-K1-E10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q133940
BLAST score
                   378
E value
                   2.0e-36
Match length
                   87
                   90
% identity
                   40S RIBOSOMAL PROTEIN S3A (S1A) >gi 70851 pir R3XL3A
NCBI Description
                   ribosomal protein S3a - African clawed frog >gi_65091_emb_CAA40592_ (X57322) ribosomal protein S1a
                   [Xenopus laevis]
                   226543
Seq. No.
Seq. ID
                   LIB3189-002-P1-K1-E11
                   BLASTX
Method
NCBI GI
                   q3831440
BLAST score
                   212
E value
                   5.0e-17
Match length
                   86
% identity
                   47
                   (AC005819) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                   >qi 4415946 qb AAD20176 (AC006418) putative cytochrome
                   P450 [Arabidopsis thaliana]
Seq. No.
                   226544
                   LIB3189-002-P1-K1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3249113
BLAST score
                   270
E value
                   8.0e-24
                   102
Match length
                    50
% identity
                   (AC003114) Strong similarity to kinesin homolog IG002P16.12
NCBI Description
                    gb 2191180 from A. thaliana BAC gb_AF007270. [Arabidopsis
                    thaliana]
                    226545
Seq. No.
                   LIB3189-002-P1-K1-E4
Seq. ID
Method
                   {\tt BLASTX}
NCBI GI
                    g3249113
BLAST score
                    239
E value
                    3.0e-20
                   105
Match length
                    47
% identity
```

(AC003114) Strong similarity to kinesin homolog IG002P16.12 NCBI Description

gb 2191180 from A. thaliana BAC gb AF007270. [Arabidopsis

thaliana]

226546 Seq. No.

Seq. ID LIB3189-002-P1-K1-E5

Method BLASTX

```
NCBI GI
                  g4263507
BLAST score
                  197
E value
                  3.0e-15
                  120
Match length
                  35
% identity
NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]
                  226547
Seq. No.
                  LIB3189-002-P1-K1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3885511
BLAST score
                  390
E value
                  7.0e - 38
Match length
                  97
                  79
% identity
NCBI Description (AF084200) similar to PSI-K subunit of photosystem I from
                  barley [Medicago sativa]
                  226548
Seq. No.
                  LIB3189-002-P1-K1-E9
Seq. ID
Method
                  BLASTX
                  g70644
NCBI GI
                  531
BLAST score
                  2.0e-54
E value
                  109
Match length
% identity
                  19
NCBI Description ubiquitin precursor - common sunflower (fragment)
                  226549
Seq. No.
                  LIB3189-002-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4432832
BLAST score
                  241
E value
                  5.0e-31
Match length
                  97
% identity
                  73
NCBI Description (AC006283) similar to protein Htf9C [Arabidopsis thaliana]
Seq. No.
                  226550
                  LIB3189-002-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q808839
BLAST score
                  184
E value
                  1.0e-13
                  103
Match length
% identity
                  45
NCBI Description (J04186) unknown protein [Saccharomyces cerevisiae]
Seq. No.
                  226551
                  LIB3189-002-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4530585
BLAST score
                  349
                  3.0e - 33
E value
Match length
                  83
```

NCBI Description (AF130978) B12D protein [Ipomoea batatas]

75

% identity

Seq. No.

226556

```
Seq. No.
                  226552
Seq. ID
                  LIB3189-002-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g2160185
                  326
BLAST score
                  2.0e-30
E value
Match length
                  86
                  72
% identity
NCBI Description (AC000132) Similar to S. pombe ISP4 (gb D83992).
                  [Arabidopsis thaliana]
Seq. No.
                  226553
                  LIB3189-002-P1-K1-F2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1362086
BLAST score
                  603
E value
                  7.0e-63
Match length
                  121
% identity
                  93
NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919 pir S65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                  [Catharanthus roseus]
Seq. No.
                 226554
                  LIB3189-002-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914370
BLAST score
                  245
E value
                  7.0e-21
                  74
Match length
                  72
% identity
NCBI Description GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
                  >gi 419754_pir_ S31083 glycerol-3-phosphate
                  O-acyltransferase (EC 2.3.1.15) precursor - Arabidopsis
                  thaliana >gi_217845_dbj_BAA00575_ (D00672)
                  glycerol-3-phosphate acyltransferase [Arabidopsis thaliana]
                  >gi 217847_dbj BAA00576 (D00673) glycerol-3-phosphate
                  acyltransferase precursor [Arabidopsis thaliana]
Seq. No.
                  226555
                  LIB3189-002-P1-K1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1709761
BLAST score
                  466
E value
                  8.0e-47
Match length
                  100
% identity
                  93
NCBI Description PROTEASOME 27 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
                  COMPLEX 27 KD SUBUNIT) >gi 1262146 emb CAA65660 (X96974)
                  proteasome subunit [Spinacia oleracea]
```

% identity

```
LIB3189-002-P1-K1-F7
Seq. ID
                  BLASTX
Method
                  g2829887
NCBI GI
BLAST score
                  440
                  9.0e-44
E value
                  123
Match length
% identity
                  70
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]
                  226557
Seq. No.
                  LIB3189-002-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3927916
BLAST score
                  471
                  2.0e-47
E value
Match length
                  88
                  98
% identity
NCBI Description (AJ130887) glycine-rich protein 2 [Fagus sylvatica]
                  226558
Seq. No.
                  LIB3189-002-P1-K1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3043428
BLAST score
                  443
E value
                  4.0e-44
                  92
Match length
% identity
                  88
NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
                  226559
Seq. No.
Seq. ID
                  LIB3189-002-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g2335099
BLAST score
                  461
E value
                  3.0e-46
Match length
                  126
                  40
% identity
NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]
                  226560
Seq. No.
Seq. ID
                  LIB3189-002-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q2828296
BLAST score
                  230
E value
                  5.0e-19
Match length
                  43
% identity
NCBI Description (AL021687) RNase L inhibitor [Arabidopsis thaliana]
                  226561
Seq. No.
                  LIB3189-002-P1-K1-G4
Seq. ID
Method
                  BLASTX
                  g2369766
NCBI GI
BLAST score
                  366
                  4.0e-35
E value
Match length
                  105
```

```
NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]
Seq. No.
                  226562
Seq. ID
                  LIB3189-002-P1-K1-G5
Method
                  BLASTX
                  q3335341
NCBI GI
BLAST score
                  140
E value
                  1.0e-08
Match length
                  96
                  38
% identity
NCBI Description (AC004512) T8F5.10 [Arabidopsis thaliana]
                  226563
Seq. No.
                  LIB3189-002-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2335101
BLAST score
                  473
                  1.0e-47
E value
Match length
                  118
                  72
% identity
NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]
                  226564
Seq. No.
Seq. ID
                  LIB3189-002-P1-K1-G9
Method
                  BLASTX
                  q1743354
NCBI GI
BLAST score
                  264
E value
                  7.0e-28
Match length
                  80
% identity
                  76
NCBI Description (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
Seq. No.
                  226565
Seq. ID
                  LIB3189-002-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q4220528
BLAST score
                  335
E value
                  2.0e-31
Match length
                  125
% identity
                  58
NCBI Description (AL035356) glucose-6-phosphate isomerase [Arabidopsis
                  thaliana]
                  226566
Seq. No.
                  LIB3189-002-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3021485
BLAST score
                  269
E value
                  1.0e-23
Match length
                  66
% identity
                  82
NCBI Description (AJ224932) histone H2B-3 [Lycopersicon esculentum]
Seq. No.
                  226567
```

Seq. ID LIB3189-002-P1-K1-H12

Method BLASTX NCBI GI g132086

Method

NCBI GI

BLASTX

g2980770

```
213
BLAST score
                  1.0e-17
E value
Match length
                  75
% identity
                  63
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1 PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 1) >gi_68053_pir__RKSYS
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor SRS1 - soybean >gi 18742 emb CAA23736 (V00458)
                  rubpcase [Glycine max]
                  226568
Seq. No.
                  LIB3189-002-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2772934
                  407
BLAST score
E value
                  7.0e-40
Match length
                  121
                  62
% identity
                  (AF030357) C-8,7 sterol isomerase; aSI1 [Arabidopsis
NCBI Description
                  thaliana]
                  226569
Seq. No.
Seq. ID
                  LIB3189-002-P1-K1-H6
Method
                  BLASTX
                  g1055368
NCBI GI
                  599
BLAST score
                  2.0e-62
E value
Match length
                  114
% identity
                  99
NCBI Description (U39567) ribulose-1,5-bisphosphate carboxylase small
                  subunit [Glycine max]
Seq. No.
                  226570
                  LIB3189-002-P1-K1-H8
Seq. ID
                  BLASTX
Method
                  g4376233
NCBI GI
BLAST score
                  517
                  8.0e-53
E value
Match length
                  101
% identity
                  93
NCBI Description (X00798) L2 protein [Nicotiana debneyi]
                  226571
Seq. No.
Seq. ID
                  LIB3189-003-P1-K1-A10
                  BLASTX
Method
NCBI GI
                  q2088654
BLAST score
                  405
                  1.0e-39
E value
Match length
                  92
% identity
                  86
NCBI Description (AF002109) 60S acidic ribosomal protein P0 isolog
                   [Arabidopsis thaliana]
Seq. No.
                  226572
Seq. ID
                  LIB3189-003-P1-K1-A11
```



BLAST score

```
2.0e-17
E value
                  79
Match length
                  59
% identity
                  (AL022198) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  226573
                  LIB3189-003-P1-K1-A2
Seq. ID
                  BLASTX
Method
                  g2501448
NCBI GI
                  144
BLAST score
                  2.0e-09
E value
                  40
Match length
                  78
% identity
NCBI Description UBIQUITIN-LIKE PROTEIN SMT3 >gi_1707372_emb_CAA67923
                   (X99609) ubiquitin-like protein [Arabidopsis thaliana]
Seq. No.
                   226574
                  LIB3189-003-P1-K1-A3
Seq. ID
                  BLASTX
Method
                   q4455208
NCBI GI
                   368
BLAST score
                   3.0e-35
E value
                  86
Match length
                   79
% identity
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                   226575
                   LIB3189-003-P1-K1-B1
Seq. ID
                   BLASTX
Method
                   g2245000
NCBI GI
                   156
BLAST score
                   3.0e-10
E value
                   136
Match length
                   30
% identity
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   226576
                   LIB3189-003-P1-K1-B6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4090257
BLAST score
                   284
                   9.0e-26
E value
Match length
                   61
% identity
NCBI Description (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
Seq. No.
                   226577
Seq. ID
                   LIB3189-003-P1-K1-C1
                   BLASTX
Method
NCBI GI
                   g2811278
BLAST score
                   345
E value
                   8.0e-33
Match length
                   99
                   67
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
```

% identity

NCBI Description

thaliana]



```
226578
Seq. No.
                  LIB3189-003-P1-K1-C11
Seq. ID
                  BLASTX
Method
                  g1718097
NCBI GI
                  272
BLAST score
                  5.0e-24
E value
                  78
Match length
                  62
% identity
                  VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
NCBI Description
                  (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016
                  lysosomal membrane protein DVA41 - slime mold
                  (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar
                  ATPase subunit DVA41 [Dictyostelium discoideum]
                  226579
Seq. No.
                  LIB3189-003-P1-K1-C2
Seq. ID
                  BLASTX
Method
                  g4539405
NCBI GI
                  348
BLAST score
                  4.0e-33
E value
                  89
Match length
                  75
% identity
                  (ALO49524) putative ribosomal protein L9, cytosolic
NCBI Description
                   [Arabidopsis thaliana]
                  226580
Seq. No.
                  LIB3189-003-P1-K1-C3
Seq. ID
Method
                  BLASTX
                   g2832625
NCBI GI
                   326
BLAST score
                   2.0e-30
E value
Match length
                   104
                   62
% identity
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
                   226581
Seq. No.
Seq. ID
                   LIB3189-003-P1-K1-D1
                   BLASTX
Method
                   q3126967
NCBI GI
                   544
BLAST score
                   6.0e-56
E value
Match length
                   113
                   17
% identity
NCBI Description (AF061807) polyubiquitin [Elaeagnus umbellata]
                   226582
Seq. No.
Seq. ID
                   LIB3189-003-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   g1076316
BLAST score
                   260
                   2.0e-22
E value
                   71
Match length
                   58
```

32307

drought-induced protein Di19 - Arabidopsis thaliana

>gi\_469110\_emb\_CAA55321\_ (X78584) Di19 [Arabidopsis



```
226583
Seq. No.
                   LIB3189-003-P1-K1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1172874
                   559
BLAST score
                   2.0e-57
E value
Match length
                   150
                   70
% identity
NCBI Description
                   DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
                   >gi 479589 pir S34823 dehydration-induced protein RD22 -
                   Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22
                   [Arabidopsis thaliana] > gi_4471\overline{3}4_prf_19134\overline{2}1A rd22 gene
                   [Arabidopsis thaliana]
                   226584
Seq. No.
                   LIB3189-003-P1-K1-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3004565
                   217
BLAST score
E value
                   1.0e-17
                   70
Match length
                   77
% identity
                  (AC003673) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   226585
                   LIB3189-003-P1-K1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   a478753
BLAST score
                   137
                   9.0e-09
E value
Match length
                   26
                   92
% identity
NCBI Description tubulin alpha-4 chain - maize (fragment)
                   226586
Seq. No.
Seq. ID
                   LIB3189-003-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   q2286153
BLAST score
                   523
E value
                   2.0e-53
Match length
                   106
% identity
                   98
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
Seq. No.
                   226587
Seq. ID
                   LIB3189-003-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g3122572
                   287
BLAST score
E value
                   2.0e-26
                   72
Match length
                   72
% identity
NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR
```

(COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I

SUBUNIT) >gi\_1084434\_pir\_\_S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi 758340 emb CAA59818\_ (X85808) 76 kDa mitochondrial

% identity

66



## complex I subunit [Solanum tuberosum]

Seq. No. 226588 Seq. ID LIB3189-003-P1-K1-E7 Method BLASTX NCBI GI g119350 BLAST score 489 E value 2.0e-49 Match length 117 % identity 83 NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi\_81608\_pir\_\_JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi 16271 emb CAA41114 (X58107) enolase [Arabidopsis thaliana] Seq. No. 226589 LIB3189-003-P1-K1-F10 Seq. ID Method BLASTX NCBI GI g3236237 BLAST score 458 1.0e-45 E value Match length 146 60 % identity NCBI Description (AC004684) putative ribotol dehydrogenase [Arabidopsis thaliana] 226590 Seq. No. Seq. ID LİB3189-003-P1-K1-F11 Method BLASTX NCBI GI g1518540 BLAST score 359 E value 2.0e-34Match length 79 87 % identity NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max] 226591 Seq. No. Seq. ID LIB3189-003-P1-K1-F2 Method BLASTX NCBI GI g4432825 BLAST score 479 E value 3.0e-48 Match length 132 70 % identity NCBI Description (AC006593) putative SOP2p protein [Arabidopsis thaliana] Seq. No. 226592 Seq. ID LIB3189-003-P1-K1-F4 Method BLASTX NCBI GI g4567249 BLAST score 433 E value 7.0e-43 117 Match length

32309

NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]

E value

Match length

% identity

2.0e-25

79 76



```
226593
Seq. No.
                   LIB3189-003-P1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2852640
                   219
BLAST score
                   9.0e-18
E value
                   101
Match length
                   45
% identity
                   (AF007157) unknown [Homo sapiens]
NCBI Description
                   226594
Seq. No.
                   LIB3189-003-P1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2129581
BLAST score
                   666
                   4.0e-70
E value
                   141
Match length
                   93
% identity
                   envelope Ca2+-ATPase precursor - Arabidopsis thaliana
NCBI Description
                   >gi 471089 dbj BAA03091 (D13984) chloroplast envelope
                   Ca2+-ATPase precursor [Arabidopsis thaliana]
                   >gi_4165448_emb_CAA49558_ (X69940) envelope Ca2+-ATPase
                    [Arabidopsis thaliana]
Seq. No.
                   226595
                   LIB3189-003-P1-K1-F9
Seq. ID
Method
                   BLASTX
                   g3335060
NCBI GI
                   178
BLAST score
E value
                   2.0e-13
Match length
                   44
                   89
% identity
                   (AF025842) plasma membrane-type calcium ATPase [Arabidopsis
NCBI Description
                   thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma
membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]
Seq. No.
                    226596
                   LIB3189-003-P1-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                    g267069
BLAST score
                    341
                    3.0e-32
E value
                   74
Match length
% identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                    tubulin alpha chain - Arabidopsis thaliana >gi_166914
                    (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                    (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                    226597
Seq. No.
                    LIB3189-003-P1-K1-G11
Seq. ID
                   BLASTX
Method
NCBI GI
                    g126894
BLAST score
                    285
```



NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi 319832 pir DEPUGW malate dehydrogenase (EC 1.1.1.37) precursor, glyoxysomal - watermelon >gi 167284 (M33148) glyoxysomal malate dehydrogenase precursor (EC 1.1.1.37) [Citrullus vulgaris] Seq. No. 226598 LIB3189-003-P1-K1-G6 Seq. ID BLASTX Method g2253384 NCBI GI BLAST score 613 5.0e-64E value Match length 136 85 % identity (AF007100) biotin carboxylase precursor [Glycine max] NCBI Description 226599 Seq. No. LIB3189-003-P1-K1-H1 Seq. ID Method BLASTX q1076678 NCBI GI BLAST score 392 3.0e-38 E value Match length 91 91 % identity ubiquitin / ribosomal protein S27a - potato (fragment) NCBI Description 226600 Seq. No. LIB3189-003-P1-K1-H3 Seq. ID Method BLASTX g267082 NCBI GI 490 BLAST score 1.0e-49 E value 95 Match length 94 % identity NCBI Description TUBULIN BETA-8 CHAIN >gi\_320189\_pir\_\_JQ1592 tubulin beta-8 chain - Arabidopsis thalīana >gī 166908 (M84705) beta-8 tubulin [Arabidopsis thaliana] 226601 Seq. No. LIB3189-003-P1-K1-H6 Seq. ID Method BLASTX NCBI GI q1632822 558 BLAST score 2.0e-57 E value 138 Match length 81 % identity NCBI Description (Y08962) transmembrane protein [Oryza sativa] >gi\_1667594 (U77297) transmembrane protein [Oryza sativa] 226602 Seq. No. LIB3189-003-P1-K1-H9 Seq. ID Method BLASTX

g4508073 NCBI GI 176 BLAST score 5.0e-13 E value Match length 62 % identity 56



```
NCBI Description (AC005882) 43220 [Arabidopsis thaliana]
Seq. No.
                  226603
                  LIB3189-004-P1-K1-A10
Seq. ID
                  BLASTX
Method
                  q445613
NCBI GI
BLAST score
                  667
                  3.0e-70
E value
                  155
Match length
                  79
% identity
                  ribosomal protein L7 [Solanum tuberosum]
NCBI Description
                  226604
Seq. No.
                  LIB3189-004-P1-K1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q82209
                  148
BLAST score
                  1.0e-09
E value
                  66
Match length
                  47
% identity
                  hypothetical protein 228 - common tobacco chloroplast
NCBI Description
                  >gi_225265_prf__1211235DA ORF 228 [Nicotiana tabacum]
                  226605
Seq. No.
                  LIB3189-004-P1-K1-A4
Seq. ID
                  BLASTX
Method
                   g3269288
NCBI GI
                   471
BLAST score
                   3.0e-47
E value
                   114
Match length
                   81
% identity
                  (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                   226606
Seq. No.
                   LIB3189-004-P1-K1-B11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2982320
BLAST score
                   228
                   9.0e-19
E value
                   116
Match length
                   43
% identity
NCBI Description (AF051245) hypothetical protein [Picea mariana]
                   226607
Seq. No.
                   LIB3189-004-P1-K1-C1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g585963
BLAST score
                   262
E value
                   6.0e-23
Match length
                   69
                   78
 % identity
NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT
Seq. No.
                   226608
                   LIB3189-004-P1-K1-C12
Seq. ID
```

BLASTX

g2244740

Method NCBI GI

```
616
BLAST score
                   3.0e-64
E value
                   138
Match length
                   87
% identity
                   (D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]
NCBI Description
                   226609
Seq. No.
                   LIB3189-004-P1-K1-C4
Seq. ID
                   BLASTX
Method
                   g730449
NCBI GI
                   545
BLAST score
                   6.0e-56
E value
                   131
Match length
                   79
% identity
                   60S RIBOSOMAL PROTEIN L13-1 (COLD INDUCED PROTEIN C24A)
NCBI Description
                   >gi_480647_pir__S37132 ribosomal protein L13.A - rape
>gi_398918_emb_CAA80341_ (Z22618) cold induced protein
                   (BnC24A) [Brassica napus]
                   226610
Seq. No.
                   LIB3189-004-P1-K1-C6
Seq. ID
                   BLASTX
Method
                   g122781
NCBI GI
                   268
BLAST score
                   2.0e-23
E value
Match length
                   60
% identity
                   80
                   POTENTIAL HEME-BINDING PROTEIN PRECURSOR (ORF 229)
NCBI Description
                   >gi 82210 pir_A05198 hypothetical protein 229 - common
                    tobacco chloroplast >gi 11844_emb_CAA77364_ (Z00044)
                    hypothetical protein [Nicotiana tabacum]
                    >gi 225212_prf__1211235AT ORF 229 [Nicotiana tabacum]
                    226611
Seq. No.
                    LIB3189-004-P1-K1-C8
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2501850
BLAST score
                    330
                    5.0e-31
E value
                    65
Match length
% identity
                    94
NCBI Description (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]
                    226612
Seq. No.
                    LIB3189-004-P1-K1-D1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g4206765
                    228
BLAST score
                    7.0e-19
E value
                    89
Match length
                    55
 % identity
                   (AF104329) putative type 1 membrane protein [Arabidopsis
NCBI Description
                    thaliana]
```

LIB3189-004-P1-K1-D12

226613

BLASTX

Seq. No.

Seq. ID

Method

```
a3128176
NCBI GI
                   376
BLAST score
                   4.0e-36
E value
                  139
Match length
                   53
% identity
                  (AC004521) unknown protein [Arabidopsis thaliana]
NCBI Description
                  226614
Seq. No.
                  LIB3189-004-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829893
BLAST score
                   639
```

E value 5.0e-67 143 Match length 87 % identity

(AC002311) phosphoglucomutase [Arabidopsis thaliana] NCBI Description

Seq. No. LIB3189-004-P1-K1-D6 Seq. ID BLASTX Method NCBI GI q3269283 BLAST score 155 E value 3.0e-10Match length 146

% identity 22

(AL030978) putative protein [Arabidopsis thaliana] NCBI Description

226616 Seq. No.

Seq. ID LIB3189-004-P1-K1-D8

226615

BLASTX Method NCBI GI q4580394 BLAST score 238 E value 3.0e-20Match length 68 % identity

(AC007171) putative fatty acid elongase [Arabidopsis NCBI Description

thaliana]

226617 Seq. No.

LIB3189-004-P1-K1-E1 Seq. ID

Method BLASTX g2370312 NCBI GI BLAST score 536 5.0e-55 E value 123 Match length % identity 80

(AJ000995) DnaJ-like protein [Medicago sativa] >gi 3202020 NCBI Description

(AF069507) DnaJ-like protein MsJ1 [Medicago sativa]

226618 Seq. No.

LIB3189-004-P1-K1-E12 Seq. ID

95

BLASTX Method g3551031 NCBI GI BLAST score 517 E value 7.0e-53 Match length 107

% identity



```
NCBI Description (AB011467) chalcone synthase [Hydrangea macrophylla]
                  226619
Seq. No.
                  LIB3189-004-P1-K1-E5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3123614
                  594
BLAST score
                  9.0e-62
E value
                  123
Match length
                   93
% identity
                  (Y17225) cyclin-dependent protein kinase p34cdc2
NCBI Description
                   [Lycopersicon esculentum]
                   226620
Seq. No.
                  LIB3189-004-P1-K1-E9
Seq. ID
Method
                  BLASTX
                   g3892713
NCBI GI
                   191
BLAST score
                   2.0e-23
E value
Match length
                  71
                   76
% identity
                  (AL033545) putative protein [Arabidopsis thaliana]
NCBI Description
                   226621
Seq. No.
                  LIB3189-004-P1-K1-F10
Seq. ID
                   BLASTX
Method
                   g267069
NCBI GI
BLAST score
                   331
                   4.0e-31
E value
                   72
Match length
                   85
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                   226622
                   LIB3189-004-P1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2129473
                   269
BLAST score
E value
                   1.0e-23
                   105
Match length
% identity
                   arabinogalactan-like protein - loblolly pine >gi_607774
NCBI Description
                   (U09556) arabinogalactan-like protein [Pinus taeda]
Seq. No.
                   226623
                   LIB3189-004-P1-K1-F4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q116923
BLAST score
                   355
E value
                   1.0e-33
                   156
Match length
                   54
 % identity
NCBI Description COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
```

>gi 111414 pir S13520 beta-COP protein - rat



>gi\_55819\_emb\_CAA40505\_ (X57228) beta COP [Rattus norvegicus]

 Seq. No.
 226624

 Seq. ID
 LIB3189-004-P1-K1-F6

 Method
 BLASTX

 NCBI GI
 g3876865

 BLAST score
 161

E value 5.0e-11
Match length 73
% identity 40

NCBI Description (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177

comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No. 226625

Seq. ID LIB3189-004-P1-K1-G11

Method BLASTX
NCBI GI g1169228
BLAST score 212
E value 7.0e-17
Match length 70
% identity 60

NCBI Description RNA HELICASE-LIKE PROTEIN DB10 >gi\_1084413\_pir\_\_S42639

helicase-like protein - Wood tobacco

>gi\_563986\_dbj\_BAA03763\_ (D16247) RNA helicase like protein

DB10 [Nicotiana sylvestris]

Seq. No. 226626

Seq. ID LIB3189-004-P1-K1-G12

Method BLASTX
NCBI GI g1172874
BLAST score 302
E value 8.0e-28
Match length 91
% identity 68

NCBI Description DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR

>gi\_479589\_pir\_\_S34823 dehydration-induced protein RD22 Arabidopsis thaliana >gi\_391608\_dbj\_BAA01546\_ (D10703) rd22
[Arabidopsis thaliana] >gi\_447134\_prf\_\_1913421A rd22 gene

[Arabidopsis thaliana]

Seq. No. 226627

Seq. ID LIB3189-004-P1-K1-G2

Method BLASTX
NCBI GI g2580499
BLAST score 320
E value 9.0e-30
Match length 79
% identity 75

NCBI Description (U67186) NADPH: ferrihemoprotein oxidoreductase

[Eschscholzia californica]

Seq. No. 226628

Seq. ID LIB3189-004-P1-K1-G4

Method BLASTX

NCBI GI



```
g2995384
NCBI GI
BLAST score
                  141
                  3.0e-09
E value
Match length
                  50
                  56
% identity
NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]
                  226629
Seq. No.
                  LIB3189-004-P1-K1-G5
Seq. ID
                  BLASTX
Method
                  g441457
NCBI GI
BLAST score
                  734
                  4.0e-78
E value
                  143
Match length
                  96
% identity
                  (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                  esculentum]
                  226630
Seq. No.
                  LIB3189-004-P1-K1-G9
Seq. ID
                  BLASTX
Method
                  g4220535
NCBI GI
                  246
BLAST score
                  2.0e-24
E value
Match length
                  97
                   61
% identity
                  (AL035356) clathrin coat assembly like protein [Arabidopsis
NCBI Description
                   thaliana]
                   226631
Seq. No.
                  LIB3189-004-P1-K1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3876865
                   173
BLAST score
                   3.0e-12
E value
Match length
                   113
% identity
                  (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177
NCBI Description
                   comes from this gene; cDNA EST EMBL: C09822 comes from this
                   gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST
                   yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co
                   226632
Seq. No.
                   LIB3189-004-P1-K1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3914435
BLAST score
                   408
E value
                   5.0e-40
                   83
Match length
% identity
                   89
NCBI Description PROFILIN 1 >gi_3021375_emb CAA11756_ (AJ223982) profilin
                   [Glycine max]
                   226633
Seq. No.
                   LIB3189-005-P1-K1-A10
Seq. ID
                   BLASTX
Method
```

g2062167



```
BLAST score
                  217
                  7.0e-18
E value
Match length
                  50
                  76
% identity
                  (ACO01645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                  thaliana]
                  226634
Seq. No.
                  LIB3189-005-P1-K1-A11
Seq. ID
                  BLASTX
Method
                  q3914437
NCBI GI
BLAST score
                  440
                  2.0e-49
E value
Match length
                  120
% identity
                  81
                  PROFILIN >gi 3183706_emb_CAA75312_ (Y15042) profilin [Hevea
NCBI Description
                  brasiliensis]
                  226635
Seq. No.
                  LIB3189-005-P1-K1-A12
Seq. ID
                  BLASTX
Method
                  g1076621
NCBI GI
BLAST score
                  323
                  3.0e-30
E value
                  66
Match length
                  89
% identity
NCBI Description cytochrome b5 - common tobacco >gi_296386_emb_CAA50575_
                  (X71441) cytochrome b5 [Nicotiana tabacum]
                  226636
Seq. No.
                  LIB3189-005-P1-K1-A3
Seq. ID
                  BLASTX
Method
                  g2765316
NCBI GI
                   276
BLAST score
                  1.0e-24
E value
Match length
                   55
% identity
                   93
NCBI Description (Y13321) asparagine synthetase 1 [Pisum sativum]
                   226637
Seq. No.
                   LIB3189-005-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2829902
BLAST score
                   353
E value
                   1.0e-33
Match length
                   87
% identity
                   79
NCBI Description (AC002311) Putative sulphate transporter protein#protein
                   [Arabidopsis thaliana]
                   226638
Seq. No.
                   LIB3189-005-P1-K1-A6
Seq. ID
                   BLASTX
Method
                   g3962377
NCBI GI
BLAST score
                   762
E value
                   2.0e-81
```

Match length



% identity NCBI Description (AJ002551) heat shock protein 70 [Arabidopsis thaliana] 226639 Seq. No. LIB3189-005-P1-K1-B1 Seq. ID BLASTX Method NCBI GI g3334113 BLAST score 466 1.0e-46 E value Match length 89 100 % identity ACYL-COA-BINDING PROTEIN (ACBP) >gi\_1006831 (U35015) NCBI Description acyl-CoA-binding protein [Gossypium hirsutum] 226640 Seq. No. LIB3189-005-P1-K1-B2 Seq. ID BLASTX Method g3367520 NCBI GI BLAST score 622 E value 5.0e-65Match length 148 78 % identity (AC004392) Similar to protein kinase APK1A, NCBI Description tyrosine-serine-threonine kinase gb\_D12522 from A. thaliana. [Arabidopsis thaliana] Seq. No. 226641 LIB3189-005-P1-K1-B3 Seq. ID Method BLASTX g1710780 NCBI GI BLAST score 502 7.0e-51E value 132 Match length 74 % identity 40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433\_ NCBI Description (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina] 226642 Seq. No. LIB3189-005-P1-K1-B5 Seq. ID Method BLASTX NCBI GI g3096947 371 BLAST score 2.0e-35 E value Match length 115 % identity 63 NCBI Description (Y16327) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana] 226643 Seq. No. LIB3189-005-P1-K1-B7 Seq. ID BLASTX Method

NCBI GI g1263291
BLAST score 411
E value 2.0e-40
Match length 83
% identity 95



```
NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]
                  226644
Seq. No.
                  LIB3189-005-P1-K1-B8
Seq. ID
                  BLASTX
Method
                  g2244754
NCBI GI
                  406
BLAST score
                  1.0e-39
E value
                  93
Match length
                  78
% identity
                  (Z97335) heat shock transcription factor homolog
NCBI Description
                   [Arabidopsis thaliana]
                  226645
Seq. No.
                  LIB3189-005-P1-K1-C1
Seq. ID
Method
                  BLASTX
                  g322750
NCBI GI
BLAST score
                  654
                  1.0e-68
E value
                  128
Match length
                   98
% identity
                  ubiquitin / ribosomal protein CEP52 - wood tobacco
NCBI Description
                   >gi 170217 (M74100) ubiquitin fusion protein [Nicotiana
                   sylvestris]
                   226646
Seq. No.
                  LIB3189-005-P1-K1-C12
Seq. ID
Method
                  BLASTX
                   g4263704
NCBI GI
                   234
BLAST score
                   2.0e-19
E value
Match length
                   79
                   53
% identity
                  (AC006223) putative sugar starvation-induced protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   226647
                   LIB3189-005-P1-K1-C2
Seq. ID
Method
                   BLASTX
                   q2618698
NCBI GI
                   543
BLAST score
E value
                   1.0e-55
                   156
Match length
% identity
NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]
                   226648
Seq. No.
                   LIB3189-005-P1-K1-C3
Seq. ID
Method
                   BLASTX
                   g133438
NCBI GI
BLAST score
                   622
E value
                   6.0e-65
Match length
                   157
                   79
 % identity
                   DNA-DIRECTED RNA POLYMERASE BETA' CHAIN
NCBI Description
```

>gi\_81504\_pir\_\_B29959 DNA-directed RNA polymerase (EC
2.7.7.6) beta' chain - spinach chloroplast >gi\_295120



## (M55297) RNA polymerase [Spinacia oleracea]

```
226649
Seq. No.
                  LIB3189-005-P1-K1-C4
Seq. ID
Method
                  BLASTX
                  g3402279
NCBI GI
                  720
BLAST score
                  2.0e-76
E value
                  154
Match length
                  87
% identity
                   (AJ000999) putative beta-subunit of K+ channels [Solanum
NCBI Description
                  tuberosum]
                   226650
Seq. No.
                  LIB3189-005-P1-K1-C8
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2244732
                   351
BLAST score
E value
                   3.0e - 33
                   73
Match length
                   95
% identity
                  (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
NCBI Description
Seq. No.
                   226651
                   LIB3189-005-P1-K1-D12
Seq. ID
                   BLASTX
Method
                   q3335337
NCBI GI
BLAST score
                   432
                   1.0e-42
E value
Match length
                   132
                   70
% identity
                  (AC004512) Similar to acyl carrier protein, mitochondrial
NCBI Description
                   precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD
                   subunit (MYACP-1), gb_L23574 from A. thaliana. ESTs
                   gb_Z30712, gb_Z30713, gb_Z26204, gb_N37975 and gb_N96330
                   come from this gene
Seq. No.
                   226652
                   LIB3189-005-P1-K1-D6
Seq. ID
                   BLASTX
Method
                   q3212877
NCBI GI
                   516
BLAST score
E value
                   1.0e-52
                   115
Match length
% identity
NCBI Description (AC004005) Lea-like protein [Arabidopsis thaliana]
                   226653
Seq. No.
                   LIB3189-005-P1-K1-D8
Seq. ID
                   BLASTX
Method
                   q3122673
NCBI GI
                   284
BLAST score
E value
                   9.0e-28
                   70
Match length
                   93
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
```



```
226654
Seq. No.
                  LIB3189-005-P1-K1-E1
Seq. ID
                  BLASTX
Method
                  g870726
NCBI GI
                  301
BLAST score
                  3.0e-27
E value
                  78
Match length
                  78
% identity
                  (L38260) biotin carboxylase subunit [Nicotiana tabacum]
NCBI Description
                  >gi_1582354_prf__2118337A Ac-CoA carboxylase:SUBUNIT=biotin
                  carboxylase [Nicotiana tabacum]
                  226655
Seq. No.
                  LIB3189-005-P1-K1-E2
Seq. ID
                  BLASTX
Method
                  g3168840
NCBI GI
                  330
BLAST score
                   7.0e-31
E value
                  97
Match length
                   67
% identity
                  (U88711) copper homeostasis factor [Arabidopsis thaliana]
NCBI Description
                   226656
Seq. No.
                  LIB3189-005-P1-K1-E7
Seq. ID
                   BLASTX
Method
                   g1174592
NCBI GI
                   477
BLAST score
                   4.0e-48
E value
                   117
Match length
                   84
% identity
                   TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin
NCBI Description
                   - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
                   sativum]
                   226657
Seq. No.
                   LIB3189-005-P1-K1-E9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2129753
BLAST score
                   730
                   1.0e-77
E value
Match length
                   149
                   93
% identity
                   threonine synthase (EC 4.2.99.2) precursor - Arabidopsis
NCBI Description
                   thaliana (fragment) >gi_1448917 (L41666) threonine synthase
                   [Arabidopsis thaliana]
Seq. No.
                   226658
                   LIB3189-005-P1-K1-F1
Seq. ID
Method
                   BLASTX
                   q3885341
NCBI GI
                   337
BLAST score
                   1.0e-31
E value
                   151
Match length
```

NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]

46

% identity

BLAST score

E value Match length 170 6.0e-12

86



```
226659
Seq. No.
                  LIB3189-005-P1-K1-F3
Seq. ID
Method
                  BLASTX
                  g4558678
NCBI GI
                  213
BLAST score
                  5.0e-17
E value
Match length
                  67
                  55
% identity
                  (AC006586) unknown protein [Arabidopsis thaliana]
NCBI Description
                  226660
Seq. No.
                  LIB3189-005-P1-K1-F6
Seq. ID
                  BLASTX
Method
                  g3928142
NCBI GI
BLAST score
                  710
                  3.0e-75
E value
                  154
Match length
% identity
                  88
                  (AJ131045) protein phosphatase [Cicer arietinum]
NCBI Description
                  226661
Seq. No.
                  LIB3189-005-P1-K1-F8
Seq. ID
Method
                  BLASTX
                  g2129575
NCBI GI
                  513
BLAST score
                   3.0e-52
E value
                  110
Match length
% identity
                  89
NCBI Description DNA repair protein homolog XPBara - Arabidopsis thaliana
                   226662
Seq. No.
                  LIB3189-005-P1-K1-F9
Seq. ID
Method
                  BLASTX
                   g2995198
NCBI GI
                   189
BLAST score
                   3.0e-14
E value
Match length
                   103
                   36
% identity
NCBI Description (Y11588) apoptosis specific protein [Homo sapiens]
                   226663
Seq. No.
                   LIB3189-005-P1-K1-G10
Seq. ID
Method
                   BLASTX
                   g3540197
NCBI GI
                   327
BLAST score
                   2.0e-30
E value
Match length
                   135
% identity
NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]
                   226664
Seq. No.
                   LIB3189-005-P1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2335053
```



```
% identity
                  43
                  (D88825) ORF3 [Aeromonas caviae]
NCBI Description
                  226665
Seq. No.
                  LIB3189-005-P1-K1-G6
Seq. ID
                  BLASTX
Method
                  g2924520
NCBI GI
                  501
BLAST score
                  6.0e-51
E value
                  106
Match length
                  92
% identity
                  (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                   [Arabidopsis thaliana]
                  226666
Seq. No.
                  LIB3189-005-P1-K1-G7
Seq. ID
                  BLASTX
Method
                  g1850546
NCBI GI
                  445
BLAST score
                  2.0e-44
E value
                  113
Match length
                   79
% identity
                  (U88045) syntaxin related protein AtVam3p [Arabidopsis
NCBI Description
                   thaliana]
                   226667
Seq. No.
                  LIB3189-005-P1-K1-G8
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4454466
BLAST score
                   244
                   9.0e-21
E value
                   74
Match length
                   59
% identity
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
                   226668
Seq. No.
Seq. ID
                   LIB3189-005-P1-K1-G9
                   BLASTX
Method
NCBI GI
                   q2583123
BLAST score
                   646
E value
                   1.0e-68
Match length
                   150
                   86
% identity
                   (AC002387) putative nucleotide sugar epimerase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   226669
                   LIB3189-005-P1-K1-H10
Seq. ID
                   BLASTX
Method
                   g3600043
NCBI GI
BLAST score
                   209
E value
                   1.0e-16
                   75
Match length
```

% identity 51
NCBI Description (AF080119) No definition line found [Arabidopsis thaliana]

Seq. No.



```
LIB3189-005-P1-K1-H11
Seq. ID
Method
                   BLASTX
                   g1332579
NCBI GI
                   497
BLAST score
                   2.0e-50
E value
Match length
                   101
                   10
% identity
                   (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
                   226671
Seq. No.
                   LIB3189-005-P1-K1-H6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2829204
BLAST score
                   481
                   2.0e-48
E value
Match length
                   115
                   85
% identity
                   (AF044204) lipid transfer protein precursor [Gossypium
NCBI Description
                   hirsutum]
                   226672
Seq. No.
                   LIB3189-005-P1-K1-H8
Seq. ID
                   BLASTX
Method
                   g1703108
NCBI GI
                   572
BLAST score
                   4.0e-59
E value
Match length
                   105
                   100
% identity
                   ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis
NCBI Description
                   thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis
                   thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis
                   thaliana]
                   226673
Seq. No.
Seq. ID
                   LIB3189-005-P1-K1-H9
Method
                  BLASTX
NCBI GI
                   q421757
BLAST score
                    567
                    9.0e-59
E value
Match length
                   104
% identity
                    96
NCBI Description tubulin alpha chain - Euglena gracilis
                    226674
Seq. No.
                    LIB3189-006-P1-K1-A11
Seq. ID
Method
                    BLASTX
NCBI GI
                    q3668089
BLAST score
                    211
E value
                    3.0e-17
                    83
Match length
% identity
                    51
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
```

Seq. No. 226675

Seq. ID LIB3189-006-P1-K1-A12

Method BLASTX



```
g3169028
NCBI GI
                  297
BLAST score
                  6.0e-27
E value
Match length
                  134
                  49
% identity
                   (AL023702) putative cationic amino acid transporter
NCBI Description
                   [Streptomyces coelicolor]
                  226676
Seq. No.
                  LIB3189-006-P1-K1-A2
Seq. ID
Method
                  BLASTX
                  q1854386
NCBI GI
                  591
BLAST score
                   2.0e-61
E value
                   148
Match length
                   76
% identity
                  (AB001375) similar to soluble NSF attachment protein [Vitis
NCBI Description
                   vinifera]
```

 Seq. No.
 226677

 Seq. ID
 LIB3189-006-P1-K1-A3

 Method
 BLASTX

 NCBI GI
 g1854386

BLAST score 205 E value 2.0e-17 Match length 91 % identity 57

NCBI Description (AB001375) similar to soluble NSF attachment protein [Vitis vinifera]

Seq. No. 226678

Seq. ID LIB3189-006-P1-K1-A4

Method BLASTX
NCBI GI g232024
BLAST score 628
E value 1.0e-65
Match length 131
% identity 90

NCBI Description PROTEIN E6 > gi 421806 pir A46130 fiber protein - upland

cotton >gi\_2129498\_pir\_\_S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi\_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi\_1000084

(U30505) E6 [Gossypium hirsutum]

Seq. No. 226679

Seq. ID LIB3189-006-P1-K1-B1

Method BLASTX
NCBI GI g232024
BLAST score 262
E value 2.0e-24
Match length 80
% identity 69

NCBI Description PROTEIN E6 >gi\_421806\_pir\_\_A46130 fiber protein - upland cotton >gi\_2129498 pir\_S65061 fiber protein E6 (clone

CKE6-1A) - upland cotton >gi\_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi\_1000084

(U30505) E6 [Gossypium hirsutum]

Seq. ID

Method



```
226680
Seq. No.
                  LIB3189-006-P1-K1-B12
Seq. ID
                  BLASTX
Method
                  g2498982
NCBI GI
                  226
BLAST score
                  9.0e-19
E value
                  83
Match length
                  49
% identity
                  TRANSCRIPTION INITIATION FACTOR TFIID 31 KD SUBUNIT
NCBI Description
                  (TAFII-31) (TAFII-32) (TAFII32) (NEURONAL CELL DEATH
                  RELATED GENE IN NEURON -7) (DN-7) >gi 1103900 (U40188)
                  induced upon programmed cell death in neuronally
                  differentiated PC12 cells [Rattus norvegicus]
                  226681
Seq. No.
                  LIB3189-006-P1-K1-C1
Seq. ID
                  BLASTX
Method
                  g232024
NCBI GI
                  601
BLAST score
                  1.0e-62
E value
Match length
                  117
                  97
% identity
                 PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland
NCBI Description
                   cotton >gi_2129498_pir__$65061 fiber protein E6 (clone
                  CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site
                   is putative; putative [Gossypium hirsutum] >gi_1000084
                   (U30505) E6 [Gossypium hirsutum]
                   226682
Seq. No.
                   LIB3189-006-P1-K1-D10
Seq. ID
                   BLASTX
Method
                   q461498
NCBI GI
                   338
BLAST score
                   5.0e-32
E value
                   93
Match length
% identity
                   72
NCBI Description ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
                   TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                   (ALAAT-2) >gi_320619_pir__S28429 alanine transaminase (EC
                   2.6.1.2) - proso millet >gi 296204 emb CAA49199 (X69421)
                   alanine aminotransferase [Panicum miliaceum]
                   226683
 Seq. No.
                   LIB3189-006-P1-K1-D12
 Seq. ID
                   BLASTX
Method
NCBI GI
                   q4406781
                   197
 BLAST score
                   4.0e-15
E value
                   132
Match length
                   45
 % identity
 NCBI Description (AC006532) putative Na+/H+ antiporter [Arabidopsis
                   thaliana]
                   226684
 Seq. No.
```

32327

LIB3189-006-P1-K1-D3

BLASTX

E value

Match length

8.0e-13



```
q1706326
NCBI GI
                  559
BLAST score
                  1.0e-57
E value
                  121
Match length
                  88
% identity
                  PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC)
NCBI Description
                  >gi_2146786_pir__S65470 pyruvate decarboxylase (EC 4.1.1.1)
                   (clone PDC1) - Garden pea >gi_1177603_emb_CAA91444_
                   (Z66543) pyruvate decarboxylase [Pisum sativum]
                  226685
Seq. No.
                  LIB3189-006-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q84373
                  275
BLAST score
                  1.0e-24
E value
                  56
Match length
                   93
% identity
NCBI Description tubulin alpha chain - Stylonychia lemnae (SGC5)
                   226686
Seq. No.
                  LIB3189-006-P1-K1-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2114046
BLAST score
                   263
                   2.0e-23
E value
Match length
                   58
                   86
% identity
                  (AB002147) water channel protein [Nicotiana excelsior]
NCBI Description
                   226687
Seq. No.
                   LIB3189-006-P1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3163946
BLAST score
                   307
E value
                   1.0e-28
Match length
                   67
% identity
NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]
Seq. No.
                   226688
                   LIB3189-006-P1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4335763
BLAST score
                   246
E value
                   6.0e-21
Match length
                   87
% identity
                   51
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]
                   226689
Seq. No.
                   LIB3189-006-P1-K1-F10
Seq. ID
                   BLASTX
Method
                   g267069
NCBI GI
                   170
BLAST score
```

Match length

% identity

60

48



```
% identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                   226690
                   LIB3189-006-P1-K1-F12
Seq. ID
                   BLASTX
Method
                   g4432841
NCBI GI
                   341
BLAST score
                   4.0e-32
E value
                   138
Match length
                   49
% identity
                   (AC006283) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   226691
Seq. No.
                   LIB3189-006-P1-K1-F6
Seq. ID
                   BLASTX
Method
                   g2911801
NCBI GI
                   276
BLAST score
                   9.0e-25
E value
                   73
Match length
                   75
% identity
                  (AF009565) alpha-tubulin [Gossypium hirsutum]
NCBI Description
                   226692
Seq. No.
                   LIB3189-006-P1-K1-G1
Seq. ID
                   BLASTX
Method
                   g2894612
NCBI GI
                    391
BLAST score
                    6.0e - 38
E value
                    110
Match length
                    67
% identity
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
                    226693
Seq. No.
                   LIB3189-006-P1-K1-G12
Seq. ID
                    BLASTX
Method
NCBI GI
                    q2497743
                    153
BLAST score
                    3.0e-10
E value
                    56
Match length
                    59
% identity
                   NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3)
NCBI Description
                    >gi_999315_bbs_166991 (S78173) LTP=lipid transfer protein
                    [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa]
                    [Gossypium hirsutum]
                    226694
Seq. No.
                    LIB3189-006-P1-K1-H1
Seq. ID
                    BLASTX
Method
NCBI GI
                    g3283409
BLAST score
                    147
                    3.0e-09
E value
```



```
(AF068754) heat shock factor binding protein 1 HSBP1 [Homo
NCBI Description
                  sapiens] >gi_4557647_ref_NP_001528.1_pHSBP1_ heat shock
                  factor binding protein
Seq. No.
                  226695
                  LIB3189-006-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3036804
                  195
BLAST score
E value
                  7.0e-15
                  67
Match length
                  57
% identity
NCBI Description (AL022373) thaumatin-like protein [Arabidopsis thaliana]
                  226696
Seq. No.
                  LIB3189-006-P1-K1-H11
Seq. ID
                  BLASTX
Method
                  g755150
NCBI GI
BLAST score
                  290
                  3.0e-26
E value
Match length
                  88
                  70
% identity
NCBI Description (U13670) vacuolar H+-ATPase proteolipid (16 kDa) subunit
                  [Gossypium hirsutum]
                  226697
Seq. No.
                  LIB3189-006-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3687251
BLAST score
                  440
E value
                  1.0e-43
                  115
Match length
                   74
% identity
NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]
Seq. No.
                  226698
Seq. ID
                  LIB3189-006-P1-K1-H5
Method
                  BLASTX
NCBI GI
                   q2129495
BLAST score
                   291
E value
                   1.0e-26
Match length
                   60
                   95
% identity
                   fiber protein E6 (clone SIE6-2A) - sea-island cotton
NCBI Description
                   >gi 1000088 (U30507) E6 [Gossypium barbadense] >gi_1000090
                   (U30508) E6 [Gossypium barbadense]
                   226699
Seq. No.
                   LIB3189-006-P1-K1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1709002
BLAST score
                   361
                   2.0e-34
E value
                  86
Match length
                   81
% identity
```

32330

ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi\_1033190

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE



(U38186) S-adenosyl methionine synthetase [Pinus banksiana]

```
226700
Seq. No.
                  LIB3189-006-P1-K1-H8
Seq. ID
                  BLASTX
Method
                  g3327868
NCBI GI
                  128
BLAST score
                  2.0e-13
E value
                  71
Match length
                  61
% identity
                  (AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis
NCBI Description
                  thaliana]
                  226701
Seq. No.
                  LIB3189-006-P1-K1-H9
Seq. ID
                  BLASTX
Method
                  g3169182
NCBI GI
                  212
BLAST score
                  5.0e-17
E value
                  42
Match length
                  86
% identity
NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]
                  226702
Seq. No.
                  LIB3189-007-P1-K1-A1
Seq. ID
                  BLASTX
Method
                  g1174592
NCBI GI
BLAST score
                   441
                   6.0e-44
E value
Match length
                   82
                   99
% identity
NCBI Description TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
                   - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                   sativum]
                   226703
Seq. No.
                   LIB3189-007-P1-K1-A11
Seq. ID
Method
                   BLASTX
                   q4098129
NCBI GI
                   639
BLAST score
                   5.0e-67
E value
                   127
Match length
% identity
                   95
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
                   226704
Seq. No.
                   LIB3189-007-P1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2245012
                   166
BLAST score
                   2.0e-11
E value
                   92
Match length
% identity
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]
                   226705
Seq. No.
                   LIB3189-007-P1-K1-A6
Seq. ID
```

NCBI GĮ



```
BLASTX
Method
                  g3420239
NCBI GI
                  264
BLAST score
                  1.0e-23
E value
                  57
Match length
                  89
% identity
                 (AF059484) actin [Gossypium hirsutum]
NCBI Description
                  226706
Seq. No.
                  LIB3189-007-P1-K1-A7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2995384
                  145
BLAST score
                  4.0e-09
E value
                  40
Match length
                  75
% identity
NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]
                  226707
Seq. No.
                  LIB3189-007-P1-K1-B1
Seq. ID
                  BLASTX
Method
                  g3650032
NCBI GI
                  237
BLAST score
                   8.0e-20
E value
                   49
Match length
                   73
% identity
NCBI Description (AC005396) gibberellin-regulated protein GAST1-like
                   [Arabidopsis thaliana]
                   226708
Seq. No.
                  LIB3189-007-P1-K1-B10
Seq. ID
Method
                   BLASTX
                   g2244750
NCBI GI
                   635
BLAST score
                   1.0e-66
E value
Match length
                   124
% identity
                   97
                  (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
NCBI Description
                   >gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                   [Arabidopsis thaliana]
                   226709
Seq. No.
                   LIB3189-007-P1-K1-B11
Seq. ID
Method
                   BLASTX
                   q1710838
NCBI GI
                   376
BLAST score
E value
                   3.0e-36
                   79
Match length
% identity
                   89
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                   HYDROLASE) (ADOHCYASE) >gi 535584 (L36119)
                   adenosylhomocysteinase [Medicago sativa]
                   226710
Seq. No.
                   LIB3189-007-P1-K1-B12
Seq. ID
                   BLASTX
Method
```

32332

g3122389



```
496
BLAST score
                  3.0e-50
E value
                  123
Match length
                  70
% identity
NCBI Description WD-40 REPEAT PROTEIN MSI3 >gi_2394233 (AF016848) WD-40
                  repeat protein [Arabidopsis thaliana]
                  226711
Seq. No.
                  LIB3189-007-P1-K1-B4
Seq. ID
                  BLASTX
Method
                  g586076
NCBI GI
BLAST score
                  633
                  3.0e-66
E value
Match length
                  119
                  97
% identity
                  TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta
NCBI Description
                  chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta
                  tubulin 1 [Lupinus albus]
                  226712
Seq. No.
                  LIB3189-007-P1-K1-B7
Seq. ID
Method
                  BLASTX
                  g481818
NCBI GI
                  179
BLAST score
E value
                  4.0e-13
                  77
Match length
% identity
                  56
NCBI Description coproporphyrinogen oxidase - soybean
                  226713
Seq. No.
                  LIB3189-007-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1203832
                  534
BLAST score
                   1.0e-54
E value
Match length
                  143
% identity
                   71
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
NCBI Description
                   [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan
                   exohydrolase [Hordeum vulgare]
Seq. No.
                   226714
                   LIB3189-007-P1-K1-C10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g629858
BLAST score
                   483
```

```
E value
                   9.0e-49
                   115
Match length
```

NCBI Description protein kinase C inhibitor - maize

Seq. No. 226715 Seq. ID LIB3189-007-P1-K1-C2 BLASTX Method

81

NCBI GI g2244749 BLAST score 489 E value 1.0e-49

% identity

% identity

100



```
Match length
                  116
                   79
% identity
NCBI Description
                  (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
                  226716
Seq. No.
                  LIB3189-007-P1-K1-C3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2564253
                  369
BLAST score
                  2.0e-35
E value
                  112
Match length
                   59
% identity
                  (Z99996) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase
NCBI Description
                   [Hordeum vulgare]
                   226717
Seq. No.
                  LIB3189-007-P1-K1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4102859
                   465
BLAST score
E value
                   9.0e-47
                   109
Match length
                   77
% identity
                  (AF016892) cytoplasmic superoxide dismutase 1 [Populus
NCBI Description
                   tremuloides]
Seq. No.
                   226718
                  LIB3189-007-P1-K1-C7
Seq. ID
                   BLASTX
Method
                   g2880049
NCBI GI
BLAST score
                   184
                   5.0e-15
E value
                   84
Match length
                   58
% identity
                  (AC002340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   226719
                   LIB3189-007-P1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2129499
BLAST score
                   575
E value
                   1.0e-59
Match length
                   129
                   86
% identity
                   fiber protein E6 (clone CKE6-4A) - upland cotton
NCBI Description
                   >gi 1000086 (U30506) E6 [Gossypium hirsutum]
Seq. No.
                   226720
                   LIB3189-007-P1-K1-E10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2244732
BLAST score
                   551
E value
                   1.0e-56
Match length
                   105
```

NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]



Seq. No. 226721 LIB3189-007-P1-K1-E11 Seq. ID Method BLASTX NCBI GI q2673913 BLAST score 4419.0e-44E value Match length 108 % identity 76 (AC002561) hypothetical protein [Arabidopsis thaliana] NCBI Description 226722 Seq. No. LIB3189-007-P1-K1-E12 Seq. ID Method BLASTX NCBI GI g629838 BLAST score 678 E value 2.0e-71 Match length 162 % identity 73 tubulin beta-4 chain - maize >gi 416145 (L10635) beta-4 NCBI Description tubulin [Zea mays] 226723 Seq. No. LIB3189-007-P1-K1-E2 Seq. ID Method BLASTX q4371290 NCBI GI BLAST score 354 2.0e-33 E value Match length 127 % identity 54 NCBI Description (AC006260) unknown protein [Arabidopsis thaliana] 226724 Seq. No. LIB3189-007-P1-K1-E5 Seq. ID Method BLASTX g3702327 NCBI GI 158 BLAST score E value 1.0e-10 Match length 105 % identity 46 NCBI Description (AC005397) unknown protein [Arabidopsis thaliana] Seq. No. 226725 LIB3189-007-P1-K1-E6 Seq. ID Method BLASTX q3775997 NCBI GI 361 BLAST score E value 1.0e-34 Match length 95 % identity 76 NCBI Description (AJ010462) RNA helicase [Arabidopsis thaliana] Seq. No. 226726 LIB3189-007-P1-K1-E8 Seq. ID Method BLASTX

NCBI GI g3334261 BLAST score 206 E value 3.0e-16

E value

Match length

6.0e-39

119



```
54
Match length
                   63
% identity
NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi_1655851 (U61973)
                  metallothionein-like protein [Malus domestica]
                  226727
Seq. No.
                  LIB3189-007-P1-K1-E9
Seq. ID
                  BLASTX
Method
                  g4544399
NCBI GI
BLAST score
                  248
                   3.0e-21
E value
Match length
                  99
                   44
% identity
                  (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                  thaliana]
                   226728
Seq. No.
                   LIB3189-007-P1-K1-F12
Seq. ID
                   BLASTX
Method
                   g2961384
NCBI GI
BLAST score
                   215
                   3.0e-17
E value
                   95
Match length
                   46
% identity
                  (AL022141) aldehyde dehydrogenase like protein [Arabidopsis
NCBI Description
                   thaliana]
                   226729
Seq. No.
                   LIB3189-007-P1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3320379
                   511
BLAST score
                   5.0e-52
E value
Match length
                   135
                   76
% identity
                  (AF014375) putative JUN kinase activation domain binding
NCBI Description
                   protein [Medicago sativa]
                   226730
Seq. No.
                   LIB3189-007-P1-K1-F4
Seq. ID
                   BLASTX
Method
                   g4249382
NCBI GI
                   267
BLAST score
                   2.0e-23
E value
                   66
Match length
% identity
                   76
                   (AC005966) Strong similarity to gi_3337350 F13P17.3
NCBI Description
                   putative permease from Arabidopsis thaliana BAC
                   gb AC004481. [Arabidopsis thaliana]
                   226731
Seq. No.
                   LIB3189-007-P1-K1-G12
Seq. ID
                   {\tt BLASTX}
Method
                   g4191784
NCBI GI
BLAST score
                   400
```



% identity (AC005917) putative WD-40 repeat protein [Arabidopsis NCBI Description thaliana] Seq. No. 226732 LIB3189-007-P1-K1-G2 Seq. ID BLASTX Method g3876865 NCBI GI BLAST score 152 6.0e-10 E value 68 Match length 41 % identity (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 NCBI Description

comes from this gene; cDNA EST EMBL: C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

226733 Seq. No.

LIB3189-007-P1-K1-H10 Seq. ID

Method BLASTX NCBI GI g3953457 162 BLAST score 5.0e-11 E value 68 Match length % identity 50

NCBI Description (AC002328) F20N2.2 [Arabidopsis thaliana]

226734 Seq. No.

LIB3189-007-P1-K1-H11 Seq. ID

Method BLASTX NCBI GI q3953457 BLAST score 155 E value 3.0e-10 Match length 60 58 % identity

NCBI Description (AC002328) F20N2.2 [Arabidopsis thaliana]

226735 Seq. No.

LIB3189-007-P1-K1-H12 Seq. ID

Method BLASTX NCBI GI g1346422 BLAST score 239 E value 1.0e-22 Match length 145 % identity 41

NCBI Description SERINE PALMITOYLTRANSFERASE 2 (LONG CHAIN BASE BIOSYNTHESIS

PROTEIN 2) (SPT 2) >gi\_2130481\_pir\_\_JC5183 serine

C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain - fission yeast (Schizosaccharomyces pombe) >gi 1001947 (U15645) serine palmitoyltransferase [Schizosaccharomyces pombe]

>gi 2414613 emb CAB16362 (Z99259) serine

palmitoyltransferase 2 [Schizosaccharomyces pombe]

Seq. No. 226736

Seq. ID LIB3189-007-P1-K1-H5

BLASTX Method NCBI GI g3914368



158 BLAST score 3.0e-17 E value 78 Match length 63 % identity GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT) NCBI Description >gi 167519 (M80571) glycerol-3-phosphate acyltransferase [Cucumis sativus] >gi 444331 prf 1906380A glycerol phosphate acyltransferase [Cucumis sativus] 226737 Seq. No. LIB3189-007-P1-K1-H7 Seq. ID BLASTX Method NCBI GI g3334115 BLAST score 550 1.0e-56 E value Match length 119 % identity 51 NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi\_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum] 226738 Seq. No. LIB3189-007-P1-K1-H9 Seq. ID BLASTX Method NCBI GI g2662343 BLAST score 395 E value 1.0e-38 Match length 82 95 % identity NCBI Description (D63581) EF-1 alpha [Oryza sativa] 226739 Seq. No. LIB3189-008-P1-K1-A1 Seq. ID Method BLASTX NCBI GI q3915847 BLAST score 204 4.0e-16 E value Match length 71 70 % identity NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana] 226740 Seq. No. Seq. ID LIB3189-008-P1-K1-A10 Method BLASTX NCBI GI g1916807 BLAST score 284 E value 2.0e-25 Match length 106 % identity 65 NCBI Description (U81162) auxin-binding protein [Prunus persica]

Seq. No. 226741

Seq. ID LIB3189-008-P1-K1-A12

Method BLASTX NCBI GI g4490332

Match length

% identity

62



```
BLAST score
E value
                   1.0e-16
Match length
                   79
% identity
                   56
NCBI Description (AL035656) putative protein [Arabidopsis thaliana]
                   226742
Seq. No.
Seq. ID
                   LIB3189-008-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   q3273828
BLAST score
                   304
E value
                   1.0e-27
Match length
                   118
% identity
NCBI Description
                  (AF068686) nodule-enhanced malate dehydrogenase [Glycine
                  max]
                   226743
Seq. No.
                   LIB3189-008-P1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3420239
BLAST score
                   208
E value
                   4.0e-17
Match length
                   50
% identity
NCBI Description (AF059484) actin [Gossypium hirsutum]
Seq. No.
                   226744
Seq. ID
                   LIB3189-008-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   q4467146
BLAST score
                   365
E value
                   5.0e-35
Match length
                   107
% identity
NCBI Description
                  (AL035540) galactosidase like protein [Arabidopsis
                   thaliana]
Seq. No.
                   226745
Seq. ID
                   LIB3189-008-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   g3128176
BLAST score
                   310
E value
                   2.0e-28
Match length
                   101
% identity
                   59
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                   226746
Seq. ID
                   LIB3189-008-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   g4204300
BLAST score
                   160
E value
                   7.0e-11
```

32339

NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]



Seq. No.

226747

```
LIB3189-008-P1-K1-B5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4406819
                  190
BLAST score
                  2.0e-14
E value
                  98
Match length
                  48
% identity
                 (AC006201) unknown protein [Arabidopsis thaliana]
NCBI Description
                  226748
Seq. No.
                  LIB3189-008-P1-K1-B6
Seq. ID
                  BLASTX
Method
                  g1518540
NCBI GI
BLAST score
                  519
                  7.0e-65
E value
                  143
Match length
                  93
% identity
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
                  226749
Seq. No.
                  LIB3189-008-P1-K1-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3551131
BLAST score
                  153
E value
                  2.0e-12
                  56
Match length
                  64
% identity
                  (AB012044) plasma membrane aquaporin (PAQ1) [Raphanus
NCBI Description
                  sativus]
                  226750
Seq. No.
                  LIB3189-008-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2529665
BLAST score
                  646
                  8.0e-68
E value
Match length
                  136
% identity
                  (AC002535) putative ribosomal protein L7A [Arabidopsis
NCBI Description
                  thaliana]
                  226751
Seq. No.
Seq. ID
                  LIB3189-008-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  q4455208
BLAST score
                  199
E value
                   1.0e-15
Match length
                  71
% identity
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                   226752
                  LIB3189-008-P1-K1-C11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2088649
```

NCBI Description



```
BLAST score
                   342
                   3.0e - 32
E value
Match length
                  107
% identity
                   63
NCBI Description (AF002109) unknown protein [Arabidopsis thaliana]
                   226753
Seq. No.
                  LIB3189-008-P1-K1-C2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2078350
BLAST score
                   157
                   1.0e-10
E value
                   35
Match length
                   83
% identity
NCBI Description (U95923) transaldolase [Solanum tuberosum]
                   226754
Seq. No.
                   LIB3189-008-P1-K1-C3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1421730
                   540
BLAST score
                   2.0e-55
E value
                   138
Match length
                   78
% identity
NCBI Description (U43082) RF2 [Zea mays]
                   226755
Seq. No.
                   LIB3189-008-P1-K1-C4
Seq. ID
                   BLASTX
Method
                   g4580460
NCBI GI
                   311
BLAST score
E value
                   1.0e-28
                   93
Match length
                   72
% identity
NCBI Description (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
                   thaliana]
                   226756
Seq. No.
Seq. ID
                   LIB3189-008-P1-K1-C6
Method
                   BLASTX
                   g3004564
NCBI GI
BLAST score
                   239
                   5.0e-20
E value
Match length
                   88
% identity
                   56
NCBI Description (AC003673) putative receptor Ser/Thr protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   226757
                   LIB3189-008-P1-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4467133
BLAST score
                   398
E value
                   1.0e-38
                   120
Match length
% identity
```

(AL035540) geranylgeranyl pyrophosphate synthase-related



## protein [Arabidopsis thaliana]

226758 Seq. No. LIB3189-008-P1-K1-D1 Seq. ID BLASTX Method g3080428 NCBI GI 341 BLAST score 5.0e-32 E value 94 Match length 68 % identity NCBI Description (AL022604) putative protein [Arabidopsis thaliana] 226759 Seq. No. LIB3189-008-P1-K1-D2 Seq. ID BLASTX Method g3080428 NCBI GI BLAST score 144 4.0e-09 E value 66 Match length % identity 48 NCBI Description (AL022604) putative protein [Arabidopsis thaliana] 226760 Seq. No. LIB3189-008-P1-K1-D5 Seq. ID Method BLASTX NCBI GI g3746069 BLAST score 222 4.0e-18 E value 129 Match length 37 % identity NCBI Description (AC005311) putative reverse transcriptase [Arabidopsis thaliana] 226761 Seq. No. LIB3189-008-P1-K1-D7 Seq. ID Method BLASTX NCBI GI g541951 BLAST score 437 3.0e-43E value Match length 133 % identity 65 NCBI Description SPCP2 protein - soybean >gi 310578 (L12258) nodulin-26 [Glycine max] 226762 Seq. No. Seq. ID LIB3189-008-P1-K1-D8 Method BLASTX NCBI GI g1345882 141 BLAST score 3.0e-09 E value Match length 30 87 % identity NCBI Description CYTOCHROME B5 226763 Seq. No.

Seq. ID LIB3189-008-P1-K1-D9

Method BLASTX



NCBI GI q3150402 BLAST score 677 E value 2.0e-71Match length 147 % identity 92 (AC004165) putative malonyl-CoA:Acyl carrier protein NCBI Description transacylase [Arabidopsis thaliana] 226764 Seq. No. Seq. ID LIB3189-008-P1-K1-E1 Method BLASTX NCBI GI g1173055 BLAST score 509 E value 9.0e-52 105 Match length 97 % identity 60S RIBOSOMAL PROTEIN L11 (L5) >gi 541961 pir S42497 NCBI Description ribosomal protein L11.e - alfalfa >gi 1076504 pir S51819 RL5 ribosomal protein - alfalfa >gi 463252 emb CAA55090 (X78284) RL5 ribosomal protein [Medicago sativa] 226765 Seq. No. LIB3189-008-P1-K1-E10 Seq. ID Method BLASTX g3355480 NCBI GI BLAST score 328 1.0e-30 E value Match length 97 64 % identity NCBI Description (AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

226766

Seq. No.

Seq. ID LIB3189-008-P1-K1-E4

Method BLASTX NCBI GI g2129499 BLAST score 457 E value 1.0e-45Match length 98 % identity 84

NCBI Description fiber protein E6 (clone CKE6-4A) - upland cotton >gi 1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No. 226767

LIB3189-008-P1-K1-E8 Seq. ID

Method BLASTX NCBI GI g1449179 BLAST score 327 E value 8.0e-33 Match length 87 % identity 83

NCBI Description (D86506) N-ethylmaleimide sensitive fusion protein

[Nicotiana tabacum]

226768 Seq. No.

Seq. ID LIB3189-008-P1-K1-F1

Method BLASTX

BLAST score

E value

586

9.0e-61



```
NCBI GI
                  g121953
BLAST score
                  175
                  1.0e-12
E value
                  43
Match length
                  81
% identity
                  HISTONE H1 >gi_81905_pir__S00033 histone H1.b - garden pea
NCBI Description
                  >gi 20762 emb CAA29123 (X05636) H1 histone (AA 1-263)
                  [Pisum sativum]
                  226769
Seq. No.
                  LIB3189-008-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3608171
BLAST score
                  367
                  3.0e - 35
E value
Match length
                  93
                  78
% identity
NCBI Description (D86306) proton-translocating inorganic pyrophosphatase
                  [Cucurbita moschata]
                  226770
Seq. No.
                  LIB3189-008-P1-K1-F11
Seq. ID
Method
                  BLASTX
                  g2661840
NCBI GI
                  424
BLAST score
                  7.0e-42
E value
Match length
                  124
% identity
                  64
NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]
                  226771
Seq. No.
                  LIB3189-008-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3420055
BLAST score
                   560
E value
                   9.0e-58
Match length
                  138
% identity
NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]
                   226772
Seq. No.
Seq. ID
                  LIB3189-008-P1-K1-F2
Method
                  BLASTX
NCBI GI
                   g3355470
BLAST score
                   255
E value
                   1.0e-34
Match length
                   98
% identity
                   73
NCBI Description
                  (AC004218) putative lysophospholipase [Arabidopsis
                   thaliana]
Seq. No.
                   226773
                  LIB3189-008-P1-K1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                   g267069
```



Match length 110 % identity TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594 NCBI Description tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana] 226774 Seq. No. LIB3189-008-P1-K1-G1 Seq. ID BLASTX Method NCBI GI g2829204 BLAST score 375 3.0e-36 E value 94 Match length % identity 83 NCBI Description (AF044204) lipid transfer protein precursor [Gossypium hirsutum] 226775 Seq. No. LIB3189-008-P1-K1-G12 Seq. ID BLASTX Method NCBI GI g2062167 BLAST score 452 4.0e-45 E value 97 Match length % identity 86 NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana] 226776 Seq. No. LIB3189-008-P1-K1-G3 Seq. ID Method BLASTX g1223922 NCBI GI BLAST score 496 E value 3.0e-50 Match length 117 % identity 74 NCBI Description (U49445) Vigna radiata vicilin peptidohydrolase [Vigna radiata] 226777 Seq. No. Seq. ID LIB3189-008-P1-K1-G4 Method BLASTX NCBI GI g3914437 BLAST score 176 3.0e-13E value Match length 50 % identity NCBI Description PROFILIN >gi\_3183706\_emb\_CAA75312\_ (Y15042) profilin [Hevea brasiliensis]

 Seq. No.
 226778

 Seq. ID
 LIB3189-008-P1-K1-G6

 Method
 BLASTX

 NCBI GI
 g2062167

BLAST score 213 E value 2.0e-17



Match length 44 % identity NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana] 226779 Seq. No. LIB3189-008-P1-K1-G7 Seq. ID Method BLASTX NCBI GI g3360289 BLAST score 161 E value 3.0e-11 Match length 64 % identity 45 NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays] 226780 Seq. No. LIB3189-008-P1-K1-H1 Seq. ID Method BLASTX NCBI GI g4539417 BLAST score 475 E value 7.0e-48 Match length 107 80 % identity NCBI Description (AL049171) putative protein [Arabidopsis thaliana] 226781 Seq. No. LIB3189-008-P1-K1-H3 Seq. ID Method BLASTX g3986110 NCBI GI BLAST score 367 E value 1.0e-35 Match length 78 90 % identity NCBI Description (AB012716) heat shock protein 70 cognate [Salix gilgiana] Seq. No. 226782 LIB3189-008-P1-K1-H7 Seq. ID Method BLASTX NCBI GI q3915873 BLAST score 497 E value 1.0e-50 Match length 99 % identity 93 NCBI Description SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) (NODULIN-100) >gi 2606081 (AF030231) sucrose synthase [Glycine max]

226783 Seq. No.

Seq. ID LIB3189-008-P1-K1-H8

Method BLASTX NCBI GI g4098129 BLAST score 403 E value 2.0e-39 86 Match length % identity 88

NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]

Method

NCBI GI

BLASTX

g3176098



```
226784
Seq. No.
                  LIB3189-008-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4262226
                  139
BLAST score
E value
                  1.0e-08
                  92
Match length
                  45
% identity
NCBI Description (AC006200) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  226785
                  LIB3189-010-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4314378
BLAST score
                  147
                   3.0e-09
E value
                  81
Match length
                   47
% identity
NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]
                  226786
Seq. No.
                  LIB3189-010-P1-K1-B11
Seq. ID
Method
                  BLASTX
                  q3786005
NCBI GI
BLAST score
                   255
                   3.0e-22
E value
Match length
                  73
                   42
% identity
NCBI Description
                  (AC005499) putative phosphoethanolamine
                  cytidylyltransferase [Arabidopsis thaliana]
Seq. No.
                   226787
Seq. ID
                  LIB3189-010-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   g4126399
BLAST score
                   456
                   1.0e-45
E value
Match length
                  111
% identity
                   81
NCBI Description (AB011794) chalcone isomerase [Citrus sinensis]
Seq. No.
                   226788
                   LIB3189-010-P1-K1-B9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3786005
BLAST score
                   374
                   5.0e-36
E value
Match length
                   100
                   42
% identity
                  (AC005499) putative phosphoethanolamine
NCBI Description
                   cytidylyltransferase [Arabidopsis thaliana]
                   226789
Seq. No.
Seq. ID
                   LIB3189-010-P1-K1-C10
```



BLAST score 356 E value 7.0e-34 Match length 123 % identity 60

NCBI Description (Y15036) annexin [Medicago truncatula]

Seq. No.

226790 LIB3189-010-P1-K1-C12

Seq. ID LIB3

Method BLASTX
NCBI GI g2129473
BLAST score 250
E value 2.0e-21
Match length 91
% identity 52

NCBI Description arabinogalactan-like protein - loblolly pine >gi\_607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No. 226791

Seq. ID LIB3189-010-P1-K1-C2

Method BLASTX
NCBI GI g3023847
BLAST score 489
E value 1.0e-60
Match length 131
% identity 34

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE

PROTEIN >gi\_2385376\_emb\_CAA69934\_ (Y08678) G protein beta

subunit-like [Medicago sativa]

Seq. No. 226792

Seq. ID LIB3189-010-P1-K1-C7

Method BLASTX
NCBI GI g2506139
BLAST score 501
E value 9.0e-51
Match length 120

% identity 83

NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)

(ARCHAIN) >gi\_1314049\_emb\_CAA91901\_ (Z67962)

archain/delta-COP [Oryza sativa]

Seq. No. 226793

Seq. ID LIB3189-010-P1-K1-C9

Method BLASTX
NCBI GI g3023847
BLAST score 247
E value 1.0e-21
Match length 62
% identity 81

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE

PROTEIN >gi\_2385376\_emb\_CAA69934\_ (Y08678) G protein beta

subunit-like [Medicago sativa]

Seq. No. 226794

Seq. ID LIB3189-010-P1-K1-D2

Method BLASTX NCBI GI g1619602



```
BLAST score
                  327
E value
                  1.0e-30
Match length
                  95
% identity
                  36
NCBI Description (Y08726) MtN3 [Medicago truncatula]
                  226795
Seq. No.
Seq. ID
                  LIB3189-010-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g2651310
BLAST score
                  202
E value
                  2.0e-16
Match length
                  57
% identity
                  61
NCBI Description (AC002336) putative PTR2-B peptide transporter [Arabidopsis
                  thaliana]
                  226796
Seq. No.
Seq. ID
                  LIB3189-010-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g3970652
BLAST score
                  513
E value
                  3.0e-52
Match length
                  129
% identity
                  76
NCBI Description (X77499) amino acid permease [Arabidopsis thaliana]
                  226797
Seq. No.
                  LIB3189-010-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4335774
BLAST score
                  193
                  1.0e-14
E value
Match length
                  116
% identity
                  42
NCBI Description (AC006284) hypothetical protein, 3' partial [Arabidopsis
                  thalianal
Seq. No.
                  226798
Seq. ID
                  LIB3189-010-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g2811278
BLAST score
                  183
E value
                  4.0e-14
Match length
                  44
% identity
                  77
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                  226799
Seq. ID
                  LIB3189-010-P1-K1-E11
Method
                  BLASTX
```

NCBI GI g3063396
BLAST score 605
E value 5.0e-63
Match length 132
% identity 85

NCBI Description (AB012947) vcCyP [Vicia faba]

% identity

NCBI Description

reinhardtii]



```
226800
Seq. No.
                  LIB3189-010-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100225
BLAST score
                  381
E value
                  1.0e-36
                  101
Match length
                   66
% identity
                  heat shock transcription factor 8 - tomato
NCBI Description
                  >gi_19260_emb_CAA47868_ (X67599) heat stress transcription
                   factor 8 [Lycopersicon esculentum]
Seq. No.
                   226801
                  LIB3189-010-P1-K1-E2
Seq. ID
Method
                  BLASTX
                  g70639
NCBI GI
BLAST score
                   381
                   6.0e-37
E value
                   95
Match length
                   21
% identity
                  ubiquitin precursor - Neurospora crassa
NCBI Description
                   >gi_295930_emb_CAA31530_ (X13140) ubiquitin [Neurospora
                   crassa]
Seq. No.
                   226802
Seq. ID
                  LIB3189-010-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   g2369714
BLAST score
                   715
E value
                   7.0e-76
Match length
                   152
% identity
                   93
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.
                   226803
Seq. ID
                   LIB3189-010-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   g115492
BLAST score
                   640
E value
                   4.0e-67
Match length
                   125
                   56
% identity
NCBI Description
                  CALMODULIN-RELATED PROTEIN >qi 169205 (M80831)
                   calmodulin-related protein [Petunia hybrida]
Seq. No.
                   226804
Seq. ID
                  LIB3189-010-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   g1353352
BLAST score
                   191
E value
                   4.0e-15
Match length
                   62
```

(U31975) alanine aminotransferase [Chlamydomonas



```
226805
Seq. No.
                  LIB3189-010-P1-K1-F11
Seq. ID
                  BLASTX
Methad
NCBI GI
                  q4510430
BLAST score
                  589
E value
                  4.0e-61
Match length
                  122
                  88
% identity
                  (AC006929) unknown protein, 3' partial [Arabidopsis
NCBI Description
                  thaliana]
                  226806
Seq. No.
                  LIB3189-010-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760320
BLAST score
                  200
E value
                  1.0e-18
Match length
                  86
                   66
% identity
                  (AC002130) F1N21.4 [Arabidopsis thaliana]
NCBI Description
                  226807
Seq. No.
                  LIB3189-010-P1-K1-F6
Seq. ID
Method
                  BLASTX
                  g3075394
NCBI GI
BLAST score
                   456
E value
                   4.0e-50
Match length
                   150
% identity
                   71
                  (ACO04484) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana] >gi 3559809 emb CAA09311 (AJ010713) fiddlehead
                  protein [Arabidopsis thaliana]
                   226808
Seq. No.
                  LIB3189-010-P1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4139264
BLAST score
                   391
                   5.0e-38
E value
Match length
                   88
% identity
                   85
NCBI Description (AF111812) actin [Brassica napus]
                   226809
Seq. No.
Seq. ID
                   LIB3189-010-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   g2791900
BLAST score
                   557
E value
                   2.0e-57
Match length
                   140
% identity
                   71
NCBI Description (AJ000057) PP7 [Arabidopsis thaliana]
Seq. No.
                   226810
```

Seq. ID LIB3189-010-P1-K1-G1

Method BLASTX NCBI GI g3033380

Match length



```
BLAST score
                      415
                      6.0e-43
  E value
  Match length
                     127
  % identity
                     66
                     (AC004238) putative coatomer epsilon subunit [Arabidopsis
NCBI Description
                     thaliana]
                     226811
  Seq. No.
                     LIB3189-010-P1-K1-G11
  Seq. ID
  Method
                     BLASTX
                     q3309269
  NCBI GI
  BLAST score
                      496
                      3.0e-50
  E value
  Match length
                     106
  % identity
                      90
                     (AF074940) ferric leghemoglobin reductase-2 precursor
  NCBI Description
                      [Glycine max]
                      226812
  Seq. No.
                      LIB3189-010-P1-K1-G12
  Seq. ID
                      BLASTX
  Method
                      g3928150
  NCBI GI
  BLAST score
                      212
                      5.0e-17
  E value
  Match length
                      66
  % identity
                      61
  NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]
                      226813
  Seq. No.
                      LIB3189-010-P1-K1-G2
  Seq. ID
                      BLASTX
  Method
                      g2464905
  NCBI GI
                      298
  BLAST score
                      5.0e-27
  E value
                      116
  Match length
  % identity
  NCBI Description (Z99708) minor allergen [Arabidopsis thaliana]
                      226814
  Seq. No.
                      LIB3189-010-P1-K1-G3
  Seq. ID
  Method
                      BLASTX
  NCBI GI
                      q464846
                      507
  BLAST score
  E value
                      2.0e-51
  Match length
                      102
                      91
  % identity
                     TUBULIN ALPHA-6 CHAIN >gi_322880_pir_S28983 tubulin alpha-6 chain - maize >gi_22158_emb_CAA44863_ (X63178)
  NCBI Description
                      alpha-tubulin #6 [Zea mays]
                      226815
  Seq. No.
                      LIB3189-010-P1-K1-G5
  Seq. ID
  Method
                      BLASTX
  NCBI GI
                      g2244792
  BLAST score
                      235
                      9.0e-20
  E value
```



% identity NCBI Description (Z97336) ankyrin homolog [Arabidopsis thaliana] 226816 Seq. No. LIB3189-010-P1-K1-G6 Seq. ID Method BLASTX g2760326 NCBI GI BLAST score 320 E value 1.0e-29 Match length 151 % identity 50 NCBI Description (AC002130) F1N21.11 [Arabidopsis thaliana] Seq. No. 226817 LIB3189-010-P1-K1-G8 Seq. ID Method BLASTX NCBI GI g4262250 BLAST score 381 E value 1.0e-36 Match length 85 % identity 85 NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana] 226818 Seq. No. Seq. ID LIB3189-010-P1-K1-G9 Method BLASTX NCBI GI g1173218 BLAST score 387 E value 1.0e-37 Match length 77 % identity 97 NCBI Description 40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana] Seq. No. 226819 Seq. ID LIB3189-010-P1-K1-H1 Method BLASTX NCBI GI q2688839 BLAST score 373 E value 9.0e-36 Match length 88 % identity 80 NCBI Description (AF003347) ATP phosphoribosyltransferase [Thlaspi goesingense] Seq. No. 226820 Seq. ID LIB3189-010-P1-K1-H10 Method BLASTX NCBI GI g4468979 BLAST score 500 E value 1.0e-50 Match length 123 79 % identity

Seq. No. 226821

NCBI Description

(AL035605) putative protein [Arabidopsis thaliana]

BLAST score

E value

154

2.0e-10



```
LIB3189-010-P1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4416307
BLAST score
                   179
E value
                   1.0e-18
Match length
                   91
                   55
% identity
NCBI Description
                  (AF105716) hypothetical protein [Zea mays]
Seq. No.
                   226822
                   LIB3189-010-P1-K1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4204300
BLAST score
                   214
E value
                   4.0e-17
Match length
                   81
                   52
% identity
NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   226823
                   LIB3189-010-P1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3757522
BLAST score
                   291
                   3.0e-26
E value
Match length
                   129
% identity
                   53
NCBI Description (AC005167) putative splicing factor [Arabidopsis thaliana]
Seq. No.
                   226824
Seq. ID.
                   LIB3189-010-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   q3618214
BLAST score
                   171
E value
                   4.0e-12
Match length
                   136
% identity
NCBI Description
                   (AL031579) dihydrofolate reductase [Schizosaccharomyces
                   pombe]
Seq. No.
                   226825
Seq. ID
                   LIB3189-011-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g4191789
BLAST score
                   197
                   2.0e-15
E value
Match length
                   106
% identity
                   45
                   (AC005917) putative transmembrane transport protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   226826
Seq. ID
                   LIB3189-011-P1-K1-A10
Method.
                   {\tt BLASTX}
NCBI GI
                   g3047085
```



53 Match length % identity NCBI Description (AF058914) No definition line found [Arabidopsis thaliana] 226827 Seq. No. Seq. ID LIB3189-011-P1-K1-A11 Method BLASTX NCBI GI q267069 BLAST score 329 E value 5.0e-31 Match length 61 95 % identity NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi\_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] > gi 166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana] Seq. No. 226828 Seq. ID LIB3189-011-P1-K1-A12 Method BLASTX NCBI GI q3914394 BLAST score 720 E value 2.0e-76 Match length 150 % identity 90 NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi\_2118335\_pir\_\_S60473 phosphoglycerate mutase (EC 5.4.2.1) - common ice plant >gi\_602426 (U16021) phosphoglyceromutase [Mesembryanthemum crystallinum] 226829 Seq. No. Seq. ID LIB3189-011-P1-K1-A2 Method BLASTX NCBI GI g2829893 BLAST score 311 E value 8.0e-29 Match length 71 % identity NCBI Description (AC002311) phosphoglucomutase [Arabidopsis thaliana] 226830 Seq. No. Seq. ID LIB3189-011-P1-K1-A3 Method BLASTX NCBI GI g4530585 BLAST score 357 E value 7.0e - 3485 Match length % identity NCBI Description (AF130978) B12D protein [Ipomoea batatas]

Seq. No. 226831

Seq. ID LIB3189-011-P1-K1-A5

Method BLASTX
NCBI GI g4455129
BLAST score 194
E value 9.0e-15



```
85
Match length
% identity
NCBI Description (AF127761) ribonucleoprotein ZRNP1 [Homo sapiens]
Seq. No.
                   226832
                   LIB3189-011-P1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2245012
BLAST score
                   179
E value
                   5.0e-13
Match length
                   62
% identity
                   58
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   226833
                   LIB3189-011-P1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2130073
BLAST score
                   252
E value
                   5.0e-22
                   65
Match length
                   78
% identity
NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
                   cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
                   C-1 [Oryza sativa] >\overline{gi}_790970_d\overline{bj}_BAA08830_ (D50301)
                   aldolase C-1 [Oryza sativa]
                   226834
Seq. No.
Seq. ID
                   LIB3189-011-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   g4490317
BLAST score
                   172
E value
                   2.0e-12
Match length
                   62
% identity
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
Seq. No.
                   226835
Seq. ID
                   LIB3189-011-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   g2244841
BLAST score
                   255
E value
                   4.0e-22
Match length
                  92
                   53
% identity
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
                   226836
Seq. No.
Seq. ID
                   LIB3189-011-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   g228316
BLAST score
                   185
E value
                   2.0e-14
```

NCBI Description albumin [Theobroma cacao]

57

58

Match length

% identity



```
Seq. No.
                  226837
Seq. ID
                  LIB3189-011-P1-K1-B10
                  BLASTX
Method
NCBI GI
                  g3914832
BLAST score
                  214
                  3.0e-17
E value
                  59
Match length
                   66
% identity
NCBI Description DNA-DIRECTED RNA POLYMERASE MITOCHONDRIAL PRECURSOR
                  >gi_1742971_emb_CAA70583_ (Y09432) mitochondrial singel
                  subunit DNA-directed RNA polymerase [Arabidopsis thaliana]
                  >gi_2330566_emb_CAA70210_ (Y09006) mitochondrial
                   single-subunit DNA-dependent RNA polymerase [Arabidopsis
                   thaliana]
Seq. No.
                  226838
                  LIB3189-011-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129840
BLAST score
                  378
                  2.0e-36
E value
                  113
Match length
                   65
% identity
NCBI Description nucleosome assembly protein 1 - soybean >gi 1161252
                  (L38856) nucleosome assembly protein 1 [Glycine max]
Seq. No.
                  226839
                  LIB3189-011-P1-K1-B2
Seq. ID
Method
                  BLASTX
                  g4006878
NCBI GI
BLAST score
                  391
E value
                   4.0e-38
Match length
                  97
% identity
                  70
NCBI Description (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
Seq. No.
                   226840
                  LIB3189-011-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4406816
BLAST score
                   589
E value
                   3.0e-61
Match length
                   119
% identity
                   91
NCBI Description (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]
Seq. No.
                   226841
Seq. ID
                   LIB3189-011-P1-K1-B7
Method
                  BLASTX
NCBI GI
                   g1199806
BLAST score
                  176
E value
                   5.0e-13
                  52
Match length
```

Seq. No. 226842

% identity

NCBI Description (X95663) elongation factor 1 alpha [Brugia pahangi]

Seq. No.

Seq. ID

226847

LIB3189-011-P1-K1-D2



```
LIB3189-011-P1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   a4098129
BLAST score
                   383
                   4.0e-37
E value
                   89
Match length
% identity
                   82
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
Seq. No.
                   226843
                   LIB3189-011-P1-K1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2827715
BLAST score
                   498
E value
                   2.0e-50
Match length
                   144
% identity
                  (AL021684) receptor protein kinase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   226844
                   LIB3189-011-P1-K1-C5
Seq. ID
Method
                   BLASTX
                   g1351408
NCBI GI
BLAST score
                   339
E value
                   8.0e-32
                   106
Match length
% identity
                    67
                   VACUOLAR PROCESSING ENZYME PRECURSOR (VPE)
NCBI Description
                   >gi_1076563_pir__S51117 cystein proteinase - sweet orange
                   >gi_633185_emb_CAA87720_ (Z47793) cystein proteinase (by
similarity) [Citrus sinensis] >gi_1588548_prf__2208463A
                    vascular processing protease [Citrus sinensis]
Seq. No.
                    226845
Seq. ID
                   LIB3189-011-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   g2911073
BLAST score
                   347
E value
                    3.0e - 33
Match length
                   82
% identity
NCBI Description (AL021960) putative protein [Arabidopsis thaliana]
Seq. No.
                    226846
Seq. ID
                   LIB3189-011-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   g3142289
BLAST score
                   151
E value
                    5.0e-10
                   44
Match length
% identity
                   (AC002411) Strong similarity to beta-keto-Coa synthase
NCBI Description
                    gb U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
```

32358



```
Method
                  BLASTX
NCBI GI
                  g3914685
BLAST score
                  292
E value
                  6.0e-27
Match length
                  68
                  82
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L17 >gi 2668748 (AF034948) ribosomal
                  protein L17 [Zea mays]
Seq. No.
                  226848
Seq. ID
                  LIB3189-011-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q126770
BLAST score
                  466
E value
                  1.0e-48
Match length
                  105
% identity
                  84
NCBI Description
                  MALATE SYNTHASE, GLYOXYSOMAL >gi 68218 pir SYCNMU malate
                  synthase (EC 4.1.3.2) - upland cotton
                  >gi_18507_emb_CAA36546_ (X52305) malate synthase (AA 1-567)
                  [Gossypium hirsutum]
Seq. No.
                  226849
Seq. ID
                  LIB3189-011-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q2935298
BLAST score
                  653
E value
                  2.0e-68
Match length
                  145
% identity
                  94
                  (AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase
NCBI Description
                  1 [Gossypium hirsutum]
                  226850
Seq. No.
Seq. ID
                  LIB3189-011-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g2244838
BLAST score
                  145
E value
                  5.0e-09
                  37
Match length
                  73
% identity
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  226851
Seq. ID
                  LIB3189-011-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g3808101
BLAST score
                  430
E value
                  2.0e-42
Match length
                  128
% identity
NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]
Seq. No.
                  226852
```

Seq. ID LIB3189-011-P1-K1-E6

Method BLASTX NCBI GI g4539305



```
403
. BLAST score
                   8.0e-45
 E value
                   135
 Match length
 % identity
                   62
 NCBI Description (AL049480) putative protein [Arabidopsis thaliana]
 Seq. No.
                   226853
                   LIB3189-011-P1-K1-E7
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2980781
                   184
 BLAST score
 E value
                   1.0e-13
                   53
 Match length
 % identity
                   58
 NCBI Description (AL022198) putative protein [Arabidopsis thaliana]
                   226854
 Seq. No.
                   LIB3189-011-P1-K1-F3
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q730645
 BLAST score
                   592
                   2.0e-61
 E value
                   133
 Match length
                   89
 % identity
                   40S RIBOSOMAL PROTEIN S15 >gi 629556 pir S43412 ribosomal
 NCBI Description
                   protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_
                    (Z23161) ribosomal protein S15 [Arabidopsis thaliana]
                   >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15
                    [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104)
                    Strong similarity to Oryza 40S ribosomal protein S15. ESTs
                    gb R29788, gb ATTS0365 come from this gene. [Arabidopsis
                   thaliana]
                   226855
 Seq. No.
                   LIB3189-011-P1-K1-F8
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q3461845
 BLAST score
                   195
 E value
                    6.0e-15
 Match length
                   74
 % identity
 NCBI Description (AC005315) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                   226856
 Seq. ID
                   LIB3189-011-P1-K1-F9
 Method
                   BLASTX
 NCBI GI
                    g4322940
 BLAST score
                    350
 E value
                    4.0e-33
 Match length
                   109
 % identity
 NCBI Description (AF096299) DNA-binding protein 2 [Nicotiana tabacum]
```

Seq. No. 226857

Seq. ID LIB3189-011-P1-K1-G1

Method BLASTX NCBI GI g3687243

Method

NCBI GI

E value

BLAST score

BLASTX

223

g2078350

3.0e-18



```
BLAST score
                  124
E value
                  1.0e-12
Match length
                  55
                  78
% identity
NCBI Description
                  (AC005169) putative ribosomal protein [Arabidopsis
                  thaliana]
                  226858
Seq. No.
Seq. ID
                  LIB3189-011-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g1703091
BLAST score
                  197
E value
                  2.0e-15
Match length
                  50
                  80
% identity
NCBI Description ACYL CARRIER PROTEIN, MITOCHONDRIAL PRECURSOR (ACP)
                  (NADH-UBIQUINONE OXIDOREDUCTASE 9.6 KD SUBUNIT) (MTACP-1)
                  >gi_903689 (L23574) acyl carrier protein precursor
                   [Arabidopsis thaliana] >gi 3341682 (AC003672) acyl carrier
                  protein [Arabidopsis thaliana]
                  226859
Seq. No.
Seq. ID
                  LIB3189-011-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q3928083
BLAST score
                  627
E value
                  1.0e-65
Match length
                  151
% identity
NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]
                  226860
Seq. No.
Seq. ID
                  LIB3189-011-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q3894099
BLAST score
                  538
E value
                   4.0e-55
Match length
                  118
% identity
                  89
NCBI Description (AJ012750) MCM3 protein [Pisum sativum]
Seq. No.
                  226861
                  LIB3189-011-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g529353
BLAST score
                  169
E value
                  9.0e-12
Match length
                  94
                  45
% identity
NCBI Description (U12757) diphenol oxidase [Acer pseudoplatanus]
Seq. No.
                  226862
Seq. ID
                  LIB3189-011-P1-K1-G4
```

32361



```
50
Match length
                  82
% identity
NCBI Description (U95923) transaldolase [Solanum tuberosum]
                  226863
Seq. No.
                  LIB3189-011-P1-K1-G5
Seq. ID
Method
                  BLASTX
                  g2829204
NCBI GI
BLAST score
                  512
E value
                  4.0e-52
                  120
Match length
                  86
% identity
NCBI Description (AF044204) lipid transfer protein precursor [Gossypium
                  hirsutum]
                  226864
Seq. No.
                  LIB3189-011-P1-K1-G7
Seq. ID
Method
                  BLASTX
                  g167367
NCBI GI
BLAST score
                   328
E value
                   9.0e-31
Match length
                  87
                  75
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                  226865
                  LIB3189-011-P1-K1-G8
Seq. ID
Method
                  BLASTX
                   g730536
NCBI GI
                   103
BLAST score
E value
                   2.0e-11
Match length
                  72
                   64
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L23 >gi_310933 (L18915) 60S ribosomal
                  protein subunit L17 [Nicotiana tabacum]
Seq. No.
                   226866
Seq. ID
                  LIB3189-011-P1-K1-G9
Method
                  BLASTX
NCBI GI
                   q2764806
BLAST score
                   189
E value
                   1.0e-14
Match length
                  45
% identity
                   71
NCBI Description (X78548) epoxide hydrolase [Glycine max]
Seq. No.
                   226867
                   LIB3189-011-P1-K1-H2
Seq. ID
Method
                   BLASTX
                   g2497743
NCBI GI
BLAST score
                   174
E value
                   1.0e-12
                   57
Match length
% identity
                   60
```

32362

>gi\_999315\_bbs\_166991 (S78173) LTP=lipid transfer protein

[Gossypium hirsutum=cotton, fiber, Peptide, 120 aa]

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3)

Method

BLASTX



## [Gossypium hirsutum]

```
Seq. No.
                   226868
                  LIB3189-011-P1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3694811
BLAST score
                   175
                   7.0e-13
E value
                   36
Match length
                   86
% identity
NCBI Description
                  (AF060481) p-hydroxyphenylpyruvate dioxygenase [Arabidopsis
                   thaliana]
Seq. No.
                   226869
                  LIB3189-011-P1-K1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4432839
BLAST score
                   296
                   5.0e-27
E value
                   59
Match length
% identity
                   52
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                   226870
                  LIB3189-012-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2388885
BLAST score
                   137
                   1.0e-08
E value
                  51
Match length
                   57
% identity
NCBI Description (Y14762) glutathione peroxidase [Lycopersicon esculentum]
                   226871
Seq. No.
                   LIB3189-012-P1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3559814
BLAST score
                   185
E value
                   8.0e-14
                   90
Match length
% identity
                   50
NCBI Description (Y15781) transketolase 1 [Capsicum annuum]
                   226872
Seq. No.
Seq. ID
                   LIB3189-012-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   q4406780
BLAST score
                   249
E value
                   1.0e-21
Match length
                   73
% identity
                   66
NCBI Description
                   (AC006532) putative multispanning membrane protein
                   [Arabidopsis thaliana]
Seq. No.
                   226873
Seq. ID
                   LIB3189-012-P1-K1-B1
```



```
NCBI GI
                   g2149640
                   477
BLAST score
E value
                   5.0e-48
Match length
                   114
% identity
                   83
NCBI Description
                   (U91995) Argonaute protein [Arabidopsis thaliana]
                   226874
Seq. No.
Seq. ID
                   LIB3189-012-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   g1171035
BLAST score
                   161
E value
                   4.0e-11
Match length
                   43
% identity
                   60
                   METALLOTHIONEIN-LIKE PROTEIN TYPE 2 PKIWI504
NCBI Description
                   >gi_1086021_pir__S48038 metallothionein-like protein - kiwi fruit >gi_450245 (L27813) metallothionein-like protein
                    [Actinidia deliciosa]
Seq. No.
                   226875
Seq. ID
                   LIB3189-012-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   q543905
BLAST score
                   503
E value
                   3.0e-51
Match length
                   94
                   94
% identity
                   BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi 347459 (L22162)
NCBI Description
                   brassinosteroid-regulated protein [Glycine max]
                   226876
Seq. No.
                   LIB3189-012-P1-K1-C9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q312179
                   570
BLAST score
                   7.0e-59
E value
Match length
                   135
                   81
% identity
NCBI Description
                   (X73151) glyceraldehyde 3-phosphate dehydrogenase
                    (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic
                   glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]
                   >gi 1185554 (U45858) glyceraldehyde-3-phosphate
                   dehydrogenase [Zea mays]
Seq. No.
                   226877
Seq. ID
                   LIB3189-012-P1-K1-D1
                   BLASTX
Method
NCBI GI
                   g2435511
BLAST score
                   255
E value
                   5.0e-22
Match length
                   93
% identity
                   (AF024504) contains similarity to prolyl 4-hydroxylase
NCBI Description
                   alpha subunit [Arabidopsis thaliana]
```

Seq. No. 226878

32364

NCBI Description



LIB3189-012-P1-K1-D12 Seq. ID Method BLASTX q3894183 NCBI GI 256 BLAST score 5.0e-22 E value Match length 141 30 % identity NCBI Description (AC005662) calmodulin-like protein [Arabidopsis thaliana] 226879 Seq. No. Seq. ID LIB3189-012-P1-K1-D4 Method BLASTX NCBI GI g3059131 BLAST score 260 8.0e-27 E value Match length 118 % identity 53 NCBI Description (AJ000478) cytochrome P450 [Helianthus tuberosus] Seq. No. 226880 LIB3189-012-P1-K1-D7 Seq. ID Method BLASTX NCBI GI g126896 BLAST score 191 5.0e-15 E value Match length 43 % identity 91 NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR >gi\_319831\_pir\_\_DEPUMW malate dehydrogenase (EC 1.1.1.37) precursor, mitochondrial - watermelon >gi 18297 emb CAA35239 (X17362) precursor protein (AA -27 to 320) [Citrullus lanatus] Seq. No. 226881 LIB3189-012-P1-K1-D8 Seq. ID Method BLASTX NCBI GI g120669 BLAST score 363 E value 4.0e-35 Match length 70 % identity 93 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora] Seq. No. 226882 Seq. ID LIB3189-012-P1-K1-D9 Method BLASTX NCBI GI q462013 BLAST score 468 E value 6.0e-47Match length 135 73 % identity

ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)

>gi 542022 pir S39558 HSP90 homolog - Madagascar



periwinkle >gi 348696 (L14594) heat shock protein 90 [Catharanthus roseus]

Seq. No. 226883 LIB3189-012-P1-K1-E11 Seq. ID Method BLASTX NCBI GI g3643603 BLAST score 555 3.0e-57 E value Match length 127 % identity

NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

226884 Seq. No.

LIB3189-012-P1-K1-E3 Seq. ID

Method BLASTX NCBI GI g3023713 BLAST score 207 E value 7.0e-17Match length 52 85 % identity

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi 780372

(U09450) enolase [Oryza sativa]

226885 Seq. No.

LIB3189-012-P1-K1-E4 Seq. ID

Method BLASTX g136057 NCBI GI BLAST score 185 2.0e-14 E value Match length 38 89 % identity

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

>gi\_99499\_pir\_\_A32187 (S)-tetrahydroberberine oxidase -

Coptis japonica >gi\_556171 (J04121) triosephosphate

isomerase [Coptis japonica]

226886 Seq. No.

LIB3189-012-P1-K1-E6 Seq. ID

BLASTX Method NCBI GI q4204300 BLAST score 354 E value 1.0e-33 Match length 104 63 % identity

NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No. 226887

LIB3189-012-P1-K1-E7 Seq. ID

Method BLASTX NCBI GI a4105696 BLAST score 523 E value 9.0e-54Match length 127 % identity

NCBI Description (AF049870) beta tubulin 1 [Arabidopsis thaliana]



```
226888
Seq. No.
                  LIB3189-012-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024629
BLAST score
                  189
                  3.0e-14
E value
                  134
Match length
                  31
% identity
                  GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-GAMMA)
NCBI Description
                  >gi_423252_pir__S32369 gamma-SNAP protein - bovine
                  >gi 298669 bbs 127528 gamma soluble NSF attachment protein,
                  gamma SNAP=N-ethyl-maleimide-sensitive fusion protein
                  attachment protein [cattle, brain, Peptide, 328 aa]
                  >gi 445846 prf 1910317C NSF attachment protein
                   (SNAP):ISOTYPE=gamma [Bos taurus]
                  226889
Seq. No.
                  LIB3189-012-P1-K1-F10
Seq. ID
                  BLASTX
Method
                  g2780365
NCBI GI
                  138
BLAST score
                  1.0e-09
E value
                  79
Match length
                  51
% identity
NCBI Description (AB007693) Elongin C [Drosophila melanogaster]
Seq. No.
                  226890
                  LIB3189-012-P1-K1-F12
Seq. ID
                  BLASTX
Method
                   g1346675
NCBI GI
BLAST score
                   628
                   1.0e-65
E value
                  132
Match length
                   89
% identity
NCBI Description
                  NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B)
                   >qi 499112 (U10283) nucleoside diphosphate kinase [Flaveria
                  bidentisl
                   226891
Seq. No.
Seq. ID
                   LIB3189-012-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   q3128228
BLAST score
                   307
                   3.0e-28
E value
Match length
                   69
% identity
NCBI Description
                   (AC004077) putative ribosomal protein L18A [Arabidopsis
                   thaliana] >gi 3337376 (AC004481) putative ribosomal protein
                   L18A [Arabidopsis thaliana]
Seq. No.
                   226892
```

 Seq. ID
 LIB3189-012-P1-K1-F5

 Method
 BLASTX

 NCBI GI
 g3024629

 BLAST score
 188

 E value
 5.0e-14



Match length 133 % identity 32

NCBI Description GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-GAMMA)

>gi\_423252\_pir\_\_S32369\_gamma-SNAP\_protein - bovine

>gi\_298669\_bbs\_127528 gamma soluble NSF attachment protein,

gamma SNAP=N-ethyl-maleimide-sensitive fusion protein attachment protein [cattle, brain, Peptide, 328 aa] >gi\_445846\_prf\_\_1910317C NSF attachment protein

(SNAP):ISOTYPE=gamma [Bos taurus]

Seq. No. 226893

Seq. ID LIB3189-012-P1-K1-F6

Method BLASTX
NCBI GI g3980396
BLAST score 460
E value 4.0e-46
Match length 111
% identity 77

NCBI Description (AC004561) putative C-4 sterol methyl oxidase [Arabidopsis

thaliana]

Seq. No. 226894

Seq. ID LIB3189-012-P1-K1-G1

Method BLASTX
NCBI GI g2507455
BLAST score 435
E value 4.0e-43
Match length 102
% identity 86

NCBI Description FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE

SYNTHETASE) (FHS) (FTHFS) >gi 322401 pir A43350

formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi\_170145 (M83940) 10-formyltetrahydrofolate synthetase

[Spinacia oleracea]

Seq. No. 226895

Seq. ID LIB3189-012-P1-K1-G11

Method BLASTX
NCBI GI g1915974
BLAST score 631
E value 5.0e-66
Match length 149
% identity 81

NCBI Description (U62329) fructokinase [Lycopersicon esculentum] >qi 2102693

(U64818) fructokinase [Lycopersicon esculentum]

Seq. No. 226896

Seq. ID LIB3189-012-P1-K1-G2

Method BLASTX
NCBI GI g2662343
BLAST score 614
E value 5.0e-64
Match length 122
% identity 97

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 226897



```
LIB3189-012-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g130720
BLAST score
                  279
                  9.0e-25
E value
Match length
                  126
% identity
                  44
NCBI Description PROTEOLIPID PROTEIN PPA1 >gi 101508 pir A34633 probable
                  H+-transporting ATPase (EC 3.6.1.35) lipid-binding protein
                  - yeast (Saccharomyces cerevisiae) >gi 172221 (M35294)
                  proteolipid protein of proton ATPase [Saccharomyces
                  cerevisiae] >gi 500700 (U10399) Ppalp: Proteolipid protein
                  of proton ATPase [Saccharomyces cerevisiae]
                  226898
Seq. No.
Seq. ID
                  LIB3189-012-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q2583123
BLAST score
                  423
E value
                  2.0e-42
Match length
                  128
% identity
                  80
NCBI Description (AC002387) putative nucleotide sugar epimerase [Arabidopsis
                  thaliana]
                  226899
Seq. No.
                  LIB3189-012-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829204
BLAST score
                  369
                  2.0e-35
E value
Match length
                  70
                  99
% identity
NCBI Description (AF044204) lipid transfer protein precursor [Gossypium
                  hirsutum]
Seq. No.
                  226900
Seq. ID
                  LIB3189-012-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g2500443
BLAST score
                  159
E value
                  7.0e-11
Match length
                  32
                  100
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S14 >gi 1762931 (U66262) ribosomal
                  protein S14 [Nicotiana tabacum]
Seq. No.
                  226901
Seq. ID
                  LIB3189-012-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  a3080402
BLAST score
                  262
```

Method BLASTX
NCBI GI g3080402
BLAST score 262
E value 3.0e-23
Match length 76
% identity 71

NCBI Description (AL022603) putative NADPH quinone oxidoreductase [Arabidopsis thaliana] >gi 4455266 emb CAB36802.1



(AL035527) putative NADPH quinone oxidoreductase [Arabidopsis thaliana]

226902 Seq. No. LIB3189-012-P1-K1-H5 Seq. ID Method BLASTX NCBI GI q3860259 BLAST score 190 E value 2.0e-14 90 Match length % identity 49 NCBI Description (AC005824) unknown protein [Arabidopsis thaliana] Seq. No. 226903 LIB3189-012-P1-K1-H6 Seq. ID Method BLASTX NCBI GI g1402833 BLAST score 166 E value 4.0e-12 Match length 41 % identity 83 NCBI Description (U60147) plasma membrane major intrinsic protein 1 [Beta vulgaris] 226904 Seq. No. Seq. ID LIB3189-012-P1-K1-H7 Method BLASTX NCBI GI g4191255 BLAST score 385 E value 2.0e-37 81 Match length % identity 89 NCBI Description (AJ132323) chalcone synthase [Casuarina glauca] 226905 Seq. No. Seq. ID LIB3189-012-P1-K1-H8 Method BLASTX NCBI GI q2267567 BLAST score 419 2.0e-41E value 92 Match length % identity 87 NCBI Description (AF009003) glycine-rich RNA binding protein 1 [Pelargonium x hortorum] >gi 2267569 (AF009004) glycine-rich RNA binding protein 2 [Pelargonium x hortorum] Seq. No. 226906 Seq. ID LIB3189-013-P1-K1-A1 Method BLASTX NCBI GI q2130017 BLAST score 391 E value 7.0e-38

Match length 122 % identity 58

NCBI Description hypothetical protein - common sunflower

>gi\_1040729 emb CAA60621 (X87143) cytochrome b5 containing

fusion protein [Helianthus annuus]



```
Seq. No.
                  226907
                  LIB3189-013-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1280611
BLAST score
                  468
                  6.0e-47
E value
Match length
                  129
                  64
% identity
                  (U53860) steroid reductase DET2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  226908
                  LIB3189-013-P1-K1-A6
Seq. ID
                  BLASTX
Method
                  q2924520
NCBI GI
                  503
BLAST score
                   4.0e-51
E value
                  108
Match length
% identity
                   91
                  (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                   [Arabidopsis thaliana]
                   226909
Seq. No.
Seq. ID
                  LIB3189-013-P1-K1-A7
                  BLASTX
Method
                   q1694976
NCBI GI
                   170
BLAST score
                   2.0e-12
E value
Match length
                   61
% identity
NCBI Description
                  (Y09482) HMG1 [Arabidopsis thaliana]
                   >qi 2832361 emb CAA74402 (Y14073) HMG protein [Arabidopsis
                   thaliana]
                   226910
Seq. No.
                   LIB3189-013-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2065531
BLAST score
                   478
E value
                   2.0e-48
Match length
                   93
% identity
                   89
                  (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
NCBI Description
                   226911
Seq. No.
                   LIB3189-013-P1-K1-A9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2129921
BLAST score
                   194
                   8.0e-15
E value
                   51
Match length
                   75
% identity
                   hypothetical protein 1 - Madagascar periwinkle >gi_758694
NCBI Description
                   (U12573) putative [Catharanthus roseus]
```

32371

226912

LIB3189-013-P1-K1-B1

Seq. No.

Seq. ID



```
Method
                  BLASTX
                  g4455800
NCBI GI
BLAST score
                  190
                  2.0e-14
E value
Match length
                  65
                  51
% identity
NCBI Description (Z97343) unnamed protein product [Arabidopsis thaliana]
Seq. No.
                  226913
                  LIB3189-013-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1174600
BLAST score
                  658
                  3.0e-69
E value
Match length
                  130
                  92
% identity
NCBI Description TUBULIN BETA CHAIN >gi_493710_dbj_BAA06382 (D30717)
                  beta-tubulin [Oryza sativa]
Seq. No.
                  226914
                  LIB3189-013-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982322
BLAST score
                  711
                  2.0e-75
E value
Match length
                  149
                  89
% identity
NCBI Description (AF051246) probable proteasome subunit [Picea mariana]
                  226915
Seq. No.
                  LIB3189-013-P1-K1-B3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1703375
BLAST score
                  288
                   4.0e-26
E value
Match length
                  64
                   94
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 965483 dbj BAA08259_ (D45420)
                  DcARF1 [Daucus carota]
                  226916
Seq. No.
Seq. ID
                  LIB3189-013-P1-K1-B4
Method
                  BLASTX
                  g4006867
NCBI GI
BLAST score
                   153
E value
                   2.0e-10
Match length
                  55
% identity
                   62
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
Seq. No.
                   226917
                  LIB3189-013-P1-K1-B5
Seq. ID
```

Method BLASTX NCBI GI g1175016 BLAST score 176 2.0e-13 E value Match length 63



```
% identity
                   48
                  WHITE PROTEIN HOMOLOG >gi 1160186 emb CAA62631 (X91249)
NCBI Description
                  white [Homo sapiens]
                  226918
Seq. No.
                  LIB3189-013-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g951427
BLAST score
                  287
                  8.0e-26
E value
Match length
                  99
% identity
                  60
                  (M59857) stearoyl-acyl-carrier protein desaturase [Ricinus
NCBI Description
                  communis]
Seq. No.
                  226919
                  LIB3189-013-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1545805
BLAST score
                  235
E value
                  1.0e-19
Match length
                  93
                  54
% identity
NCBI Description (D64052) cytochrome P450 like TBP [Nicotiana tabacum]
Seq. No.
                  226920
Seq. ID
                  LIB3189-013-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g2811278
BLAST score
                  243
                  5.0e-21
E value
Match length
                  63
                  76
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                  226921
                  LIB3189-013-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g218157
BLAST score
                  608
E value
                  2.0e-63
Match length
                  133
                  90
% identity
NCBI Description (D13512) cytoplasmic aldolase [Oryza sativa]
                  226922
Seq. No.
                  LIB3189-013-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q730583
BLAST score
                  275
E value
                   2.0e-24
Match length
                  76
% identity
                  75
NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P2 >qi 551267 emb CAA55047
```

argentatum]

(X78213) 60s acidic ribosomal protein P2 [Parthenium



```
Seq. No.
                  226923
                  LIB3189-013-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3915031
BLAST score
                  759
                  5.0e-81
E value
Match length
                  145
% identity
                  99
NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
                  (STEAROYL-ACP DESATURASE) >gi 1217628 emb CAA65232
                   (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase
                   [Gossypium hirsutum]
                  226924
Seq. No.
Seq. ID
                  LIB3189-013-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q4454014
BLAST score
                  259
E value
                  2.0e-22
Match length
                  123
% identity
                  44
NCBI Description (AL035396) putative protein [Arabidopsis thaliana]
Seq. No.
                  226925
                  LIB3189-013-P1-K1-E1
Seq. ID
Method
                  BLASTX
                  q3702327
NCBI GI
BLAST score
                  290
E value
                  5.0e-26
Match length
                  96
% identity
                  62
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                  226926
Seq. No.
                  LIB3189-013-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1703375
BLAST score
                  488
E value
                  2.0e-49
Match length
                  96
                  99
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 965483 dbj BAA08259 (D45420)
                  DcARF1 [Daucus carota]
Seq. No.
                  226927
                  LIB3189-013-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2497543
BLAST score
                  500
E value
                  1.0e-50
Match length
                  122
% identity
                  83
```

Seq. No. 226928

(Z29492) pyruvate kinase [Nicotiana tabacum]

pyruvate kinase - common tobacco >qi 444023 emb CAA82628

NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 542061 pir S41379



LIB3189-013-P1-K1-E8

Seq. ID

```
Method
                  BLASTX
                  g730583
NCBI GI
BLAST score
                  219
E value
                  4.0e-18
                  56
Match length
                  79
% identity
NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P2 >gi_551267 emb CAA55047
                  (X78213) 60s acidic ribosomal protein P2 [Parthenium
                  argentatum]
                  226929
Seq. No.
                  LIB3189-013-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1362086
BLAST score
                  150
E value
                  4.0e-10
Match length
                  29
                  97
% identity
NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_2129919_pir__S65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 886471_emb_CAA58474_ (X83499) methionine synthase
                  [Catharanthus roseus]
                  226930
Seq. No.
Seq. ID
                  LIB3189-013-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g3785983
BLAST score
                  247
E value
                  3.0e-21
Match length
% identity
NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  226931
Seq. ID
                  LIB3189-013-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g1703375
BLAST score
                  680
E value
                  9.0e-72
Match length
                  134
% identity
                  99
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483 dbj BAA08259 (D45420)
                  DcARF1 [Daucus carota]
Seq. No.
                  226932
Seq. ID
                  LIB3189-013-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g3879754
BLAST score
                  218
E value
                  1.0e-17
Match length
                  107
                  42
% identity
```

NCBI Description (Z72514) Similarity to Rabbit glycogenin (SW:GLYG RABIT)



## [Caenorhabditis elegans]

```
Seq. No.
                  226933
                  LIB3189-013-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2369714
BLAST score
                  295
                   9.0e-27
E value
Match length
                  111
% identity
                  (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
Seq. No.
                   226934
                  LIB3189-013-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2267567 '
BLAST score
                   273
E value
                   1.0e-24
Match length
                  73
% identity
                   74
                   (AF009003) glycine-rich RNA binding protein 1 [Pelargonium
NCBI Description
                  x hortorum] >gi 2267569 (AF009004) glycine-rich RNA binding
                  protein 2 [Pelargonium x hortorum]
                   226935
Seq. No.
                  LIB3189-013-P1-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4193382
BLAST score
                   379
                   2.0e-36
E value
Match length
                   85
                   82
% identity
                   (AF083336) ribosomal protein S27 [Arabidopsis thaliana]
NCBI Description
                   >gi 4193384 (AF083337) ribosomal protein S27 [Arabidopsis
                   thaliana]
                   226936
Seq. No.
Seq. ID
                   LIB3189-013-P1-K1-G4
                   BLASTX
Method
NCBI GI
                   q4115377
BLAST score
                   428
                   3.0e-42
E value
Match length
                   122
% identity
                   72
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
                   226937
Seq. No.
Seq. ID
                   LIB3189-013-P1-K1-G5
Method
                   BLASTX
                   g862640
NCBI GI
                   398
BLAST score
                   8.0e-39
E value
Match length
                   92
% identity
                   85
                   (U20182) MADS-box protein AGL11 [Arabidopsis thaliana]
NCBI Description
```

AGL11 [Arabidopsis thaliana]

>gi\_4538999\_emb\_CAB39620.1\_ (AL049481) MADS-box protein



```
226938
Seq. No.
Seq. ID
                  LIB3189-013-P1-K1-G9
                  BLASTX
Method
                  q3880625
NCBI GI
BLAST score
                  158
E value
                  8.0e-11
Match length
                  60
                  50
% identity
                  (Z93785) predicted using Genefinder; similar to RNA
NCBI Description
                  recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST
                  EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823
                  comes from this gene; cDNA EST EMBL: D27559 comes from this
                  ge
                  226939
Seq. No.
Seq. ID
                  LIB3189-013-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  q1362086
BLAST score
                  330
                  5.0e-31
E value
Match length
                  78
% identity
                  85
NCBI Description
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919 pir S65957
                   5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 886471 emb CAA58474 (X83499) methionine synthase
                   [Catharanthus roseus]
                  226940
Seq. No.
Seq. ID
                  LIB3189-014-P1-K1-A1
Method
                  BLASTX
NCBI GI
                   g4512671
                  297
BLAST score
                   4.0e-27
E value
                  84
Match length
% identity
                   68
                  (AC006931) unknown protein [Arabidopsis thaliana]
NCBI Description
                  226941
Seq. No.
Seq. ID
                  LIB3189-014-P1-K1-A11
                  BLASTX
Method
NCBI GI
                  g2492953
BLAST score
                  147
E value
                   7.0e-10
Match length
                   66
                   52
% identity
                  CHORISMATE SYNTHASE 2 PRECURSOR
NCBI Description
                   (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 2)
```

>gi\_542027\_pir\_\_S40409 chorismate synthase (EC 4.6.1.4) 2 precursor - tomato >gi\_410484\_emb\_CAA79854\_ (Z21791)

chorismate synthase 2 [Lycopersicon esculentum]

Seq. No. 226942

Seq. ID LIB3189-014-P1-K1-A12

Seq. ID

Method

NCBI GI



```
Method
                  BLASTX
NCBI GI
                  q2506139
BLAST score
                   452
E value
                   5.0e-45
Match length
                  106
% identity
                  85
NCBI Description
                  COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
                   (ARCHAIN) >gi 1314049 emb CAA91901 (Z67962)
                  archain/delta-COP [Oryza sativa]
                  226943
Seq. No.
Seq. ID
                  LIB3189-014-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g3075398
BLAST score
                  354
E value
                  1.0e-33
Match length
                  114
% identity
                  56
NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]
                  226944
Seq. No.
                  LIB3189-014-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2119719
BLAST score
                  250
                  5.0e-22
E value
Match length
                  56
% identity
                  89
NCBI Description
                  heat-shock cognate protein 70-3 - tomato >gi 762844
                  (L41253) Hsc70 [Lycopersicon esculentum]
Seq. No.
                  226945
Seq. ID
                  LIB3189-014-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g3901014
BLAST score
                  235
E value
                  1.0e-19
Match length
                  55
% identity
                  76
NCBI Description
                  (AJ130886) metallothionein-like protein class II [Fagus
                  sylvatica]
Seq. No.
                  226946
Seq. ID
                  LIB3189-014-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g543905
BLAST score
                  778
E value
                  3.0e-83
Match length
                  146
% identity
NCBI Description
                  BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi 347459 (L22162)
                  brassinosteroid-regulated protein [Glycine max]
                  226947
Seq. No.
```

32378

LIB3189-014-P1-K1-B1

BLASTX

g4567203



261 1.0e-22

BLAST score

E value

```
Match length
                  52
                   94
% identity
                  (AC007168) putative beta-hydroxyacyl-ACP dehydratase
NCBI Description
                   [Arabidopsis thaliana]
                  226948
Seq. No.
                  LIB3189-014-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4467157
BLAST score
                  346
                   1.0e-32
E value
Match length
                  113
% identity
                   60
NCBI Description
                  (AL035540) disease resistance response like protein
                   [Arabidopsis thaliana]
                   226949
Seq. No.
                  LIB3189-014-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2959767
BLAST score
                   398
                   5.0e-39
E value
                   101
Match length
% identity
                   50
                  (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi 3738292
NCBI Description
                   (AC005309) glutathione-conjugate transporter AtMRP4
                   [Arabidopsis thaliana]
                   226950
Seq. No.
                  LIB3189-014-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2832664
BLAST score
                  183
                   1.0e-13
E value
Match length
                   91
% identity
                   42
NCBI Description
                  (AL021710) pollen-specific protein - like [Arabidopsis
                   thaliana]
                   226951
Seq. No.
Seq. ID
                  LIB3189-014-P1-K1-B9
Method
                   BLASTX
                   g3980380
NCBI GI
BLAST score
                  200
E value
                   1.0e-15
Match length
                   44
                   91
% identity
NCBI Description (AC004561) putative enolase [Arabidopsis thaliana]
Seq. No.
                   226952
Seq. ID
                  LIB3189-014-P1-K1-C11
Method
                  BLASTX
NCBI GI
                   g2213628
BLAST score
                  136
E value
                   1.0e-09
```



```
Match length
                  109
% identity
                   45
NCBI Description (AC000103) F21J9.20 [Arabidopsis thaliana]
                  226953
Seq. No.
                  LIB3189-014-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3738320
BLAST score
                  201
                  1.0e-15
E value
Match length
                  115
% identity
                  40
                  (AC005170) putative cinnamoyl CoA reductase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  226954
Seq. ID
                  LIB3189-014-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g1703375
BLAST score
                  332
E value
                  2.0e-33
Match length
                  89
% identity
                  91
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 965483 dbj BAA08259 (D45420)
                  DcARF1 [Daucus carota]
Seq. No.
                  226955
Seq. ID
                  LIB3189-014-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g3175990
BLAST score
                  270
E value
                  5.0e-24
Match length
                  59
                  90
% identity
NCBI Description (AJ005836) GDP dissociation inhibitor [Cicer arietinum]
                  226956
Seq. No.
Seq. ID
                  LIB3189-014-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g121631
BLAST score
                  305
E value
                  7.0e-28
Match length
                  97
% identity
                  62
NCBI Description GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR
                  >gi_72323 pir KNNT2S glycine-rich protein 2 - wood tobacco
                  >gi 19743 emb_CAA42622_ (X60007) nsGRP-2 [Nicotiana
                  sylvestris]
Seq. No.
                  226957
Seq. ID
                  LIB3189-014-P1-K1-D2
Method
                  BLASTX
```

NCBI GI g3025205
BLAST score 177
E value 5.0e-13
Match length 73
% identity 51



NCBI Description HYPOTHETICAL 65.1 KD PROTEIN SLR1919

>gi\_1652223\_dbj\_BAA17147\_ (D90903) ABC1-like [Synechocystis

sp.]

Seq. No. 226958

Seq. ID LIB3189-014-P1-K1-D5

Method BLASTX
NCBI GI g2815493
BLAST score 316
E value 4.0e-29
Match length 80
% identity 70

NCBI Description SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)

(CP-MI) >gi 1731988 emb CAA70816 (Y09603) serine

carboxypeptidase I, CP-MI [Hordeum vulgare]

Seq. No. 226959

Seq. ID LIB3189-014-P1-K1-E1

Method BLASTX
NCBI GI g1928981
BLAST score 526
E value 8.0e-54
Match length 112
% identity 93

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

Seq. No. 226960

Seq. ID LIB3189-014-P1-K1-E12

Method BLASTX
NCBI GI g1888357
BLAST score 443
E value 5.0e-44
Match length 146
% identity 59

NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]

>gi 1890154 emb CAA72432 (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

Seq. No. 226961

Seq. ID LIB3189-014-P1-K1-E6

Method BLASTX
NCBI GI g1888357
BLAST score 151
E value 6.0e-10
Match length 58
% identity 47

NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]

>gi\_1890154\_emb\_CAA72432\_ (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

Seq. No. 226962

Seq. ID LIB3189-014-P1-K1-E8

Method BLASTX
NCBI GI g2935298
BLAST score 288
E value 5.0e-26

32381



```
Match length
                  79
% identity
                  70
                  (AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase
NCBI Description
                  1 [Gossypium hirsutum]
                  226963
Seq. No.
                  LIB3189-014-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  a2662341
BLAST score
                  647
                  5.0e-68
E value
                  128
Match length
% identity
                  95
NCBI Description (D63580) EF-1 alpha [Oryza sativa]
                  >gi 2662345 dbj BAA23659 (D63582) EF-1 alpha [Oryza
                  satīva] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha
                  [Oryza sativa]
Seq. No.
                  226964
                  LIB3189-014-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4105696
                  577
BLAST score
E value
                  1.0e-59
Match length
                  113
% identity
NCBI Description (AF049870) beta tubulin 1 [Arabidopsis thaliana]
Seq. No.
                  226965
Seq. ID
                  LIB3189-014-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q3776082
BLAST score
                  244
E value
                  1.0e-20
Match length
                  66
% identity
                  71
NCBI Description (Y18250) MtN30 [Medicago truncatula]
Seq. No.
                  226966
                  LIB3189-014-P1-K1-F8
Seq. ID
Method
                  BLASTX
                  g3860258
NCBI GI
BLAST score
                  283
E value
                  2.0e-25
                  90
Match length
                  60
% identity
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.
                  226967
                  LIB3189-014-P1-K1-G10
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g1843527
BLAST score 443
E value 4.0e-44
Match length 115
% identity 77

NCBI Description (U73747) annexin [Gossypium hirsutum]

Match length

% identity

139 52



```
226968
Seq. No.
Seq. ID
                  LIB3189-014-P1-K1-G11
                  BLASTX
Method
NCBI GI
                  g1085384
BLAST score
                  318
E value
                  2.0e-29
Match length
                  74
                  74
% identity
NCBI Description Sm protein F - human >gi 806564 emb CAA59688 (X85372) Sm
                  protein F [Homo sapiens]
                  >gi_4507131_ref_NP_003086.1_pSNRPF_ small nuclear
                  ribonucleoprotein polypeptide F
                  226969
Seq. No.
Seq. ID
                  LIB3189-014-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g2494162
BLAST score
                  316
                  4.0e-29
E value
Match length
                  141
                  44
% identity
                  HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II
NCBI Description
                  PRECURSOR >gi 3879803 emb CAA87414 (Z47356) similar to
                  DNAJ [Caenorhabditis elegans]
                  226970
Seq. No.
                  LIB3189-014-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3915826
BLAST score
                  506
                  2.0e-51
E value
Match length
                  116
% identity
                  82
NCBI Description 60S RIBOSOMAL PROTEIN L5
Seq. No.
                  226971
Seq. ID
                  LIB3189-014-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g416758
BLAST score
                  254
                  7.0e-22
E value
Match length
                  95
% identity
                  54
NCBI Description SERINE CARBOXYPEPTIDASE PRECURSOR >qi 166674 (M81130)
                  carboxypeptidase Y-like protein [Arabidopsis thaliana]
                  >gi 445120 prf 1908426A carboxypeptidase Y [Arabidopsis
                  thaliana]
                  226972
Seq. No.
Seq. ID
                  LIB3189-014-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g3721926
BLAST score
                  278
E value
                  2.0e-30
```

32383



NCBI Description (AB017480) chloroplast FtsH protease [Nicotiana tabacum]
Seq. No. 226973
Seq. ID LIB3189-014-P1-K1-H10

Method BLASTX
NCBI GI g266972
BLAST score 196
E value 3.0e-15
Match length 54
% identity 63

NCBI Description 40S RIBOSOMAL PROTEIN S29 >gi\_631884\_pir\_\_S30298 ribosomal protein S29 - rat >gi 1362934 pir S55919 ribosomal protein

S29 - human >gi\_57133\_emb\_CAA41778 (X59051) ribosomal

protein S29 [Rattus norvegicus] >gi\_550027 (U14973)

ribosomal protein S29 [Homo sapiens] >gi\_1220361 (L31610) homologous to antisense sequence of krev-1, anti oncogene [Homo sapiens] >gi\_1220418 (L31609) S29 ribosomal protein [Mus musculus] >gi\_1513230 (U66372) ribosomal protein S29 [Bos taurus] >gi\_1096945 prf\_2113200H ribosomal protein S29 [Homo sapiens] >gi\_4506717 ref\_NP\_001023.1\_pRPS29\_

ribosomal protein S29

Seq. No. 226974

Seq. ID LIB3189-014-P1-K1-H4

Method BLASTX
NCBI GI g2494162
BLAST score 179
E value 3.0e-13
Match length 105
% identity 34

NCBI Description HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II

PRECURSOR >gi\_3879803\_emb\_CAA87414\_ (Z47356) similar to

DNAJ [Caenorhabditis elegans]

Seq. No. 226975

Seq. ID LIB3189-014-P1-K1-H6

Method BLASTX
NCBI GI g464985
BLAST score 313
E value 2.0e-29
Match length 67
% identity 90

% identity 90

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN

LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A)

>gi 398699 emb CAA78713 (Z14989) ubiquitin conjugating

enzyme homolog [Arabidopsis thaliana]

Seq. No. 226976

Seq. ID LIB3189-014-P1-K1-H8

Method BLASTX
NCBI GI g2511590
BLAST score 377
E value 2.0e-36
Match length 102
% identity 75

NCBI Description (Y13692) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana] >qi 3421111



(AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis thaliana]

 Seq. No.
 226977

 Seq. ID
 LIB3189-014-P1-K1-H9

 Method
 BLASTX

 NCBI GI
 g2369766

BLAST score 403 E value 2.0e-39 Match length 107 % identity 70

NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No. 226978

Seq. ID LIB3189-015-P1-K1-A3

Method BLASTX
NCBI GI g218157
BLAST score 198
E value 2.0e-15
Match length 56
% identity 73

NCBI Description (D13512) cytoplasmic aldolase [Oryza sativa]

Seq. No. 226979

Seq. ID LIB3189-015-P1-K1-A4

Method BLASTX
NCBI GI g1117780
BLAST score 362
E value 1.0e-34
Match length 106
% identity 68

NCBI Description (D49367) 4-coumarate:CoA ligase [Lithospermum

erythrorhizon]

Seq. No. 226980

Seq. ID LIB3189-015-P1-K1-A5

Method BLASTX
NCBI GI g1669601
BLAST score 414
E value 8.0e-41
Match length 93
% identity 81

NCBI Description (D88747) AR401 [Arabidopsis thaliana]

Seq. No. 226981

Seq. ID LIB3189-015-P1-K1-B11

Method BLASTX
NCBI GI g1881378
BLAST score 478
E value 3.0e-48
Match length 106
% identity 90

NCBI Description (AB001582) QM family protein [Solanum melongena]

Seq. No. 226982

Seq. ID LIB3189-015-P1-K1-B2

Method BLASTX



```
NCBI GI
                  g3023187
BLAST score
                  359
                  1.0e-34
E value
Match length
                  83
% identity
                  87
                  14-3-3-LIKE PROTEIN (G-BOX BINDING FACTOR) >gi 1773328
NCBI Description
                  (U80070) 14-3-3-like protein [Mesembryanthemum
                  crystallinum]
                  226983
Seq. No.
                  LIB3189-015-P1-K1-B3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2499489
BLAST score
                  154
                  9.0e-11
E value
                  53
Match length
                  62
% identity
NCBI Description
                  PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
                  BETA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                  (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                  (PPI-PFK) >qi 483536 emb CAA83683 (Z32850)
                  pyrophosphate-dependent phosphofructokinase beta subunit
                  [Ricinus communis]
                  226984
Seq. No.
                  LIB3189-015-P1-K1-B5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2129559
BLAST score
                  452
E value
                  3.0e-45
Match length
                  107
                  80
% identity
                  cellulase homolog OR16pep - Arabidopsis thaliana
NCBI Description
                  >qi 1022807 (U37702) cellulase [Arabidopsis thaliana]
                  >gi 3493633 (AF074092) cellulase [Arabidopsis thaliana]
                  >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana]
                  >gi 3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN
                  [Arabidopsis thaliana]
Seq. No.
                  226985
Seq. ID
                  LIB3189-015-P1-K1-B6
                  BLASTX
Method
NCBI GI
                  q3023187
BLAST score
                  196
                  3.0e-15
E value
                  69
Match length
                  65
% identity
                  14-3-3-LIKE PROTEIN (G-BOX BINDING FACTOR) >gi 1773328
NCBI Description
                  (U80070) 14-3-3-like protein [Mesembryanthemum
```

crystallinum]

226986 Seq. No.

LIB3189-015-P1-K1-B7 Seq. ID

Method BLASTX g2262173 NCBI GI 238 BLAST score E value 3.0e-20



```
Match length
                   73
% identity
NCBI Description
                  (AC002329) NADPH thioredoxin reductase [Arabidopsis
                  thaliana]
                  226987
Seq. No.
                  LIB3189-015-P1-K1-C1
Seq. ID
Method
                  BLASTX
                  q3080414
NCBI GI
                  244
BLAST score
                  1.0e-27
E value
                  74
Match length
                  72
% identity
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
                  226988
Seq. No.
Seq. ID
                  LIB3189-015-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  q2642158
                  472
BLAST score
E value
                  1.0e-47
                  110
Match length
                  77
% identity
NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]
                  226989
Seq. No.
                  LIB3189-015-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1657948
BLAST score
                   243
                   8.0e-30
E value
                   98
Match length
                   71
% identity
NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
                   226990
Seq. No.
Seq. ID
                  LIB3189-015-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   g1518540
BLAST score
                   225
E value
                   2.0e-26
Match length
                  73
% identity
                   88
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
Seq. No.
                   226991
                  LIB3189-015-P1-K1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2500354
BLAST score
                   589
                   5.0e-65
E value
Match length
                  135
                   90
% identity
```

Seq. No. 226992

(AB001891) QM family protein [Solanum melongena]

NCBI Description 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462



```
LIB3189-015-P1-K1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2245021
BLAST score
                  325
                  1.0e-35
E value
Match length
                  120
                  68
% identity
NCBI Description (Z97341) heat shock protein 110 homolog [Arabidopsis
                  thaliana]
                  226993
Seq. No.
                  LIB3189-015-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2497753
BLAST score
                  196
                  4.0e-15
E value
                  50
Match length
                  64
% identity
NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
                  >gi_1321915 emb CAA65477 (X96716) lipid transfer protein
                  [Prunus dulcis]
Seq. No.
                  226994
Seq. ID
                  LIB3189-015-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q586004
                  276
BLAST score
                  1.0e-24
E value
Match length
                  64
                  84
% identity
NCBI Description SUPEROXIDE DISMUTASE [CU-ZN] >gi_421962_pir_ S34267
                  superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato
                  >gi 542090 pir S40404 superoxide dismutase (EC 1.15.1.1)
                  (Cu-Zn) - sweet potato >gi 311971 emb CAA51654 (X73139)
                  superoxide dismutase [Ipomoea batatas]
Seq. No.
                  226995
                  LIB3189-015-P1-K1-D4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1771162
BLAST score
                  159
E value
                  1.0e-20
Match length
                  115
                  49
% identity
NCBI Description (X98930) SBT2 [Lycopersicon esculentum]
                  >gi 3687307 emb CAA07000 (AJ006379) subtilisin-like
                  protease [Lycopersicon esculentum]
Seq. No.
                  226996
Seq. ID
                  LIB3189-015-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g710626
BLAST score
                  287
E value
                  8.0e-26
Match length
                  86
% identity
                  65
NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi 3241941
```



(AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi\_3894181 (AC005662) ERD15 protein [Arabidopsis thaliana]

```
Seq. No.
               ~ 226997
                  LIB3189-015-P1-K1-D6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4567283
                  160
BLAST score
                  3.0e-11
E value
                  80
Match length
                  49
% identity
NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]
                  226998
Seq. No.
Seq. ID
                  LIB3189-015-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q3860274
BLAST score
                  196
E value
                  3.0e-15
                  53
Match length
                  68
% identity
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4314397 gb AAD15607 (AC006232) putative zinc finger
                  protein [Arabidopsis thaliana]
Seq. No.
                  226999
                  LIB3189-015-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q508304
BLAST score
                  152
                  4.0e-10
E value
                  38
Match length
                  79
% identity
NCBI Description (L22305) corC [Medicago sativa]
                  227000
Seq. No.
                  LIB3189-015-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3819164
BLAST score
                  183
                  9.0e-14
E value
                  57
Match length
% identity
                  68
                  (AJ012318) cytosolic chaperonin, delta-subunit [Glycine
NCBI Description
                  max]
                  227001
Seq. No.
                  LIB3189-015-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2961346
BLAST score
                  382
                  4.0e-37
E value
Match length
                  104
% identity
                   64
                  (AL022140) pectinesterase like protein [Arabidopsis
NCBI Description
```

thaliana]

NCBI Description



```
Seq. No.
                  227002
Seq. ID
                  LIB3189-015-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g1351303
BLAST score
                  312
                  7.0e-29
E value
                  103
Match length
                  65
% identity
NCBI Description
                  INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE PRECURSOR (IGPS)
                  >gi 619732 (U18770) indole-3-glycerol phosphate synthase
                   [Arabidopsis thaliana]
                  227003
Seq. No.
Seq. ID
                  LIB3189-015-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g1771162
BLAST score
                  341
E value
                  5.0e-32
Match length
                  131
% identity
                  53
                  (X98930) SBT2 [Lycopersicon esculentum]
NCBI Description
                  >gi_3687307_emb_CAA07000 (AJ006379) subtilisin-like
                  protease [Lycopersicon esculentum]
Seq. No.
                  227004
Seq. ID
                  LIB3189-015-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g3063637
BLAST score
                  203
                  7.0e-16
E value
                  58
Match length
% identity
NCBI Description (AF056204) thioesterase homolog [Gossypium hirsutum]
Seq. No.
                  227005
Seq. ID
                  LIB3189-015-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g1703375
BLAST score
                  252
E value
                  5.0e-22
                  52
Match length
                  98
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 1 >qi 965483 dbj BAA08259 (D45420)
                  DcARF1 [Daucus carota]
Seq. No.
                  227006
Seq. ID
                  LIB3189-015-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g3834310
BLAST score
                  290
E value
                  3.0e-26
Match length
                  81
% identity
                  60
```

(AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb\_D83004 from Homo sapiens. ESTs gb\_T88233, gb\_Z24464, gb\_N37265, gb\_H36151, gb\_Z34711, gb\_AA040983, and gb\_T22122





## come from this gene. [Arabidopsis thaliana]

```
227007
Seq. No.
Seq. ID
                  LIB3189-015-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g3493172
BLAST score
                  256
E value
                  2.0e-31
                  85
Match length
% identity
                  89
NCBI Description (U89609) fiber annexin [Gossypium hirsutum]
Seq. No.
                  227008
                  LIB3189-015-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462748
BLAST score
                  442
E value
                  6.0e-44
Match length
                  94
% identity
                  91
                  (AC002292) putative Clathrin Coat Assembly protein
NCBI Description
                  [Arabidopsis thaliana]
                  227009
Seq. No.
                  LIB3189-015-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173055
BLAST score
                  611
E value
                  9.0e-66
Match length
                  153
                  89
% identity
                  60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__$42497
NCBI Description
                  ribosomal protein L11.e - alfalfa >gi_1076504 pir_ S51819
                  RL5 ribosomal protein - alfalfa >gi 463252 emb CAA55090
                  (X78284) RL5 ribosomal protein [Medicago sativa]
Seq. No.
                  227010
Seq. ID
                  LIB3189-015-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g4337025
BLAST score
                  372
E value
                  7.0e-36
Match length
                  106
% identity
                  68
NCBI Description (AF123253) AIM1 protein [Arabidopsis thaliana]
Seq. No.
                  227011
                  LIB3189-015-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2062167
BLAST score
                  386
                  2.0e-37
E value
Match length
                  79
                  89
% identity
NCBI Description
                  (AC001645) Proline-rich protein APG isolog [Arabidopsis
```

thaliana]



```
227012
Seq. No.
Seq. ID
                  LIB3189-015-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g2149380
BLAST score
                  518
E value
                  7.0e-53
                  139
Match length
                  76
% identity
NCBI Description (U85036) syntaxin homolog [Arabidopsis thaliana]
                  227013
Seq. No.
Seq. ID
                  LIB3189-015-P1-K1-H3
                  BLASTX
Method
                  g4558665
NCBI GI
                  556
BLAST score
                  3.0e-57
E value
                  143
Match length
                  81
% identity
NCBI Description (AC007063) putative white protein [Arabidopsis thaliana]
                  227014
Seq. No.
                  LIB3189-015-P1-K1-H5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2500517
BLAST score
                  151
                  3.0e-11
E value
                  53
Match length
                  61
% identity
NCBI Description EUKARYOTIC INITIATION FACTOR 4A-9 (EIF-4A-9)
                  >gi_485951_emb_CAA55736_ (X79135) NeIF-4A9 [Nicotiana
                  tabacum]
                  227015
Seq. No.
                  LIB3189-015-P1-K1-H7
Seq. ID
Method
                  BLASTX
                  q3269284
NCBI GI
BLAST score
                  334
                  3.0e-31
E value
                  88
Match length
% identity
                  77
NCBI Description (AL030978) histone H2A- like protein [Arabidopsis thaliana]
                  227016
Seq. No.
                  LIB3189-016-P1-K1-A1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q729623
BLAST score
                  454
                  2.0e-45
E value
Match length
                  106
                  85
% identity
                  78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 5 PRECURSOR (GRP
NCBI Description
                  78-5) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG
                  5) (BIP 5) >gi_100340_pir__S21880 heat shock protein BiP
                  homolog blp5 - common tobacco >gi 19813 emb CAA42660
                   (X60058) luminal binding protein (BiP) [Nicotiana tabacum]
```

227017

Seq. No.

Seq. ID

Method



```
LIB3189-016-P1-K1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2244847
BLAST score
                  304
                  1.0e-27
E value
Match length
                  103
                  57
% identity
NCBI Description (297337) hydroxyproline-rich glycoprotein homolog
                  [Arabidopsis thaliana]
                  227018
Seq. No.
Seq. ID
                  LIB3189-016-P1-K1-A5
                  BLASTX
Method
NCBI GI
                  g2244835
BLAST score
                  212
E value
                  5.0e-17
                  58
Match length
                  74
% identity
NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana]
                  227019
Seq. No.
Seq. ID
                  LIB3189-016-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  q267069
BLAST score
                  524
                  1.0e-53
E value
                  97
Match length
                  98
% identity
NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir JQ1594
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  227020
Seq. No.
Seq. ID
                  LIB3189-016-P1-K1-A8
                  BLASTX
Method
NCBI GI
                  g2541876
BLAST score
                  291
E value
                  4.0e-26
Match length
                  128
% identity
NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein
                  [Nicotiana tabacum]
Seq. No.
                  227021
                  LIB3189-016-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2791834
BLAST score
                  641
E value
                  1.0e-78
Match length
                  149
% identity
                  89
NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta]
Seq. No.
                  227022
```

32393

LIB3189-016-P1-K1-B12

BLASTX



```
q3650032
NCBI GI
BLAST score
                  229
                  7.0e-19
E value
                  49
Match length
                  69
% identity
                  (AC005396) gibberellin-regulated protein GAST1-like
NCBI Description
                  [Arabidopsis thaliana]
                  227023
Seq. No.
Seq. ID
                  LIB3189-016-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q484656
                  451
BLAST score
                  3.0e-45
E value
                  105
Match length
% identity
                  monodehydroascorbate reductase (NADH) (EC 1.6.5.4) -
NCBI Description
                  cucumber >gi_452165_dbj_BAA05408 (D26392)
                  monodehydroascorbate reductase [Cucumis sativus]
                  227024
Seq. No.
                  LIB3189-016-P1-K1-B4
Seq. ID
Method
                  BLASTX
                  g2213595
NCBI GI
                  353
BLAST score
                  1.0e-33
E value
                  113
Match length
% identity
                  63
NCBI Description (ACO00348) T7N9.15 [Arabidopsis thaliana]
                  227025
Seq. No.
                  LIB3189-016-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g542157
BLAST score
                  531
E value
                  2.0e-54
Match length
                  120
% identity
                  82
NCBI Description ribosomal 5S RNA-binding protein - Rice
Seq. No.
                  227026
                  LIB3189-016-P1-K1-B9
Seq. ID
Method
                  BLASTX
                  g267069
NCBI GI
                   635
BLAST score
                  2.0e-66
E value
Match length
                  119
                  98
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                   227027
Seq. No.
                   LIB3189-016-P1-K1-C10
Seq. ID
```

BLASTX

g495725

Method

NCBI GI



```
374
BLAST score
                  2.0e-36
E value
Match length
                  80
% identity
                  86
                 (L25042) acetyl-CoA carboxylase [Medicago sativa]
NCBI Description
                  227028
Seq. No.
                  LIB3189-016-P1-K1-C2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1684851
BLAST score
                  235
                  1.0e-19
E value
Match length
                  83
                  58
% identity
NCBI Description (U77935) DnaJ-like protein [Phaseolus vulgaris]
                  227029
Seq. No.
                  LIB3189-016-P1-K1-C3
Seq. ID
                  BLASTX
Method
                  g3386598
NCBI GI
                  513
BLAST score
```

3.0e-52 E value 146 Match length 69 % identity

NCBI Description (AC004665) putative cytochrome p450 [Arabidopsis thaliana]

227030 Seq. No. Seq. ID LIB3189-016-P1-K1-C5 BLASTX Method NCBI GI q4105772

BLAST score 388 2.0e-37 E value Match length 86 % identity 43

NCBI Description (AF049917) PGP9B [Petunia x hybrida]

227031 Seq. No.

LIB3189-016-P1-K1-C6 Seq. ID

Method BLASTX NCBI GI g2493144 BLAST score 484 9.0e-49 E value Match length 135 55 % identity

NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE

16 KD PROTEOLIPID SUBUNIT) >gi 2118221 pir S60132

H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi 926937 (144585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis

thaliana]

Seq. No. 227032

LIB3189-016-P1-K1-C8 Seq. ID

Method BLASTX NCBI GI g2244736 808 BLAST score E value 9.0e-87

E value

Match length

% identity

7.0e-58

NCBI Description (AF043284) expansin [Gossypium hirsutum]

123 85



```
151
Match length
                  97
% identity
                 (D88415) expansin [Gossypium hirsutum]
NCBI Description
                  227033
Seq. No.
Seq. ID
                  LIB3189-016-P1-K1-C9
Method
                  BLASTX
                  g4050007
NCBI GI
BLAST score
                  153
                  2.0e-14
E value
                  52
Match length
                  61
% identity
                 (AF082027) alpha tubulin [Notothenia coriiceps]
NCBI Description
Seq. No.
                  227034
Seq. ID
                  LIB3189-016-P1-K1-D2
                  BLASTX
Method
                  g3915847
NCBI GI
BLAST score
                  364
                  7.0e-35
E value
                  89
Match length
% identity
                  82
                 40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
NCBI Description
                  40S ribosomal protein S2 [Arabidopsis thaliana]
Seq. No.
                  227035
                  LIB3189-016-P1-K1-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3024526
BLAST score
                  232
E value
                  2.0e-19
                  79
Match length
% identity
                  61
                  RAS-RELATED PROTEIN RAB11 >qi 2118459 pir S59942 small
NCBI Description
                  GTP-binding protein Rabl1 - Arabidopsis thaliana >gi 451860
                  (L18883) small GTP-binding protein [Arabidopsis thaliana]
                  227036
Seq. No.
                  LIB3189-016-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3668089
BLAST score
                  140
E value
                  1.0e-08
Match length
                  59
                  41
% identity
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.
                  227037
                  LIB3189-016-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2811278
BLAST score
                  561
```

32396

% identity

57



```
227038
Seq. No.
Seq. ID
                  LIB3189-016-P1-K1-E12
                  BLASTX
Method
                  g1246823
NCBI GI
                  579
BLAST score
                  6.0e-60
E value
                  125
Match length
                  84
% identity
                  (X89865) unknown [Phoenix dactylifera]
NCBI Description
                  227039
Seq. No.
                  LIB3189-016-P1-K1-E2
Seq. ID
                  BLASTX
Method
                  g232031
NCBI GI
BLAST score
                  220
                  8.0e-18
E value
                   67
Match length
                   60
% identity
                  ELONGATION FACTOR 1 BETA' >gi_322851_pir__$29224
NCBI Description
                   translation elongation factor eEF-1 beta chain - rice
                   >gi 218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'
                   [Oryza sativa]
                   227040
Seq. No.
                   LIB3189-016-P1-K1-E4
Seq. ID
                  BLASTX
Method
                   g3643609
NCBI GI
BLAST score
                   316
                   6.0e-31
E value
                   132
Match length
                   61
% identity
                  (AC005395) putative Cys3His zinc finger protein
NCBI Description
                   [Arabidopsis thaliana]
                   227041
Seq. No.
Seq. ID
                   LIB3189-016-P1-K1-F10
                   BLASTX
Method
NCBI GI
                   g267069
BLAST score
                   712
                   1.0e-75
E value
Match length
                   133
                   98
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >qi 320183 pir JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                   227042
Seq. No.
Seq. ID
                   LIB3189-016-P1-K1-F11
                   BLASTX
Method
NCBI GI
                   q3757520
BLAST score
                   169
                   3.0e-12
E value
Match length
                   65
```

NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

BLAST score

E value

220 2.0e-18



```
227043
Seq. No.
Seq. ID
                  LIB3189-016-P1-K1-F12
                  BLASTX
Method
NCBI GI
                  g3176098
BLAST score
                  450
                  8.0e-45
E value
                  133
Match length
                  39
% identity
NCBI Description
                  (Y15036) annexin [Medicago truncatula]
                  227044
Seq. No.
Seq. ID
                  LIB3189-016-P1-K1-F2
                  BLASTX
Method
                  g2129473
NCBI GI
BLAST score
                  253
                  7.0e-22
E value
                  90
Match length
                  54
% identity
                  arabinogalactan-like protein - loblolly pine >gi 607774
NCBI Description
                   (U09556) arabinogalactan-like protein [Pinus taeda]
Seq. No.
                  227045
Seq. ID
                  LIB3189-016-P1-K1-F6
                  BLASTX
Method
NCBI GI
                  q2811278
BLAST score
                  712
                  2.0e-75
E value
                  144
Match length
                  90
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
                  227046
Seq. No.
                  LIB3189-016-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539371
BLAST score
                  260
E value
                  2.0e-22
Match length
                  94
                  55
% identity
NCBI Description (AL049525) putative protein [Arabidopsis thaliana]
Seq. No.
                  227047
                  LIB3189-016-P1-K1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2804278
BLAST score
                  506
                  2.0e-51
E value
Match length
                  145
                  70
% identity
NCBI Description (AB003516) squalene epoxidase [Panax ginseng]
Seq. No.
                  227048
Seq. ID
                  LIB3189-016-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  q2244749
```

Seq. ID



```
57
Match length
                  75
% identity
NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
                  227049
Seq. No.
                  LIB3189-016-P1-K1-G10
Seq. ID
                  BLASTX
Method
                  g4432845
NCBI GI
                  236
BLAST score
                  1.0e-19
E value
                  107
Match length
                  50
% identity
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
                  227050
Seq. No.
                  LIB3189-016-P1-K1-G12
Seq. ID
                  BLASTX
Method
                  g4539301
NCBI GI
                  275
BLAST score
                  3.0e-24
E value
                  110
Match length
                  47
% identity
                  (AL049480) putative mitochondrial protein [Arabidopsis
NCBI Description
                  thaliana]
                  227051
Seq. No.
                  LIB3189-016-P1-K1-G2
Seq. ID
                  BLASTX
Method
                  q1350680
NCBI GI
                  486
BLAST score
                  5.0e-49
E value
                  142
Match length
                   65
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L1
                   227052
Seq. No.
                  LIB3189-016-P1-K1-G6
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3434986
                   451
BLAST score
                   7.0e-45
E value
                   126
Match length
% identity
NCBI Description (AB016895) Pop3 [Schizosaccharomyces pombe]
                   227053
Seq. No.
                   LIB3189-016-P1-K1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2811278
BLAST score
                   176
                   8.0e-15
E value
Match length
                   44
                   95
 % identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
                   227054
 Seq. No.
```

LIB3189-016-P1-K1-H11



```
BLASTX
Method
NCBI GI
                  q129881
                  668
BLAST score
                  2.0e-70
E value
                  146
Match length
                  89
% identity
                  PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
NCBI Description
                  ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                  (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                  (PPI-PFK) >gi_482294 pir A36094
                  pyrophosphate--fructose-6-phosphate 1-phosphotransferase
                   (EC 2.7.1.90) alpha chain - potato (cv. Kennebec)
                  >gi 169538 (M55190) pyrophosphate-fructose 6-phosphate
                  1-phosphotransferase alpha-subunit [Solanum tuberosum]
                  227055
Seq. No.
                  LIB3189-016-P1-K1-H12
Seq. ID
                  BLASTX
Method
                  g2088651
NCBI GI
                  180
BLAST score
                  2.0e-13
E value
                  89
Match length
                  44
% identity
                  (AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
                   [Arabidopsis thaliana]
                  227056
Seq. No.
                  LIB3189-016-P1-K1-H2
Seq. ID
                  BLASTX
Method
                   q2497753
NCBI GI
                   364
BLAST score
                   1.0e-34
E value
Match length
                   117
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
NCBI Description
                   >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein
                   [Prunus dulcis]
                   227057
Seq. No.
                   LIB3189-016-P1-K1-H4
 Seq. ID
                   BLASTX
Method
                   g2673868
NCBI GI
                   334
 BLAST score
                   3.0e-31
 E value
                   93
Match length
 % identity
                   75
NCBI Description (Y14856) fimbriata-associated protein [Antirrhinum majus]
                   227058
 Seq. No.
                   LIB3189-016-P1-K1-H9
 Seq. ID
                   BLASTX
 Method
                   g4138722
 NCBI GI
                   274
 BLAST score
                   3.0e-24
 E value
                   99
 Match length
```

NCBI Description (Y09590) hexose transporter [Vitis vinifera]

61

% identity



```
227059
Seq. No.
                  LIB3189-017-P1-K1-A10
Seq. ID
Method
                  BLASTX
                  q3650032
NCBI GI
                  267
BLAST score
                  2.0e-23
E value
                  60
Match length
                   67
% identity
                  (ACO05396) gibberellin-regulated protein GAST1-like
NCBI Description
                   [Arabidopsis thaliana]
                   227060
Seq. No.
                   LIB3189-017-P1-K1-A2
Seq. ID
                   BLASTX
Method
                   g3126969
NCBI GI
                   169
BLAST score
                   4.0e-12
E value
                   92
Match length
% identity
                   46
                   (AF061808) chalcone isomerase [Elaeagnus umbellata]
NCBI Description
                   227061
Seq. No.
                   LIB3189-017-P1-K1-A4
Seq. ID
                   BLASTX
Method
                   g267069
NCBI GI
                   531
BLAST score
                   2.0e-54
E value
                   98
Match length
                   99
% identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                   227062
Seq. No.
                   LIB3189-017-P1-K1-A5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4185819
BLAST score
                   192
                   1.0e-14
E value
                   47
Match length
                   68
 % identity
                   (AF116845) metallothionein-like type 1 protein [Ipomoea
NCBI Description
                   batatas]
                   227063
 Seq. No.
                   LIB3189-017-P1-K1-A7
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q3786001
                    638
 BLAST score
                   7.0e-67
 E value
 Match length
                    144
. % identity
                    81
 NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]
```

Seq. No.



```
LIB3189-017-P1-K1-A8
Seq. ID
                  BLASTX
Method
                  q2811278
NCBI GI
                  447
BLAST score
                  1.0e-44
E value
                  118
Match length
                  72
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
                  227065
Seq. No.
                  LIB3189-017-P1-K1-A9
Seq. ID
Method
                  BLASTX
                  q3869088
NCBI GI
                  570
BLAST score
                  6.0e-59
E value
                  111
Match length
                  98
% identity
NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
                  227066
Seq. No.
                  LIB3189-017-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1350720
                  455
BLAST score
                  2.0e-45
E value
                  111
Match length
                   77
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L32
                   227067
Seq. No.
                   LIB3189-017-P1-K1-B6
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2497753
BLAST score
                   324
                   5.0e-30
E value
                   97
Match length
                   57
 % identity
NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRF
                                                                     <sup>7</sup>P 3)
                   >gi_1321915_emb_CAA65477_ (X96716) .
                                                                     protein
                   [Prunus dulcis]
                   227068
 Seq. No.
                   LIB3189-017-P1-K1-C12
 Seq. ID
                   BLASTX
 Method
                   g1914683
 NCBI GI
                   339
 BLAST score
                   7.0e-32
 E value
                   122
 Match length
                   60
 % identity
 NCBI Description (Y12013) RAD23, ... m I [Daucus carota]
                   227069
 Seq. No.
 Seq. ID
                   LIB3189-017-P1-K1-C2
                   BLASTX
 Method
                   g3860247
 NCBI GI
```

1.0e-40

BLAST score

E value



87 Match length % identity NCBI Description (AC005824) unknown protein [Arabidopsis thaliana] 227070 Seq. No. LIB3189-017-P1-K1-C5 Seq. ID Method BLASTX g401322 NCBI GI 582 BLAST score E value 2.0e-60 Match length 112 % identity 99 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD NCBI Description SUBUNIT) >gi\_167313 (L03186) vacuolar H+-ATPase catalytic subunit [Gossypium hirsutum] 227071 Seq. No. LIB3189-017-P1-K1-C7 Seq. ID BLASTX Method q730512 NCBI GI 504 BLAST score E value 3.0e-51 Match length 117 88 % identity RAS-RELATED PROTEIN RIC2 >gi\_481506\_pir\_\_S38741 GTP-binding NCBI Description protein ric2 - rice >gi 218228\_dbj\_BAA02904\_ (D13758) ras-related GTP binding protein [Oryza sativa] 227072 Seq. No. LIB3189-017-P1-K1-C9 Seq. ID BLASTX Method NCBI GI q1174592 BLAST score 514 1.0e-52 E value 101 Match length 97 % identity TUBULIN ALPHA-1 CHAIN >gi\_2119270 pir\_\_S60233 alpha-tubulin NCBI Description - garden pea  $>gi_525332$  ( $\overline{U}12589$ )  $\overline{a}lpha$ -tubulin [Pisum sativum] 227073 Seq. No. LIB3189-017-P1-K1-D1 Seq. ID BLASTX Method

g1928981 NCBI GI 347 BLAST score 5.0e-33 E value 77 Match length 91 % identity

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

227074 Seq. No.

LIB3189-017-P1-K1-D10 Seq. ID

BLASTX Method q4454051 NCBI GI 531 BLAST score 2.0e-54 E value

% identity

96



```
115
Match length
                  84
% identity
                   (AL035394) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
                  227075
Seq. No.
                  LIB3189-017-P1-K1-D11
Seq. ID
                  BLASTX
Method
                   g3603473
NCBI GI
BLAST score
                   345
                   8.0e-33
E value
                   91
Match length
                   68
% identity
                  (AF090698) elicitor-responsive gene-3 [Oryza sativa]
NCBI Description
                   227076
Seq. No.
                   LIB3189-017-P1-K1-D12
Seq. ID
                   BLASTX
Method
                   g1172811
NCBI GI
BLAST score
                   368
E value
                   2.0e-35
Match length
                   84
                   85
% identity
                   60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34)
NCBI Description
                   >gi_1076751_pir__S49575 ribosomal protein L10.e, cytosolic
                   - rice >gi 575355 emb CAA57339 (X81691) putative tumor
                   suppresser [Oryza sativa]
                   227077
Seq. No.
Seq. ID
                   LIB3189-017-P1-K1-D3
Method
                   BLASTX
                   q4006890
NCBI GI
                   282
BLAST score
                   2.0e-25
E value
                   93
Match length
                   67
% identity
                  (Z99708) ubiquitin--protein ligase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   227078
Seq. No.
                   LIB3189-017-P1-K1-D6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3860247
                   430
BLAST score
                   1.0e-52
E value
Match length
                   115
% identity
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.
                   227079
                   LIB3189-017-P1-K1-E10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3219761
BLAST score
                   427
E value
                   6.0e-43
Match length
                   97
```



Seq. No.

227080

```
LIB3189-017-P1-K1-E2
Seq. ID
                  BLASTX
Method
                  g1346675
NCBI GI
                  501
BLAST score
                  6.0e-51
E value
                  107
Match length
                  90
% identity
                  NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B)
NCBI Description
                  >gi 499112 (U10283) nucleoside diphosphate kinase [Flaveria
                  bidentis]
                  227081
Seq. No.
                  LIB3189-017-P1-K1-E8
Seq. ID
                  BLASTX
Method
                  g2281338
NCBI GI
                  320
BLAST score
                  1.0e-29
E value
                  79
Match length
                  77
% identity
NCBI Description (U83621) putative pectate lyase [Arabidopsis thaliana]
                  227082
Seq. No.
                  LIB3189-017-P1-K1-F11
Seq. ID
                  BLASTX
Method
                  g3123515
NCBI GI
                  534
BLAST score
                  9.0e-55
E value
Match length
                  114
                  91
% identity
NCBI Description (Y08761) Mago Nashi-like protein [Euphorbia lagascae]
                  227083
Seq. No.
                  LIB3189-017-P1-K1-F12
Seq. ID
                  BLASTX
Method
                  q3687251
NCBI GI
                  228
BLAST score
                  3.0e-28
E value
                  95
Match length
% identity
                  63
NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]
                  227084
Seq. No.
                  LIB3189-017-P1-K1-F4
Seq. ID
                  BLASTX
Method
                  g2979559
NCBI GI
BLAST score
                  174
                  1.0e-12
E value
Match length
                   65
                  63
% identity
NCBI Description (AC003680) putative DNA binding protein [Arabidopsis
                  thaliana]
                  227085
Seq. No.
                  LIB3189-017-P1-K1-F5
Seq. ID
```

NCBI Description ACTIN 66 >gi 1498351 (U60491) actin [Nicotiana tabacum]

Seq. ID

Method



```
BLASTX
Method
                  g2507281
NCBI GI
                  357
BLAST score
                  3.0e-34
E value
                  73
Match length
                  90
% identity
                  GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi 1668706 emb CAA66048
NCBI Description
                  (X97380) atran2 [Arabidopsis thaliana]
                  227086
Seq. No.
                  LIB3189-017-P1-K1-F6
Seq. ID
                  BLASTX
Method
                  q1168196
NCBI GI
BLAST score
                  368
                  2.0e-35
E value
Match length
                  102
                  78
% identity
NCBI Description 14-3-3-LIKE PROTEIN >gi_555974 (U15036) 14-3-3-like protein
                  [Pisum sativum]
                  227087
Seq. No.
                  LIB3189-017-P1-K1-G1
Seq. ID
                  BLASTX
Method
                  q728882
NCBI GI
                  226
BLAST score
                  1.0e-33
E value
                  92
Match length
                  83
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 3 >gi 541846_pir _S41938
                  ADP-ribosylation factor 3 - Arabidopsis thaliana
                  >gi_453191_emb_CAA54564_ (X77385) ADP-ribosylation factor 3
                  [Arabidopsis thaliana]
                  227088
Seq. No.
Seq. ID
                  LIB3189-017-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2815905
                  277
BLAST score
                  1.0e-24
E value
Match length
                  95
                   61
% identity
NCBI Description (AF043734) Pros45 proteosome subunit homolog [Drosophila
                  melanogaster]
                  227089
Seq. No.
Seq. ID
                  LIB3189-017-P1-K1-G7
                  BLASTX
Method
                  q2661840
NCBI GI
BLAST score
                   305
                   5.0e-28
E value
Match length
                  75
% identity
NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]
Seq. No.
                  227090
```

.LIB3189-017-P1-K1-H1

BLASTX

Seq. No.

Seq. ID

Method



```
q4510428
NCBI GI
BLAST score
                  269
                  2.0e-31
E value
                  120
Match length
                  62
% identity
                  (AC006929) putative argonaute protein [Arabidopsis
NCBI Description
                  thaliana]
                  227091
Seq. No.
                  LIB3189-018-P1-K1-A1
Seq. ID
                  BLASTX
Method
                  g1076678
NCBI GI
BLAST score
                  269
                  3.0e-24
E value
                  66
Match length
                  82
% identity
                  ubiquitin / ribosomal protein S27a - potato (fragment)
NCBI Description
                  227092
Seq. No.
Seq. ID
                  LIB3189-018-P1-K1-A12
                  BLASTX
Method
                  g3785971
NCBI GI
BLAST score
                  406
                  1.0e-39
E value
Match length
                  141
                   60
% identity
                  (AC005560) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4262248_gb_AAD14541_ (AC006200) hypothetical protein
                   [Arabidopsis thaliana]
                   227093
Seq. No.
                   LIB3189-018-P1-K1-A3
Seq. ID
                   BLASTX
Method
                   q4544399
NCBI GI
BLAST score
                   564
                   3.0e-58
E value
                   147
Match length
                   72
% identity
                  (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   227094
                   LIB3189-018-P1-K1-A5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q549063
BLAST score
                   455
                   2.0e-45
E value
Match length
                   125
                   74
% identity
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
                   factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
                   227095
```

32407

LIB3189-018-P1-K1-B11

BLASTX .



```
q4559384
NCBI GI
                   592
BLAST score
                  2.0e-61
E value
                  167
Match length
                   69
% identity
                  (AC006526) unknown protein [Arabidopsis thaliana]
NCBI Description
                   227096
Seq. No.
                   LIB3189-018-P1-K1-B12
Seq. ID
                   BLASTX
Method
                   q4539301
NCBI GI
BLAST score
                   158
                   2.0e-10
E value
                   94
Match length
                   38
% identity
                   (AL049480) putative mitochondrial protein [Arabidopsis
NCBI Description
                   thaliana]
                   227097
Seq. No.
                   LIB3189-018-P1-K1-B6
Seq. ID
                   BLASTX
Method
                   q3212877
NCBI GI
BLAST score
                   232
                   2.0e-32
E value
                   106
Match length
                   72
% identity
                  (AC004005) Lea-like protein [Arabidopsis thaliana]
NCBI Description
                   227098
Seq. No.
                   LIB3189-018-P1-K1-B7
Seq. ID
                   BLASTX
Method
                   g3169182
NCBI GI
BLAST score
                   360
                   3.0e - 34
E value
Match length
                   78
 % identity
                  (AC004401) unknown protein [Arabidopsis thaliana]
NCBI Description
                   227099
 Seq. No.
                   LIB3189-018-P1-K1-B8
 Seq. ID
                   BLASTX
Method
                   g3759177
 NCBI GI
                   323
 BLAST score
                   7.0e-30
 E value
                   92
Match length
                   73
 % identity
                   (AB018408) 3-phosphoserine phosphatase [Arabidopsis
 NCBI Description
                   thaliana] >gi_3759179_dbj_BAA33807_ (AB018409)
                   3-phosphoserin phosphatase [Arabidopsis thaliana]
                   227100
 Seq. No.
                   LIB3189-018-P1-K1-C1
 Seq. ID
                   BLASTX
 Method
                   q2995384
 NCBI GI
                   178
 BLAST score
                   2.0e-13
 E value
```

Match length



```
% identity
NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]
                  227101
Seq. No.
                  LIB3189-018-P1-K1-C10
Seq. ID
                  BLASTX
Method
                  g3912950
NCBI GI
BLAST score
                  456
                  1.0e-45
E value
                  109
Match length
% identity
                  83
                  14-3-3-LIKE PROTEIN E >gi_2689479 (U91726) 14-3-3 isoform e
NCBI Description
                  [Nicotiana tabacum]
                  227102
Seq. No.
                  LIB3189-018-P1-K1-C11
Seq. ID
                  BLASTX
Method
                  g1346802
NCBI GI
                  318
BLAST score
                  1.0e-29
E value
                  87
Match length
% identity
                   68
                  PROFILIN 1 >gi 1076516_pir S49351 profilin - kidney bean
NCBI Description
                  >qi 556836 emb CAA57508 (X81982) profilin [Phaseolus
                   vulgaris]
                   227103
Seq. No.
                   LIB3189-018-P1-K1-C2
Seq. ID
                   BLASTX
Method
                   g4538913
NCBI GI
                   348
BLAST score
E value
                   9.0e-33
                   79
Match length
% identity
                   84
                  (AL049482) putative protein [Arabidopsis thaliana]
NCBI Description
                   227104
Seq. No.
                   LIB3189-018-P1-K1-C4
Seq. ID
                   BLASTX
Method
                   g2829204
NCBI GI
                   251
BLAST score
                   6.0e-22
E value
                   59
Match length
                   88
 % identity
                   (AF044204) lipid transfer protein precursor [Gossypium
NCBI Description
                   hirsutum]
                   227105
Seq. No.
                   LIB3189-018-P1-K1-C5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g312179
 BLAST score
                   265
                   1.0e-23
 E value
Match length
                   57
                   89
 % identity
 NCBI Description (X73151) glyceraldehyde 3-phosphate dehydrogenase
                   (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic
```

Seq. No.

Seq. ID

Method

NCBI GI

E value

BLAST score

Match length

% identity

Seq. No.

Seq. ID

Method

NCBI GI

E value

BLAST score

Match length

% identity

Seq. No.

Seq. ID

Method

NCBI GI

E value

Seq. No.

Seq. ID

Method

NCBI GI

E value

BLAST score

Match length

% identity

BLAST score

Match length

% identity



glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays] >gi\_1185554 (U45858) glyceraldehyde-3-phosphate dehydrogenase [Zea mays] 227106 LIB3189-018-P1-K1-C7 BLASTX g3128176 325 3.0e - 30111 57 NCBI Description (AC004521) unknown pro n [Arabidopsis thaliana] 227107 LIB3189-018-P1-K1-C9 BLASTX g3738304 163 4.0e-11 124 31 NCBI Description (AC005309) hypothetical protein [Arabi \_\_\_ana] 227108 LIB3189-018-P1-K1-D11 BLASTX q3237190 214 4.0e-17 86 49 NCBI Description (AB014760) cystein proteinase inhibitor [Cucumis sativus] 227109 LIB3189-018-P1-K1-D2 BLASTX q4220512 398 6.0e-39 98 76 NCBI Description (AL035356) putative pectate lyase [Arabidopsis thaliana] 227110 LIB3189-018-P1-K1-D4 BLASTX g3219271 432 1.0e-42

Seq. No.

Seq. ID

"Method NCBI GI BLAST score E value 161 Match length 57 % identity

NCBI Description (AB015315) MAP kinase kinase 4 [Arabidopsis thaliana]

227111 Seq. No.

LIB3189-018-P1-K1-D8 Seq. ID

BLASTX Method

NCBI GI



```
NCBI GI
                     g4204312
                     325
  BLAST score
                     2.0e-30
E value
  Match length
                     102
  % identity
                     69
                     (AC003027) lcl prt seq No definition line found
  NCBI Description
                     [Arabidopsis thaliana]
  Seq. No.
                     227112
                     LIB3189-018-P1-K1-E12
  Seq. ID
  Method
                     BLASTX
                     g729480
  NCBI GI
  BLAST score
                     440
  E value
                     1.0e-43
  Match leng.h
                     126
  % identity
                     71
                    FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOR (FNR)
  NCBI Description
                     >gi_435647_dbj_BAA04232 (D17410) ferredoxin-NADP+
reductase [Oryza sativa] >gi_902936_dbj_BAA07479 (D38445)
                     root ferredoxin-NADP+ reductase [Oryza sativa]
                     >gi_1096932_prf__2113196A ferredoxin-NADP oxidoreductase
                      [Oryza sativa]
  Seq. No.
                     227113
                     LIB3189-018-P1-K1-E4
  Seq. ID
                     BLASTX
  Method
  NCBI T
                     q4454466
  BLAS
                     197
                     4.0e-15
  E valu-
                     52
  Match length
  % identity
                     69
  NCBI Description (AC006234) unknown protein [Arabidopsis
                     227114
  Seq. No.
  Seq. ID
                     LIB3189-018-P1-K1-E9
  Method
                     BLASTX
  NCBI GI
                     g2894378
                     211
  BLAST score
  E value
                     7.0e-17
  Match length
                     88
                     52
   % identity
  NCBI Description (Y14573) putative ribophorin I homologue [Hordeum vulgare]
  Seg. No.
                     227115
  Seq. ID
                     LIB3189-018-P1-K1-F10
  Method
                     BLASTX
  NCBI GI
                     g3075398
                     450
  BLAST score
  E value
                     9.0e-45
  Match length
                     162
                     58
  % identity
  NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]
  Seq. No.
                     227116
  Seq. ID
                     LIB3189-018-P1-K1-F11
  Method
                     BLASTX
```

g1362086



```
638
BLAST score
                  8.0e-67
.E value
                  130
Match length
% identity
                  92
NCBI Description
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919 pir S65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >qi 886471 emb CAA58474 (X83499) methionine synthase
                  [Catharanthus roseus]
                  227117
Seq. No.
Seq. ID
                  LIB3189-018-P1-K1-F12
                  BLASTX
Method
NCBI GI
                  g4539301
                  179
BLAST score
E value
                  4.0e-13
                  96
Match length
                  42
% identity
NCBI Description
                  (AL049480) putative mitochondrial protein [Arabidopsis
                  thaliana]
Seq. No.
                  227118
                  LIB3189-018-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1168470
BLAST score
                  140
                  1.0e-08
E value
                  75
Match length
% identity
                  41
NCBI Description PROTEIN KINASE APK1A >gi 282877 pir S28615 protein kinase,
                  tyrosine/serine/threonine-specific (EC 2.7.1.-) -
                  Arabidopsis thaliana >gi 217829 dbj BAA02092 (D12522)
                  protein tyrosine-serine-threonine kinase [Arabidopsis
                  thaliana]
Seq. No.
                  227119
Seq. ID
                  LIB3189-018-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  q3876865
BLAST score
                  188
E value
                   4.0e-14
Match length
                  150
                  35
% identity
NCBI Description (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177
```

C.C.

(281534) predicted using Genefinder; cDNA EST EMBL:C081// comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No. 227120 Seq. ID LIB318

Seq. ID LIB3189-018-P1-K1-G1

Method BLASTX
NCBI GI g3915847
BLAST score 534
E value 1.0e-54
Match length 117

% identity



% identity NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi\_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana] 227121 Seq. No. Seq. ID LIB3189-018-P1-K1-G11 BLASTX Method NCBI GI g1619297 BLAST score 616 E value 3.0e-64 115 Match length % identity 99 NCBI Description (Y08490) alpha-tubulin 2 [Hordeum vulgare] Seq. No. 227122 LIB3189-018-P1-K1-G12 Seq. ID Method BLASTX q3695023 NCBI GI BLAST score 166 E value 1.0e-11 Match length 50 58 % identity NCBI Description (AF055850) unknown [Arabidopsis thaliana] Seq. No. 227123 Seq. ID LIB3189-018-P1-K1-G2 Method BLASTX g538213 NCBI GI BLAST score 519 E value 6.0e-53 Match length 123 % identity 79 NCBI Description (L36229) cytosolic copper/zinc-superoxide dismutase [Ipomoea batatas] >gi\_1582361 prf \_2118341A Cu/Zn-superoxide dismutase [Ipomoea batatas] Seq. No. 227124 LIB3189-018-P1-K1-G3 Seq. ID BLASTX Method NCBI GI q4006858 BLAST score 345 E value 2.0e-32 Match length 107 % identity 63 NCBI Description (Z99707) cold acclimation protein homolog [Arabidopsis thaliana] Seq. No. 227125 Seq. ID LIB3189-018-P1-K1-G7 Method BLASTX NCBI GI q3650037 BLAST score 474 E value 1.0e-47 Match length 116

32413

NCBI Description (AC005396) auxin-responsive GH3-like protein [Arabidopsis

thaliana]

NCBI GI

E value

BLAST score

g3334405

1.0e-67

645



```
227126
Seq. No.
Seq. ID
                  LIB3189-018-P1-K1-G9
                  BLASTX
Method
NCBI GI
                  g266972
BLAST score
                  195
E value
                  5.0e-15
                  54
Match length
% identity
                  63
NCBI Description 40S RIBOSOMAL PROTEIN S29 >gi 631884 pir S30298 ribosomal
                  protein S29 - rat >gi 1362934 pir S55919 ribosomal protein
                  S29 - human >gi 57133 emb CAA41778 (X59051) ribosomal
                  protein S29 [Rattus norvegicus] >gi 550027 (U14973)
                  ribosomal protein S29 [Homo sapiens] >gi 1220361 (L31610)
                  homologous to antisense sequence of krev-1, anti oncogene
                  [Homo sapiens] >gi 1220418 (L31609) S29 ribosomal protein
                  [Mus musculus] >gi 1513230 (U66372) ribosomal protein S29
                  [Bos taurus] >gi 1096945 prf 2113200H ribosomal protein
                  S29 [Homo sapiens] >gi 4506717 ref NP 001023.1 pRPS29
                  ribosomal protein S29
                  227127
Seq. No.
Seq. ID
                  LIB3189-018-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g1350720
BLAST score
                  241
                  3.0e-22
E value
                  71
Match length
                 77
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L32
Seq. No.
                  227128
Seq. ID
                  LIB3189-018-P1-K1-H4
                 BLASTX
Method
NCBI GI
                  q3695023
BLAST score
                  287
                  9.0e-26
E value
Match length
                  117
% identity
NCBI Description (AF055850) unknown [Arabidopsis thaliana]
                  227129
Seq. No.
                  LIB3189-018-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4490331
BLAST score
                  234
E value
                  6.0e-20
Match length
                  60
% identity
                  77
NCBI Description (AL035656) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  227130
                  LIB3189-018-P1-K1-H8
Seq. ID
Method
                  BLASTX
```

32414



```
134
Match length
% identity
                   99
                  VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
NCBI Description
                   >gi 2267583 (AF009338) vacuolar H+-ATPase subunit E
                   [Gossypium hirsutum]
                   227131
Seq. No.
Seq. ID
                   LIB3189-021-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   q82665
BLAST score
                   157
                   4.0e-11
E value
Match length
                   35
                   86
% identity
NCBI Description ADP, ATP carrier protein G1 - maize
Seq. No.
                   227132
Seq. ID
                  LIB3189-021-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q2497753
                   240
BLAST score
                   4.0e-31
E value
                   124
Match length
% identity
                   55
NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
                   >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein
                   [Prunus dulcis]
Seq. No.
                   227133
                   LIB3189-021-P1-K1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3759184
BLAST score
                   249
E value
                   3.0e-21
Match length
                   95
                   55
% identity
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
                   227134
Seq. ID
                   LIB3189-021-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   g133728
BLAST score
                   575
E value
                   2.0e-59
Match length
                   124
% identity
                   90
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S11 >gi 81525 pir B23525
                   ribosomal protein S11 - spinach chloroplast >gi_12264_emb_CAA27213_ (X03496) pot. ribosomal protein S11
                   (aa 1-138) [Spinacia oleracea]
                   227135
Seq. No.
Seq. ID
                   LIB3189-021-P1-K1-A7
```

Seq. ID LIBSING-UZI-PI-KI-A

Method BLASTX
NCBI GI g2392769
BLAST score 139
E value 9.0e-14



```
74
Match length
                  64
% identity
                  (AC002534) putative histone deacetylase [Arabidopsis
NCBI Description
                  thaliana]
                  227136
Seq. No.
                  LIB3189-021-P1-K1-A8
Seq. ID
                  BLASTX
Method
                  g3450889
NCBI GI
                  223
BLAST score
                  9.0e-25
E value
                  90
Match length
                  70
% identity
                  (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
NCBI Description
                  227137
Seq. No.
                  LIB3189-021-P1-K1-B12
Seq. ID
                  BLASTX
Method
                   g2497743
NCBI GI
                   168
BLAST score
                   4.0e-12
E value
                   31
Match length
                   100
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3)
NCBI Description
                   >gi_999315_bbs_166991 (S78173) LTP=lipid transfer protein
                   [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa]
                   [Gossypium hirsutum]
                   227138
Seq. No.
                   LIB3189-021-P1-K1-B9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2947060
                   461
BLAST score
                   4.0e-46
E value
                   99
Match length
                   83
% identity
NCBI Description (AC002521) putative membrane protein [Arabidopsis thaliana]
                   227139
Seq. No.
                   LIB3189-021-P1-K1-C11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1871192
                   264
 BLAST score
                   3.0e-23
 E value
                   72
Match length
 % identity
NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis
                   thaliana]
                   227140
 Seq. No.
                   LIB3189-021-P1-K1-C12
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g294668
                   481
 BLAST score
                   2.0e-48
 E value
                   130
 Match length
```

% identity

April 1

```
NCBI Description (L13242) beta-ketoacyl-ACP synthase [Ricinus communis]
                  227141
Seq. No.
                  LIB3189-021-P1-K1-C2
Seq. ID
```

BLASTX Method g730456 NCBI GI 254 BLAST score 3.0e-22E value 67 Match length 69 % identity NCBI Description 40S RIBOSOMAL PROTEIN S19

227142 Seq. No. LIB3189-021-P1-K1-C4 Seq. ID BLASTX Method g310317 NCBI GI 146 BLAST score 9.0e-10 E value

37 Match length 76 % identity

(L19598) beta-tubulin [Oryza sativa] NCBI Description

227143 Seq. No.

LIB3189-021-P1-K1-D1 Seq. ID

BLASTX Method q4218120 NCBI GI 526 BLAST score 1.0e-53 E value Match length 138 74 % identity

(AL035353) Proline-rich APG-like protein [Arabidopsis NCBI Description

thaliana]

227144 Seq. No.

LIB3189-021-P1-K1-D10 Seq. ID

BLASTX Method g120669 NCBI GI 189 BLAST score E value 8.0e-15 41 Match length 83 % identity

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >qi 19566 emb CAA42905\_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

227145 Seq. No.

LIB3189-021-P1-K1-D11 Seq. ID

Method BLASTX g3859944 NCBI GI 413 BLAST score 1.0e-40 E value Match length 102 83 % identity

(AF084570) FKBP12 interacting protein [Arabidopsis NCBI Description

thaliana]

Match length

57

```
227146
Seq. No.
                   LIB3189-021-P1-K1-D12
Seq. ID
                   BLASTX
Method
                   g1172817
NCBI GI
                   251
BLAST score
                   1.0e-21
E value
                   69
Match length
                   72
% identity
                  60S RIBOSOMAL PROTEIN L11B (L16B) >gi_550547_emb_CAA57396_
NCBI Description
                   (X81800) ribosomal protein L16 [Arabidopsis thaliana]
                   >gi_4539392_emb_CAB37458.1_ (AL035526) ribosomal protein
                   L11, cytosolic [Arabidopsis thaliana]
                   227147
Seq. No.
                   LIB3189-021-P1-K1-E1
Seq. ID
                   BLASTX
Method
                   g3650032
NCBI GI
                   237
BLAST score
                   8.0e-20
E value
                   49
Match length
                   73
% identity
                  (AC005396) gibberellin-regulated protein GAST1-like
NCBI Description
                   [Arabidopsis thaliana]
                   227148
Seq. No.
                   LIB3189-021-P1-K1-E11
Seq. ID
Method
                   BLASTX
                   g1279206
NCBI GI
                   270
BLAST score
                   2.0e-24
E value
Match length
                   59
                   90
% identity
NCBI Description (X97446) alpha-tubulin [Avena sativa]
                   227149
Seq. No.
                   LIB3189-021-P1-K1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   a133409
BLAST score
                    398
                    1.0e-38
E value
Match length
                   87
                    86
% identity
                   DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN
NCBI Description
                   >gi_66962_pir__RNNTA DNA-directed RNA polymerase (EC 2.7.7.6) alpha chain - common tobacco chloroplast
                    >qi 11860 emb CAA77376 (Z00044) RNA polymerase alpha
                    subunit [Nicotiana tabacum] >gi_225228_prf__1211235BK RNA
                    polymerase alpha [Nicotiana tabacum]
                    227150
Seq. No.
                    LIB3189-021-P1-K1-E4
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1172817
BLAST score
                    182
                    2.0e-13
E value
```

32418

- 555530



```
% identity
                  60S RIBOSOMAL PROTEIN L11B (L16B) >gi_550547 emb_CAA57396
NCBI Description
                  (X81800) ribosomal protein L16 [Arabidopsis thaliana]
                  >gi 4539392_emb_CAB37458.1_ (AL035526) ribosomal protein
                  L11, cytosolic [Arabidopsis thaliana]
                  227151
Seq. No.
                  LIB3189-021-P1-K1-F11
Seq. ID
Method
                  BLASTX
                  q2624326
NCBI GI
BLAST score
                  142
                  2.0e-09
E value
Match length
                  36
                  75
% identity
NCBI Description (AJ002893) OsGRP1 [Oryza sativa]
                  227152
Seq. No.
                  LIB3189-021-P1-K1-F7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3152606
                  154
BLAST score
                   3.0e-10
E value
Match length
                   41
% identity
                   (AC004482) putative ring zinc finger protein [Arabidopsis
NCBI Description
                   thaliana]
                   227153
Seq. No.
                   LIB3189-021-P1-K1-G1
Seq. ID
                   BLASTX
Method
                   q1703108
NCBI GI
                   568
BLAST score
                   1.0e-58
E value
Match length
                   104
% identity
                   100
                   ACTIN 2/7 > gi_2129525_pir_S71210 actin 2 - Arabidopsis
NCBI Description
                   thaliana >gi 2129528 pir S68107 actin 7 - Arabidopsis
                   thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis
                   thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis
                   thaliana]
                   227154
 Seq. No.
                   LIB3189-021-P1-K1-G7
 Seq. ID
                   BLASTX
 Method
NCBI GI
                   q548774
```

Method BLASTX
NCBI GI g548774
BLAST score 539
E value 3.0e-55
Match length 138
% identity 76

NCBI Description 60S RIBOSOMAL PROTEIN L7A >gi\_542158\_pir\_\_S38360 ribosomal

protein L7a - rice >gi\_303855\_dbj\_BAA02156\_ (D12631)

ribosomal protein L7A [Oryza sativa]

Seq. No. 227155

Seq. ID LIB3189-021-P1-K1-G8

Method BLASTX NCBI GI g132944



```
584
BLAST score
                  1.0e-60
E value
                  116
Match length
                   93
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi_81658_pir_ JQ0772 ribosomal
NCBI Description
                  protein L3 (ARP2) - Arabidopsis thaliana >gi_806279
                   (M32655) ribosomal protein [Arabidopsis thaliana]
                   227156
Seq. No.
                  LIB3189-021-P1-K1-H11
Seq. ID
                  BLASTX
Method
NCBI GI
                   q1771162
                   339
BLAST score
                   7.0e-32
E value
                   84
Match length
                   73
% identity
                   (X98930) SBT2 [Lycopersicon esculentum]
NCBI Description
                   >gi 3687307_emb_CAA07000_ (AJ006379) subtilisin-like
                   protease [Lycopersicon esculentum]
Seq. No.
                   227157
                   LIB3189-021-P1-K1-H3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1495251
BLAST score
                   428
E value
                   3.0e-42
                   129
Match length
                   66
% identity
NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]
                   227158
Seq. No.
                   LIB3189-021-P1-K1-H5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4204300
                   199
BLAST score
E value
                   9.0e-16
                   76
Match length
% identity
                   (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   227159
Seq. No.
                   LIB3189-021-P1-K1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4325369
                   150
BLAST score
E value
                   5.0e-10
Match length
                   75
 % identity
                   51
                   (AF128396) T3H13.3 gene product [Arabidopsis thaliana]
NCBI Description
                   227160
Seq. No.
                   LIB3189-022-P1-K1-A12
Seq. ID
                   BLASTX
Method
                   g2341034
NCBI GI
BLAST score
                   222
                   1.0e-18
E value
```

50

Match length

```
% identity
                  90
NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]
                  227161
Seq. No.
                  LIB3189-022-P1-K1-A3
Seq. ID
Method
                  BLASTX
                  g3915823
NCBI GI
                  200
BLAST score
                  4.0e-16
E value
Match length
                  46
                  80
% identity
NCBI Description [Segment 1 of 2] 60S RIBOSOMAL PROTEIN L5
                  227162
Seq. No.
Seq. ID
                  LIB3189-022-P1-K1-A5
Method
                  BLASTX
                  g3377797
NCBI GI
BLAST score
                  154
E value
                  2.0e-10
Match length
                  47
% identity
                  70
```

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

 Seq. No.
 227163

 Seq. ID
 LIB3189-022-P1-K1-B4

 Method
 BLASTX

 NCBI GI
 g924951

NCBI GI g924951 BLAST score 352 E value 3.0e-33 Match length 148 % identity 45

NCBI Description (U30324) class I chitinase [Theobroma cacao]

Seg. No. 227164

Seq. ID LIB3189-022-P1-K1-B7

Method BLASTX
NCBI GI g4454026
BLAST score 416
E value 8.0e-41
Match length 129
% identity 64

NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No. 227165

Seq. ID LIB3189-022-P1-K1-B8

Method BLASTX
NCBI GI g4454026
BLAST score 194
E value 3.0e-15
Match length 72
% identity 57

NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]



```
227166
Seq. No.
                  LIB3189-022-P1-K1-C8
Seq. ID
Method
                  BLASTX
                  g4510395
NCBI GI
                  276
BLAST score
                  7.0e-25
E value
                  73
Match length
                  73
% identity
                   (AC006587) putative beta-galactosidase precursor
NCBI Description
                   [Arabidopsis thaliana]
                  227167
Seq. No.
                  LIB3189-022-P1-K1-D11
Seq. ID
                  BLASTX
Method
                  g2435395
NCBI GI
BLAST score
                  254
                   4.0e-22
E value
                   51
Match length
                   88
% identity
                  (U63550) pectate lyase [Fragaria x ananassa]
NCBI Description
                   227168
Seq. No.
                  LIB3189-022-P1-K1-D12
Seq. ID
                   BLASTX
Method
                   g3694872
NCBI GI
                   497
BLAST score
E value
                   2.0e-50
                   110
Match length
                   83
% identity
                  (AF092547) profilin [Ricinus communis]
NCBI Description
                   227169
Seq. No.
                   LIB3189-022-P1-K1-D2
Seq. ID
Method
                   BLASTX
                   g3377797
NCBI GI
BLAST score
                   284
E value
                   1.0e-25
                   82
Match length
                   69
% identity
                   (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                   by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                   H36046; coded for by A. thaliana cDNA T44067; coded for by
                   A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                   R90691 [Ara
                   227170
Seq. No.
                   LIB3189-022-P1-K1-D3
Seq. ID
Method
                   BLASTX
                   g3650032
NCBI GI
                   233
BLAST score
                   2.0e-19
E value
Match length
                   49
                   71
 % identity
                   (AC005396) gibberellin-regulated protein GAST1-like
NCBI Description
```

Seq. No. 227171

[Arabidopsis thaliana]



```
Seq. ID
                  LIB3189-022-P1-K1-D4
Method
                  BLASTX
                  g586076
NCBI GI
                  570
BLAST score
                  6.0e-59
E value
Match length
                  114
                  93
% identity
                  TUBULIN BETA-1 CHAIN >gi 486734 pir S35142 tubulin beta
NCBI Description
                  chain - white lupine >gi 402636 emb CAA49736 (X70184) Beta
                  tubulin 1 [Lupinus albus]
                  227172
Seq. No.
Seq. ID
                  LIB3189-022-P1-K1-E6
                  BLASTX
Method
NCBI GI
                  q3924612
BLAST score
                  442
                  7.0e-44
E value
Match length
                  125
% identity
                  71
NCBI Description
                  (AF069442) mitochondrial elongation factor Tu [Arabidopsis
                  thaliana] >gi_4263511_gb_AAD15337_ (AC004044) mitochondrial
                  elongation factor Tu [Arabidopsis thaliana]
Seq. No.
                  227173
Seq. ID
                  LIB3189-022-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g1129145
BLAST score
                  183
E value
                  4.0e-14
Match length
                  62
% identity
NCBI Description (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]
                  227174
Seq. No.
Seq. ID
                  LIB3189-022-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g3860272
BLAST score
                  228
                  5.0e-19
E value
Match length
                  51
% identity
                  88
NCBI Description
                  (AC005824) putative suppressor protein [Arabidopsis
                  thaliana] >gi 4314399 gb AAD15609 (AC006232) putative skd1
                  protein [Arabidopsis thaliana]
Seq. No.
                  227175
Seq. ID
                  LIB3189-022-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q115515
BLAST score
                  235
E value
                  3.0e-20
Match length
                  48
% identity
                  52
```

max] >gi 170074 (L014 $\overline{3}$ 2) calmodulin [Glycine max]



```
>gi_506852 (L20507) calmodulin [Vigna radiata] >gi_4103957
(AF030032) calmodulin [Phaseolus vulgaris]
>gi_1583767_prf__2121384A calmodulin [Glycine max]
>gi_1583769_prf__2121384C calmodulin [Glycine max]
```

Seq. No. 227176

Seq. ID LIB3189-022-P1-K1-F3

Method BLASTX
NCBI GI g1617036
BLAST score 302
E value 1.0e-27
Match length 67
% identity 79

NCBI Description (Y08624) Ted2 [Vigna unguiculata]

Seq. No. 227177

Seq. ID LIB3189-022-P1-K1-F5

Method BLASTX
NCBI GI g3334115
BLAST score 539
E value 2.0e-55
Match length 113
% identity 57

NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)

(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi\_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium

hirsutum]

Seq. No. 227178

Seq. ID LIB3189-022-P1-K1-F6

Method BLASTX
NCBI GI g3334115
BLAST score 306
E value 1.0e-28
Match length 62
% identity 41

NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)

(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi\_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium

hirsutum]

Seq. No. 227179

Seq. ID LIB3189-022-P1-K1-F8

Method BLASTX
NCBI GI g120669
BLAST score 245
E value 2.0e-21
Match length 54
% identity 85

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 227180

Seq. ID LIB3189-022-P1-K1-F9



```
BLASTX
Method
NCBI GI
                  q2244750
                  535
BLAST score
E value
                  8.0e-61
Match length
                  127
                  94
% identity
NCBI Description
                  (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                  >qi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                  [Arabidopsis thaliana]
                  227181
Seq. No.
                  LIB3189-022-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1703375
BLAST score
                  580
                  5.0e-60
E value
Match length
                  117
                  97
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 965483 dbj BAA08259 (D45420)
                  DcARF1 [Daucus carota]
                  227182
Seq. No.
Seq. ID
                  LIB3189-022-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g1658197
BLAST score
                  619
                  5.0e-67
E value
Match length
                  146
% identity
                  86
NCBI Description (U74630) calreticulin [Ricinus communis] >gi 1763297
                  (U74631) calreticulin [Ricinus communis]
Seq. No.
                  227183
Seq. ID
                  LIB3189-022-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q586076
BLAST score
                  538
                  3.0e-55
E value
Match length
                  101.
                  96
% identity
NCBI Description TUBULIN BETA-1 CHAIN >gi 486734 pir S35142 tubulin beta
                  chain - white lupine >gi 402636 emb CAA49736 (X70184) Beta
                  tubulin 1 [Lupinus albus]
Seq. No.
                  227184
                  LIB3189-022-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3202042
BLAST score
                  197
E value
                  3.0e-15
Match length
                  126
% identity
                  45
                  (AF069324) 26S proteasome regulatory subunit S5A
NCBI Description
                  [Mesembryanthemum crystallinum]
```

Seq. No. 227185

Seq. ID LIB3189-022-P1-K1-H7



```
BLASTX
Method
                  q2129499
NCBI GI
                  551
BLAST score
                  1.0e-56
E value
Match length
                  120
                  87
% identity
                  fiber protein E6 (clone CKE6-4A) - upland cotton
NCBI Description
                  >gi 1000086 (U30506) E6 [Gossypium hirsutum]
                  227186
Seq. No.
                  LIB3189-023-P1-K1-A10
Seq. ID
                  BLASTX
Method
                   g3450842
NCBI GI
                   290
BLAST score
                   4.0e-26
E value
Match length
                   121
                   46
% identity
                  (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                   sativa]
                   227187
Seq. No.
                   LIB3189-023-P1-K1-A11
Seq. ID
                   BLASTX
Method
                   g3334322
NCBI GI
                   363
BLAST score
                   1.0e-34
E value
                   103
Match length
                   57
% identity
NCBI Description GTP-BINDING PROTEIN SAR1B >gi_2108347 (U55036) small
                   GTP-binding protein Bsarlb [Brassica rapa]
                   227188
Seq. No.
                   LIB3189-023-P1-K1-A12
Seq. ID
                   BLASTX
Method
                   q4204285
NCBI GI
BLAST score
                   243
 E value
                   4.0e-22
                   90
Match length
                   63
 % identity
 NCBI Description (AC003027) lcl_prt_seq No definition line found
                   [Arabidopsis thaliana]
                   227189
 Seq. No.
                   LIB3189-023-P1-K1-A2
 Seq. ID
                   BLASTX
 Method
                   g2244736
 NCBI GI
 BLAST score
                   712
                   2.0e-75
 E value
                   134
 Match length
                   97
 % identity
 NCBI Description (D88415) expansin [Gossypium hirsutum]
                   227190
 Seq. No.
                   LIB3189-023-P1-K1-A3
 Seq. ID
                   BLASTX
 Method
```

g120669

407

NCBI GI

BLAST score



E value 7.0e-40 Match length 100 77 % identity GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description >gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora] 227191 Seq. No. Seq. ID LIB3189-023-P1-K1-A5 Method BLASTX NCBI GI q2288986 BLAST score 149 E value 4.0e-10 Match length 47 62 % identity NCBI Description (AC002335) glyoxalase II isolog [Arabidopsis thaliana] Seq. No. 227192 LIB3189-023-P1-K1-A7 Seq. ID Method BLASTX NCBI GI g1922278 BLAST score 246 E value 2.0e-21 Match length 49 % identity 90 NCBI Description (Z86091) TCTP protein [Fragaria x ananassa] Seq. No. 227193 LIB3189-023-P1-K1-A8 Seq. ID Method BLASTX NCBI GI g2244736 BLAST score 654 E value 1.0e-68 Match length 124 96 % identity NCBI Description (D88415) expansin [Gossypium hirsutum] 227194 Seq. No. Seq. ID LIB3189-023-P1-K1-A9 Method BLASTX NCBI GI g2160174 BLAST score 203 E value 8.0e-16 Match length 91 % identity 49 NCBI Description (AC000132) Identical to A. thaliana PUR2 (gb X74766). ESTs gb ATTS3927,gb N96446 come from this gene. [Arabidopsis thaliana] 227195 Seq. No.

Seq. ID LIB3189-023-P1-K1-B10

Method BLASTX
NCBI GI g4185511
BLAST score 420
E value 2.0e-41



Match length 83 % identity (AF102822) actin depolymerizing factor 4 [Arabidopsis NCBI Description thaliana] 227196 Seq. No. LIB3189-023-P1-K1-B12 Seq. ID BLASTX Method g4455225 NCBI GI BLAST score 330 1.0e-30 E value 101 Match length 55 % identity (AL035440) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 227197 LIB3189-023-P1-K1-B2 Seq. ID BLASTX Method g3876865 NCBI GI 161 BLAST score 5.0e-11 E value 73 Match length 40 % identity (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 NCBI Description comes from this gene; cDNA EST EMBL: C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co 227198 Seq. No. LIB3189-023-P1-K1-B9 Seq. ID Method BLASTX NCBI GI g1170168 151 BLAST score 6.0e-10 E value 80 Match length 49 % identity HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT1 (HD-ZIP PROTEIN 1) NCBI Description >gi\_549883 (U09332) homeobox protein [Arabidopsis thaliana] 549884 (U09333) homeobox protein [Arabidopsis thaliana] >gi 2245105 emb CAB10527 (Z97343) unnamed protein product [Arabidopsis thaliana] 227199 Seq. No. LIB3189-023-P1-K1-C1 Seq. ID Method BLASTX NCBI GI g2894558 331 BLAST score 7.0e-31 E value 81 Match length % identity NCBI Description (AL021890) putative protein [Arabidopsis thaliana]

227200 Seq. No.

LIB3189-023-P1-K1-C10 Seq. ID

BLASTX Method NCBI GI g4530585 357 BLAST score

NCBI Description



```
E value
                   7.0e-34
Match length
                   85
% identity
                   74
NCBI Description (AF130978) B12D protein [Ipomoea batatas]
Seq. No.
                   227201
Seq. ID
                   LIB3189-023-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   g4544428
BLAST score
                   341
E value
                   4.0e-32
Match length
                   102
% identity
                   64
NCBI Description (AC006955) unknown protein [Arabidopsis thaliana]
Seq. No.
                   227202
Seq. ID
                   LIB3189-023-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g3650032
BLAST score
                   256
E value
                   4.0e-22
                   56
Match length
                   70
% identity
NCBI Description (AC005396) gibberellin-regulated protein GAST1-like
                   [Arabidopsis thaliana]
Seq. No.
                   227203
Seq. ID
                  LIB3189-023-P1-K1-C4
Method
                  BLASTX
NCBI GI
                   g3641836
BLAST score
                   216
E value
                   2.0e-22
Match length
                  105
% identity
                   50
NCBI Description (AL023094) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   227204
Seq. ID
                  LIB3189-023-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g4206112
BLAST score
                  321
E value
                  9.0e-30
Match length
                  62
% identity
NCBI Description (AF097662) alpha tubulin [Mesembryanthemum crystallinum]
Seq. No.
                  227205
Seq. ID
                  LIB3189-023-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g3135264
BLAST score
                  457
E value
                  1.0e-45
Match length
                  105
% identity
                  81
```

(AC003058) unknown protein [Arabidopsis thaliana]

Seq. ID

Method

BLASTX



```
227206
Seq. No.
                   LIB3189-023-P1-K1-D6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2811278
                   187
BLAST score
                   1.0e-14
E value
                   43
Match length
                   84
% identity
                   (AF043284) expansin [Gossypium hirsutum]
NCBI Description
                   227207
Seq. No.
                   LIB3189-023-P1-K1-D9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2811278
                   523
BLAST score
                   2.0e-53
E value
Match length
                   128
                   76
% identity
                   (AF043284) expansin [Gossypium hirsutum]
NCBI Description
                   227208
Seq. No.
                   LIB3189-023-P1-K1-E11
Seq. ID
Method
                   BLASTX
                   g4337175
NCBI GI
                   448
BLAST score
                   1.0e-44
E value
Match length
                   126
% identity
                   68
                   (AC006416) ESTs gb T20589, gb T04648, gb AA597906,
NCBI Description
                   gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
                   gb_AA720210 come from this gene. [Arabidopsis thaliana]
                    227209
Seq. No.
                   LIB3189-023-P1-K1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1350956
                    483
BLAST score
                    9.0e - 49
E value
                   100
Match length
                    94
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)
                    227210
Seq. No.
                    LIB3189-023-P1-K1-E5
Seq. ID
                    BLASTX
Method
NCBI GI
                    g3021513
BLAST score
                    348
E value
                    5.0e-33
Match length
                    108
% identity
                   (X96728) isocitrate dehydrogenase (NADP+) [Nicotiana
NCBI Description
                    tabacum]
                    227211
Seq. No.
                    LIB3189-023-P1-K1-E7
```

% identity

83



```
NCBI GI
                  g2464905
BLAST score
                  139
E value
                  8.0e-09
Match length
                  74
% identity
                  43
NCBI Description (Z99708) minor allergen [Arabidopsis thaliana]
Seq. No.
                  227212
Seq. ID
                  LIB3189-023-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g2924258
BLAST score
                  378
E value
                  2.0e-36
Match length
                  116
% identity
                  66
NCBI Description (Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum]
Seq. No.
                  227213
Seq. ID
                  LIB3189-023-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g4098129
BLAST score
                  581
E value
                  4.0e-60
Match length
                  115
% identity
                  91
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
Seq. No.
                  227214
Seq. ID
                  LIB3189-023-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g3687237
BLAST score
                  611
E value
                  1.0e-63
Match length
                  137
% identity
                  77
NCBI Description (AC005169) putative Cys3His zinc-finger protein
                 [Arabidopsis thaliana]
Seq. No.
                  227215
Seq. ID
                  LIB3189-023-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q3687237
BLAST score
                  437
E value
                  1.0e-43
Match length
                  87
% identity
                  80
NCBI Description (AC005169) putative Cys3His zinc-finger protein
                  [Arabidopsis thaliana]
Seq. No.
                  227216
Seq. ID
                  LIB3189-023-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g3319882
BLAST score
                  643
E value
                  2.0e-67
Match length
                  150
```

32431



```
NCBI Description (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
                   arietinum]
Seq. No.
                   227217
Seq. ID
                  LIB3189-023-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g3759184
BLAST score
                  269
E value
                  1.0e-23
Match length
                  123
% identity
                  53
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
                  227218
Seq. ID
                  LIB3189-023-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g3319774
BLAST score
                  201
E value
                  1.0e-15
Match length
                  44
% identity
                  84
NCBI Description (Y16228) TOM7 protein [Solanum tuberosum]
Seq. No.
                  227219
Seq. ID
                  LIB3189-023-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g2330739
BLAST score
                  276
E value
                  2.0e-24
Match length
                  78
% identity
                  63
NCBI Description (Z98598) putative transcriptional regulator
                  [Schizosaccharomyces pombe]
Seq. No.
                  227220
Seq. ID
                  LIB3189-023-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g547683
BLAST score
                  388
                  6.0e-38
E value
Match length
                  78
% identity
                  96
NCBI Description HEAT SHOCK COGNATE PROTEIN 80 >gi_170456 (M96549) heat
                  shock cognate protein 80 [Solanum lycopersicum]
                  >gi_445601_prf__1909348A heat shock protein hsp80
                  [Lycopersicon esculentum]
Seq. No.
                  227221
Seq. ID
                  LIB3189-023-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g1729874
BLAST score
                  267
E value
                  1.0e-23
Match length -
                  77
% identity
                  69
```

(CCT-GAMMA) >gi\_1078806\_pir\_ A55423 TpCCT-gamma protein -

NCBI Description T-COMPLEX PROTEIN 1, GAMMA SUBUNIT (TCP-1-GAMMA)

Seq. ID



Tetrahymena pyriformis (SGC5) >gi\_2654380\_emb\_CAA84368\_(Z34885) TCP1gamma protein [Tetrahymena pyriformis]

```
Seq. No.
                    227222
 Seq. ID
                    LIB3189-023-P1-K1-G4
 Method
                    BLASTX
 NCBI GI
                    g3687251
 BLAST score
                    454
 E value
                    2.0e-45
 Match length
                    110
 % identity
                    78
 NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]
 Seq. No.
                   227223
 Seq. ID
                   LIB3189-023-P1-K1-G7
 Method
                   BLASTX
 NCBI GI
                   g2245128
 BLAST score
                    436
 E value
                    4.0e-43
 Match length
                   131
 % identity
                    63
 NCBI Description (Z97344) peroxidase [Arabidopsis thaliana]
 Seq. No.
                   227224
 Seq. ID
                   LIB3189-023-P1-K1-H3
Method
                   BLASTX
 NCBI GI
                   q129960
BLAST score
                   237
 E value
                   8.0e-20
Match length
                   81
 % identity
                   51
NCBI Description 4-NITROPHENYLPHOSPHATASE (PNPPASE)
 Seq. No.
                   227225
 Seq. ID
                   LIB3189-023-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g2213595
BLAST score
                   375
E value
                   5.0e-36
Match length
                   132
 % identity
                   55
NCBI Description (AC000348) T7N9.15 [Arabidopsis thaliana]
Seq. No.
                   227226
Seq. ID
                   LIB3189-024-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   g303750
BLAST score
                   218
E value
                   6.0e-18
Match length
                   42
% identity
                   100
NCBI Description
                   (D12548) GTP-binding protein [Pisum sativum]
                   >gi_738940_prf 2001457H GTP-binding protein [Pisum
                   sativum]
Seq. No.
                   227227
```

LIB3189-024-P1-K1-A12

BLAST score

Match length

E value

142

57

9.0e-09



```
Method
                   BLASTX
NCBI GI
                   g4580389
BLAST score
                   469
E value
                   5.0e-47
Match length
                   106
% identity
                   81
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]
Seq. No.
                   227228
Seq. ID
                   LIB3189-024-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   q1531674
BLAST score
                   700
E value
                   3.0e-74
Match length
                   136
% identity
                   97
NCBI Description (U68462) actin [Striga asiatica]
Seq. No.
                   227229
Seq. ID
                   LIB3189-024-P1-K1-B5
Method
                  BLASTX
NCBI GI
                   q2827559
BLAST score
                   169
E value
                   7.0e-12
Match length
                   109
% identity
                   39
NCBI Description
                   (AL021635) predicted protein [Arabidopsis thaliana]
                   >gi_3292808_emb_CAA19798_ (AL031018) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                   227230
Seq. ID
                  LIB3189-024-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g1402878
BLAST score
                  196
E value
                  3.0e-15
Match length
                  99
% identity
                   44
NCBI Description (X98130) unknown [Arabidopsis thaliana]
Seq. No.
                  227231
Seq. ID
                  LIB3189-024-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g2288997
BLAST score
                  190
E value
                  2.0e-14
Match length
                  54
% identity
NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  227232
Seq. ID
                  LIB3189-024-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g3935165
```

32434



% identity NCBI Description (AC004557) F17L21.8 [Arabidopsis thaliana] Seq. No. 227233 LIB3189-024-P1-K1-E1 Seq. ID Method BLASTX NCBI GI g2497753 BLAST score 258 E value 2.0e-22 Match length 87 % identity 53 NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi\_1321915\_emb\_CAA65477 (X96716) lipid transfer protein [Prunus dulcis] Seq. No. 227234 Seq. ID LIB3189-024-P1-K1-E3 Method BLASTX NCBI GI g3377764 BLAST score 338 E value 1.0e-31 Match length 68 % identity NCBI Description (AF079851) nodule-enhanced sucrose synthase [Pisum sativum] Seq. No. 227235 Seq. ID LIB3189-024-P1-K1-E9 Method BLASTX NCBI GI g2950472 BLAST score 191 E value 1.0e-14 Match length 81 % identity 47 NCBI Description (AL022070) putative autophagocytosis protein [Schizosaccharomyces pombe] Seq. No. 227236 Seq. ID LIB3189-024-P1-K1-F1 Method BLASTX NCBI GI g2642215 BLAST score 308 E value 4.0e-28 Match length 77 % identity 77 NCBI Description (AF030386) NOI protein [Arabidopsis thaliana] 227237

Seq. No.

Seq. ID LIB3189-024-P1-K1-F2

Method BLASTX NCBI GI g3158376 BLAST score 212 E value 7.0e-17 Match length 72 % identity 62

NCBI Description (AF035385) unknown [Arabidopsis thaliana]

Seq. No. 227238

32435

NCBI Description



```
Seq. ID
                   LIB3189-024-P1-K1-F6
Method
                   BLASTX
NCBI GI
                   g2829902
BLAST score
                   616
E value
                   2.0e-64
Match length
                   138
% identity
                   83
NCBI Description (AC002311) Putative sulphate transporter protein#protein
                   [Arabidopsis thaliana]
Seq. No.
                   227239
Seq. ID
                   LIB3189-024-P1-K1-G1
Method
                   BLASTX
                   q4455364
NCBI GI
BLAST score
                   493
E value
                   8.0e-50
Match length
                   147
% identity
                   59
NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis
                   thaliana]
                   227240
Seq. No.
Seq. ID
                   LIB3189-024-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   q4056469
BLAST score
                   524
E value
                   2.0e-53
Match length
                   104
% identity
NCBI Description
                  (AC005990) Strong similarity to gb_M95166 ADP-ribosylation
                   factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,
                   gb_AA712956, gb_T46403, gb T46050, gb AI100391 and
                   gb_Z25043 come from t
Seq. No.
                   227241
Seq. ID
                   LIB3189-024-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   q1172558
BLAST score
                   174
E value
                   1.0e-12
Match length
                   72
% identity
                   47
NCBI Description OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT
                   ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                   >gi_480122_pir__S36454 porin por1 - garden pea
                   >gi 396819 emb CAA80988 (Z25540) Porin [Pisum sativum]
Seq. No.
                   227242
Seq. ID
                   LIB3189-024-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   g3080420
BLAST score
                   476
E value
                   8.0e-50
Match length
                   120
% identity
                   83
```

(AL022604) putative sugar transporter protein [Arabidopsis



## thaliana]

```
Seq. No.
                   227243
Seq. ID
                   LIB3189-024-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g3885334
BLAST score
                   145
E value
                   4.0e-09
Match length
                   41
% identity
                   66
NCBI Description (AC005623) putative argonaute protein [Arabidopsis
                   thaliana
Seq. No.
                   227244
Seq. ID
                  LIB3189-024-P1-K1-H6
Method
                  BLASTX
NCBI GI
                   g4559358
BLAST score
                   383
E value
                   5.0e-37
Match length
                  100
% identity
                   72
NCBI Description (AC006585) putative steroid binding protein [Arabidopsis
                   thaliana]
Seq. No.
                   227245
Seq. ID
                  LIB3189-024-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g3334113
BLAST score
                   401
E value
                   3.0e-39
                  78
Match length
% identity
                  97
NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >gi 1006831 (U35015)
                  acyl-CoA-binding protein [Gossypium hirsutum]
Seq. No.
                  227246
Seq. ID
                  LIB3189-025-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g3668089
BLAST score
                  171
E value
                  4.0e-12
Match length
                  86
% identity
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.
                  227247
Seq. ID
                  LIB3189-025-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g1169009
BLAST score
                  238
E value
                  4.0e-20
Match length
                  107
% identity
                  48
NCBI Description
                  CAFFEIC ACID 3-O-METHYLTRANSFERASE
```

3-O-METHYLTRANSFERASE) (COMT) >gi\_542009\_pir\_\_S40146 catechol O-methyltransferase (EC 2.1.1.6) - cider tree

(S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID



>gi 437777 emb CAA52814\_ (X74814) 0-Methyltransferase [Eucalyptus gunnii]

Seq. No. 227248

Seq. ID LIB3189-025-P1-K1-B1

Method BLASTX NCBI GI g3377805 BLAST score 168 E value 3.0e-12 Match length 47

% identity NCBI Description (AF075597) contains similarity to several apoptosis or

programmed cell death proteins such as rat apoptosis

protein RP-8 (GB:M80601) [Arabidopsis thaliana]

>gi 3912928 gb AAC78712.1\_ (AF001308) putative zinc finger

protein [Arabidopsis thaliana]

Seq. No. 227249

Seq. ID LIB3189-025-P1-K1-B10

Method BLASTX NCBI GI q4510373 BLAST score 234 E value 2.0e-30 Match length 126 % identity 60

NCBI Description (AC007017) putative harpin-induced protein [Arabidopsis

thaliana]

Seq. No. 227250

Seq. ID LIB3189-025-P1-K1-B2

Method BLASTX NCBI GI g1620898 BLAST score 560 E value 1.0e-57 Match length 138 % identity 80

NCBI Description (D87957) protein involved in sexual development [Homo .

sapiens]

Seq. No.

227251

Seq. ID LIB3189-025-P1-K1-B3

Method BLASTX NCBI GI g2160169 BLAST score 194 E value 8.0e-15 Match length 75 % identity

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 227252

Seq. ID LIB3189-025-P1-K1-B4

Method BLASTX NCBI GI g2623310 BLAST score 349 E value 4.0e - 33Match length 100 % identity 67

32438



NCBI Description (AC002409) unknown protein [Arabidopsis thaliana] >gi\_3402721 (AC004261) unknown protein [Arabidopsis

thaliana]

Seq. No. 227253

Seq. ID LIB3189-025-P1-K1-B5

Method BLASTX
NCBI GI 94510373
BLAST score 220
E value 3.0e-28
Match length 82
% identity 80

NCBI Description (AC007017) putative harpin-induced protein [Arabidopsis

thaliana]

Seq. No. 227254

Seq. ID LIB3189-025-P1-K1-B8

Method BLASTX
NCBI GI g2088649
BLAST score 304
E value 1.0e-27
Match length 90
% identity 66

NCBI Description (AF002109) unknown protein [Arabidopsis thaliana]

Seq. No. 227255

Seq. ID LIB3189-025-P1-K1-B9

Method BLASTX
NCBI GI g133409
BLAST score 595
E value 7.0e-62
Match length 129
% identity 88

NCBI Description DNA-DIRECTED RNA POLYMERASE ALPHA CHAIN

>gi\_66962\_pir\_\_RNNTA DNA-directed RNA polymerase (EC
2.7.7.6) alpha chain - common tobacco chloroplast
>gi\_11860\_emb\_CAA77376\_ (Z00044) RNA polymerase alpha
subunit [Nicotiana tabacum] >gi\_225228\_prf\_\_1211235BK RNA

polymerase alpha [Nicotiana tabacum]

Seq. No. 227256

Seq. ID LIB3189-025-P1-K1-C5

Method BLASTX
NCBI GI g167367
BLAST score 259
E value 5.0e-23
Match length 61
% identity 80

NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 227257

Seq. ID LIB3189-025-P1-K1-D3

Method BLASTX
NCBI GI g2605621
BLAST score 382
E value 2.0e-37
Match length 80

32439



```
% identity
NCBI Description (D88619) OSMYB3 [Oryza sativa]
                  227258
Seq. No.
Seq. ID
                  LIB3189-025-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g4538897
                  522
BLAST score
E value
                  3.0e-53
Match length
                  151
% identity
                  64
NCBI Description (AL049482) AX110P-like protein [Arabidopsis thaliana]
Seq. No.
                  227259
Seq. ID
                  LIB3189-025-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g1350944
BLAST score
                  301
E value
                  7.0e-28
Match length
                  63
% identity
                  94
NCBI Description 40S RIBOSOMAL PROTEIN S17
Seq. No.
                  227260
Seq. ID
                  LIB3189-025-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g2961300
BLAST score
                  387
E value
                  1.0e-37
Match length
                  78
                  96
% identity
NCBI Description (AJ225027) ribosomal protein L24 [Cicer arietinum]
Seq. No.
                  227261
Seq. ID
                  LIB3189-025-P1-K1-G8
                  BLASTX
Method
NCBI GI
                  q3851001
BLAST score
                  395
E value
                  2.0e-38
Match length
                  96
% identity
                  81
NCBI Description
                 (AF069909) pyruvate dehydrogenase E1 beta subunit isoform 2
                  [Zea mays]
Seq. No.
                  227262
Seq. ID
                  LIB3189-025-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q2130073
BLAST score
                  387
                  1.0e-37
E value
Match length
                  86
```

% identity 90

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice \( \grace{qi}\_786178\_\text{dbj}\_BAA08845 \) (D50307) aldolase

C-1 [Oryza sativa] >gi\_790970\_dbj\_BAA08830\_ (D50301)

aldolase C-1 [Oryza sativa]

NCBI Description

227268

Seq. No.



```
Seq. No.
                   227263
Seq. ID
                   LIB3189-026-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   g3415117
BLAST score
                   251
E value
                   2.0e-21
Match length
                   71
% identity
                   66
NCBI Description (AF081203) villin 3 [Arabidopsis thaliana]
Seq. No.
                   227264
Seq. ID
                   LIB3189-026-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   g3024126
BLAST score
                   572
E value
                   4.0e-59
Match length
                   118
% identity
                   92
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine
                   synthetase 1 [Catharanthus roseus]
Seq. No.
                   227265
Seq. ID
                   LIB3189-026-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   g140207
BLAST score
                   147
E value
                   6.0e-10
Match length
                   38
% identity
                   63
NCBI Description PROBABLE 40S RIBOSOMAL PROTEIN S9 >gi 102109 pir S12674
                   ribosomal protein S9.e - Trypanosoma brucei >gi_10399_emb_CAA36818_ (X52586) ald orfU protein (AA 1 -
                   190) [Trypanosoma brucei]
Seq. No.
                   227266
Seq. ID
                   LIB3189-026-P1-K1-B4
                   BLASTX
Method
NCBI GI
                   g3603401
BLAST score
                   230
E value
                   1.0e-19
Match length
                   60
% identity
NCBI Description (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]
Seq. No.
                   227267
Seq. ID
                   LIB3189-026-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   g2244867
BLAST score
                   200
E value
                   9.0e-16
Match length
                   101
% identity
                   43
```

(Z97337) hydroxynitrile lyase [Arabidopsis thaliana]

% identity



```
LIB3189-026-P1-K1-B7
Seq. ID
Method
                  BLASTX
                  g3915847
NCBI GI
BLAST score
                  391
E value
                  5.0e-38
Match length
                  85
                  87
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
                  40S ribosomal protein S2 [Arabidopsis thaliana]
Seq. No.
                  227269
Seq. ID
                  LIB3189-026-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  q3785978
BLAST score
                  234
E value
                  1.0e-19
                  91
Match length
% identity
                  56
NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]
Seq. No.
                  227270
Seq. ID
                  LIB3189-026-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g1171965
BLAST score
                  227
E value
                  3.0e-19
Match length
                  52
                  87
% identity
NCBI Description PHOSPHATIDYLINOSITOL 3-KINASE, ROOT ISOFORM (PI3-KINASE)
                  (PTDINS-3-KINASE) (PI3K) (SPI3K-5) >gi 736339 (L27265)
                  phosphatidylinositol 3-kinase [Glycine max]
Seq. No.
                  227271
Seq. ID
                  LIB3189-026-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g1362086
BLAST score
                  195
                 1.0e-15
E value
Match length
                  46
                  87
% identity
NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_2129919_pir__$65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                  [Catharanthus roseus]
Seq. No.
                  227272
Seq. ID
                  LIB3189-026-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g3650032
BLAST score
                  141
E value
                  3.0e-09
Match length
                  38
```

NCBI Description (AC005396) gibberellin-regulated protein GAST1-like

Match length

% identity

49

88



## [Arabidopsis thaliana]

```
Seq. No.
                  227273
Seq. ID
                  LIB3189-026-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g267122
BLAST score
                  172
E value
                  8.0e-13
Match length
                  50
% identity
                  66
NCBI Description
                  THIOREDOXIN H-TYPE (TRX-H) >gi 478400 pir JQ2242
                  thioredoxin h - Arabidopsis thaliana
                  >gi_16552_emb_CAA78462_ (Z14084) Thioredoxin H [Arabidopsis
                  thaliana] >gi_1388080 (U35827) thioredoxin h [Arabidopsis
                  thalianal
Seq. No.
                  227274
Seq. ID
                  LIB3189-026-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g942594
BLAST score
                  196
E value
                  1.0e-15
Match length
                  49
% identity
                  78
NCBI Description (U30456) heat shock cognate protein [Urechis caupo]
Seq. No.
                  227275
Seq. ID
                  LIB3189-026-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g1076696
BLAST score
                  174
E value
                  5.0e-13
Match length
                  42
% identity
                  74
NCBI Description cyprosin - cardoon >gi 556819 emb CAA57510 (X81984)
                  cyprosin [Cynara cardunculus]
Seq. No.
                  227276
Seq. ID
                  LIB3189-026-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g3024017
BLAST score
                  377
E value
                  3.0e-38
Match length
                  95
% identity
                  81
NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)
                  (EIF-4C) > gi_2565421 (AF026804) eukaryotic translation
                  initiation factor eIF-1A [Onobrychis viciifolia]
Seq. No.
                  227277
                  LIB3189-026-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q267069
BLAST score
                  238
E value
                  2.0e-20
```

% identity

86

NCBI Description (Z73948) RAB8E [Lotus japonicus]



```
NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
                    tubulin alpha chain - Arabidopsis thaliana >gi 166914
                    (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                    (M84697) alpha-4 tubulin [Arabidopsis thaliana]
 Seq. No.
                   227278
                   LIB3189-026-P1-K1-H8
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g3451072
                   230
 BLAST score
 E value
                    3.0e-19
 Match length
                   69
 % identity
 NCBI Description (AL031326) putative protein [Arabidopsis thaliana]
                   227279
 Seq. No.
                   LIB3189-027-P1-K1-A6
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2388574
 BLAST score
                   151
 E value
                    2.0e-10
 Match length
                    46
 % identity
                    65
 NCBI Description (AC000098) Strong similarity to Phalaenopsis homeobox
                   protein (gb U34743). [Arabidopsis thaliana]
Seq. No.
                    227280
                   LIB3189-027-P1-K1-B3
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g2062167
 BLAST score
                   354
 E value
                    3.0e-35
 Match length
                   107
 % identity
                    73
 NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis
                    thaliana]
                    227281
 Seq. No.
 Seq. ID
                   LIB3189-027-P1-K1-B6
 Method
                   BLASTX
 NCBI GI
                    g3420008
 BLAST score
                   193
                    7.0e-15
 E value
 Match length
                   77
 % identity
                    47
 NCBI Description (AF000307) steroid sulfotransferase 3 [Brassica napus]
                   227282
 Seq. No.
 Seq. ID
                   LIB3189-027-P1-K1-C1
 Method
                   BLASTX
 NCBI GI
                   g1370198
 BLAST score
                   239
 E value
                   1.0e-20
 Match length
                   57
```

Match length

% identity

64

59



```
Seq. No.
                   227283
Seq. ID
                   LIB3189-027-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   g2499610
BLAST score
                   571
E value
                   5.0e-59
Match length
                   148
% identity
                   78
NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 6 (MAP KINASE 6)
                   (ATMPK6) >gi_629547_pir__S40472 mitogen-activated protein kinase 6 (EC 2.7.1.-) - Arabidopsis thaliana
                   >gi 457404 dbj BAA04869 (D21842) MAP kinase [Arabidopsis
                   thaliana] >gi 2281091 (AC002333) MAP Kinase 6 [Arabidopsis
                   thaliana!
Seq. No.
                   227284
Seq. ID
                   LIB3189-027-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   g167367
BLAST score
                   290
E value
                   3.0e-26
                   58
Match length
% identity
                   95
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                   227285
Seq. ID
                   LIB3189-027-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   g1707955
BLAST score
                   557
E value
                   2.0e-57
Match length
                   111
                   95
% identity
NCBI Description GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME 1
                   (GLUTAMATE--AMMONIA LIGASE) >gi 1134896 emb CAA63981
                   (X94320) glutamine synthetase [Vitis vinifera]
Seq. No.
                   227286
Seq. ID
                   LIB3189-027-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   g2961377
BLAST score
                   185
E value
                   7.0e-14
Match length
                   122
% identity
NCBI Description
                  (AL022141) putative receptor protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   227287
Seq. ID
                   LIB3189-027-P1-K1-F8
Method
                   BLASTX
                   q3337361
NCBI GI
BLAST score
                   213
E value
                   5.0e-17
```

NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. ID

Method



```
Seq. No.
                   227288
Seq. ID
                   LIB3189-027-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   g2340166
BLAST score
                   212
E value
                   6.0e-17
Match length
                   92
% identity
                   52
NCBI Description
                  (AF008124) glutathione S-conjugate transporting ATPase
                   [Arabidopsis thaliana] >gi_2459949 (AF008125) multidrug
                   resistance-associated protein homolog [Arabidopsis
                   thalianal
Seq. No.
                   227289
Seq. ID
                  LIB3189-027-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g4098129
BLAST score
                  446
E value
                   2.0e-44
Match length
                  83
% identity
                  100
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
Seq. No.
                  227290
Seq. ID
                  LIB3189-027-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g1694621
BLAST score
                  187
E value
                   4.0e-14
                  76
Match length
% identity
                  53
NCBI Description (D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]
Seq. No.
                  227291
Seq. ID
                  LIB3189-027-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g2961300
BLAST score
                  483
E value
                  8.0e-49
Match length
                  117
% identity
                  80
NCBI Description (AJ225027) ribosomal protein L24 [Cicer arietinum]
Seq. No.
                  227292
Seq. ID
                  LIB3189-027-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g2661840
BLAST score
                  366
                  5.0e-35
E value
Match length
                  98
% identity
                  68
NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]
Seq. No.
                  227293
```

32446

LIB3189-027-P1-K1-H5

BLASTX

BLAST score

E value

228

3.0e-19



```
NCBI GI
                   g3914394
BLAST score
                   292
E value
                   2.0e-36
Match length
                   97
                   74
% identity
NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
                   (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
                  >gi_2118335 pir S60473 phosphoglycerate mutase (EC
                   5.4.2.1) - common ice plant >gi_602426 (U16021)
                  phosphoglyceromutase [Mesembryanthemum crystallinum]
Seq. No.
                  227294
Seq. ID
                  LIB3189-027-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g3986695
BLAST score
                  537
E value
                  4.0e-55
Match length
                  121
% identity
                  90
NCBI Description (AF101423) ribosomal protein L12 [Cichorium intybus]
Seq. No.
                  227295
Seq. ID
                  LIB3189-027-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g1694621
BLAST score
                  387
E value
                  2.0e-37
Match length
                  115
% identity
NCBI Description (D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]
Seq. No.
                  227296
Seq. ID
                  LIB3189-028-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  q1293835
BLAST score
                  225
E value
                  2.0e-18
Match length
                  135
% identity
                  33
NCBI Description (U56965) C15H9.5 gene product [Caenorhabditis elegans]
Seq. No.
                  227297
Seq. ID
                  LIB3189-028-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g1917019
BLAST score
                  559
E value
                  1.0e-57
Match length
                  118
% identity
                  89
NCBI Description (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
Seq. No.
                  227298
Seq. ID
                  LIB3189-028-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g3785989
```

NCBI Description

bisulcatus]



```
Match length
                  68
                  68
% identity
NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]
                  227299
Seq. No.
Seq. ID
                  LIB3189-028-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g167367
BLAST score
                  534
E value
                  1.0e-54
                  126
Match length
                  84
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                  227300
Seq. No.
Seq. ID
                  LIB3189-028-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g2829204
BLAST score
                  189
E value
                  1.0e-14
Match length
                  35
                  100
% identity
NCBI Description (AF044204) lipid transfer protein precursor [Gossypium
                  hirsutum
                  227301
Seq. No.
Seq. ID
                  LIB3189-028-P1-K1-C7
                  BLASTX
Method
NCBI GI
                  g71498
BLAST score
                  261
E value
                  1.0e-22
Match length
                  116
% identity
                  50
NCBI Description heat shock protein 17.7 - garden pea
                  227302
Seq. No.
Seq. ID
                  LIB3189-028-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g1364059
BLAST score
                  231
E value
                  3.0e-19
Match length
                  109
% identity
                  44
NCBI Description
                  dioscorin class A precursor - Dioscorea cayenensis
                  >gi_433463_emb_CAA53781 (X76187) storage protein
                  [Dioscorea cayenensis]
                  227303
Seq. No.
Seq. ID
                  LIB3189-028-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q4006848
BLAST score
                  153
E value
                  5.0e-10
Match length
                  37
% identity
                  78
```

32448

(AJ131433) selenocysteine methyltransferase [Astragalus

Match length

% identity

133

92



```
Seq. No.
                  227304
Seq. ID
                  LIB3189-028-P1-K1-D7
                  BLASTX
Method
NCBI GI
                  g3420239
BLAST score
                  153
E value
                   2.0e-10
Match length
                  31
                  97
% identity
NCBI Description (AF059484) actin [Gossypium hirsutum]
                  227305
Seq. No.
Seq. ID
                  LIB3189-028-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g4508073
BLAST score
                  309
E value
                   2.0e-28
Match length
                  95
% identity
                  62
NCBI Description (AC005882) 43220 [Arabidopsis thaliana]
                  227306
Seq. No.
Seq. ID
                  LIB3189-028-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g3288113
BLAST score
                  386
                  2.0e-37
E value
Match length
                  106
                  74
% identity
NCBI Description (Z97067) elongation factor 1-beta [Beta vulgaris]
                  227307
Seq. No.
Seq. ID
                  LIB3189-028-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g1076708
BLAST score
                  643
E value
                  2.0e-67
Match length
                  129
% identity
                   28
NCBI Description seed tetraubiquitin - common sunflower
                   >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max]
                  >gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max] >gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin
                   [Helianthus annuus] >gi_994785_dbj BAA05085 (D26092)
                   Ubiquitin [Glycine max] >gi 4263514 gb AAD15340 (AC004044)
                   putative polyubiquitin [Arabidopsis thaliana]
                   >gi 1096513 prf 2111434A tetraubiquitin [Helianthus
                   annuus]
                   227308
Seq. No.
                  LIB3189-028-P1-K1-F6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2129499
BLAST score
                  655
E value
                  7.0e-69
```

Match length

% identity

77

10



```
fiber protein E6 (clone CKE6-4A) - upland cotton
NCBI Description
                  >gi 1000086 (U30506) E6 [Gossypium hirsutum]
Seq. No.
                  227309
                  LIB3189-028-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g167367
BLAST score
                  666
E value
                  3.0e-70
Match length
                  125
                  98
% identity
NCBI Description
                 (L08199) peroxidase [Gossypium hirsutum]
                  227310
Seq. No.
Seq. ID
                  LIB3189-028-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  q1762945
BLAST score
                  347
E value
                  8.0e-33
Match length
                  103
% identity
                  61
NCBI Description
                  (U66269) ORF; able to induce HR-like lesions [Nicotiana
                  tabacum]
Seq. No.
                  227311
                  LIB3189-028-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3023751
BLAST score
                  499
                  1.0e-50
E value
Match length
                  136
                  71
% identity
NCBI Description
                  70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS
                  ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383
                  peptidylprolyl isomerase (EC 5.2.1.8) - wheat
                  >gi_854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase
                   [Triticum aestivum]
Seq. No.
                  227312
Seq. ID
                  LIB3189-028-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g4193388
BLAST score
                  280
E value
                  4.0e-25
Match length
                  80
% identity
                  69
NCBI Description
                  (AF091455) translationally controlled tumor protein [Hevea
                  brasiliensis]
                  227313
Seq. No.
Seq. ID
                  LIB3189-028-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g1304128
BLAST score
                  304
E value
                  6.0e-28
```

32450





```
NCBI Description (D63791) polyubiquitin [Homo sapiens]
Seq. No.
                  227314
Seq. ID
                  LIB3189-028-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g2262158
BLAST score
                  333
E value
                  4.0e-31
Match length
                  126
% identity
                  58
NCBI Description (AC002329) putative mitochondrial phosphate translocator
                  protein [Arabidopsis thaliana]
Seq. No.
                  227315
Seq. ID
                  LIB3189-028-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g992706
BLAST score
                  528
E value
                  3.0e-54
Match length
                  113
% identity
                  91
NCBI Description (U33758) UBC13 [Arabidopsis thaliana]
Seq. No.
                  227316
Seq. ID
                  LIB3189-028-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g730583
BLAST score
                  241
E value
                  2.0e-20
Match length
                  62
% identity
                  77
NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P2 >gi_551267_emb_CAA55047
                  (X78213) 60s acidic ribosomal protein P2 [Parthenium
                  argentatum]
Seq. No.
                  227317
Seq. ID
                  LIB3189-028-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g1402878
BLAST score
                  241
E value
                  2.0e-20
Match length
                  86
% identity
                  56
NCBI Description (X98130) unknown [Arabidopsis thaliana]
Seq. No.
                  227318
Seq. ID
                  LIB3189-028-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g4325338
BLAST score
                  499
E value
                  1.0e-50
Match length
                  118
% identity
                  76
NCBI Description
                 (AF128392) No definition line found [Arabidopsis thaliana]
Seq. No.
```

32451

227319

LIB3189-028-P1-K1-H3

Seq. ID



```
Method
                   BLASTX
NCBI GI
                   g3935145
BLAST score
                   231
E value
                   3.0e-19
                  95
Match length
                   50
% identity
NCBI Description (AC005106) T25N20.9 [Arabidopsis thaliana]
Seq. No.
                   227320
Seq. ID
                  LIB3189-028-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g1332579
BLAST score
                  189
E value
                   2.0e-14
Match length
                  83
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
Seq. No.
                   227321
Seq. ID
                  LIB3189-028-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g2129735
BLAST score
                  349
E value
                   4.0e-33
Match length
                  113
% identity
                   57
NCBI Description serine/threonine-specific kinase (EC 2.7.1.-) precursor -
                  Arabidopsis thaliana >gi_1405837_emb_CAA62824_ (X91630)
                   receptor-like kinase [Arabidopsis thaliana] >qi 2150023
                   (AF001168) receptor-like kinase LECRK1 [Arabidopsis
                  thaliana]
Seq. No.
                  227322
Seq. ID
                  LIB3189-028-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g2980767
BLAST score
                  220
E value
                  5.0e-24
                  111
Match length
% identity
                  62
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]
Seq. No.
                  227323
Seq. ID
                  LIB3189-030-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g2369766
BLAST score
                  378
E value
                  1.0e-36
Match length
                  106
% identity
NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]
Seq. No.
                  227324
```

Seq. ID LIB3189-030-P1-K1-A4

Method BLASTX NCBI GI q3869088 BLAST score 582



```
E value
                   2.0e-60
Match length
                  117
% identity
                  96
NCBI Description
                 (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
Seq. No.
                  227325
Seq. ID
                  LIB3189-030-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g730645
BLAST score
                  171
E value
                  1.0e-12
Match length
                  38
% identity
                  89
NCBI Description
                  40S RIBOSOMAL PROTEIN S15 >gi_629556_pir S43412 ribosomal
                  protein S15 - Arabidopsis thaliana >gi 313152 emb CAA80679
                   (Z23161) ribosomal protein S15 [Arabidopsis thaliana]
                  >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15
                   [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104)
                  Strong similarity to Oryza 40S ribosomal protein S15. ESTs
                   gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  227326
Seq. ID
                  LIB3189-030-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q4538913
BLAST score
                  244
E value
                  8.0e-21
Match length
                  62
% identity
                  79
NCBI Description (AL049482) putative protein [Arabidopsis thaliana]
Seq. No.
                  227327
Seq. ID
                  LIB3189-030-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g3204125
BLAST score
                  345
E value
                  2.0e-32
Match length
                  83
% identity
                  81
NCBI Description
                 (AJ006766) putative Pi starvation-induced protein [Cicer
                  arietinum]
Seq. No.
                  227328
Seq. ID
                  LIB3189-030-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g1843527
BLAST score
                  293
E value
                  8.0e-27
Match length
                  74
% identity
```

NCBI Description (U73747) annexin [Gossypium hirsutum]

Seq. No. 227329

Seq. ID LIB3189-030-P1-K1-B8

Method BLASTX NCBI GI g464981



BLAST score E value 2.0e-21 Match length 48 % identity 96

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 227330

Seq. ID LIB3189-030-P1-K1-C11

Method BLASTX NCBI GI g464621 BLAST score 215 E value 1.0e-17 66 Match length 59 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir S28586

ribosomal protein ML16 - common ice plant >gi\_19539\_emb\_CAA49175\_ (X69378) ribosomal protein YL16

[Mesembryanthemum crystallinum]

Seq. No. 227331

Seq. ID LIB3189-030-P1-K1-C12

Method BLASTX NCBI GI q3882081 BLAST score 491 E value 9.0e-50 Match length 101 % identity 36

NCBI Description (AJ012552) polyubiquitin [Vicia faba]

Seq. No. 227332

Seq. ID LIB3189-030-P1-K1-C3

Method BLASTX NCBI GI g2661840 BLAST score 373 E value 9.0e-36 Match length 99 % identity 72

NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]

Seq. No. 227333

Seq. ID LIB3189-030-P1-K1-C4

Method BLASTX q3421140 NCBI GI BLAST score 338 E value 8.0e-32 Match length 118 % identity

NCBI Description (AF045668) arginine decarboxylase [Polanisia dodecandra]

Seq. No. 227334

Seq. ID LIB3189-030-P1-K1-D1

Method BLASTX NCBI GI q4008159 BLAST score 517 E value 1.0e-52



```
Match length
                  139
% identity
                  94
NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]
Seq. No.
                  227335
Seq. ID
                  LIB3189-030-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  q124226
BLAST score
                  332
E value
                  4.0e-31
                  70
Match length
% identity
                  93
NCBI Description INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D)
                  >gi_100278 pir S21059 translation initiation factor
                  eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_
                   (X63542) eukaryotic initiation factor 5A (2) [Nicotiana
                  plumbaginifolia]
Seq. No.
                  227336
Seq. ID
                  LIB3189-030-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q4406372
BLAST score
                  445
E value
                  3.0e-44
Match length
                  139
% identity
                  65
NCBI Description (AF109156) thiosulfate sulfurtransferase [Datisca
                  glomerata]
Seq. No.
                  227337
Seq. ID
                  LIB3189-030-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g4455150
BLAST score
                  296
                  7.0e-27
E value
Match length
                  126
% identity
                  48
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
Seq. No.
                  227338
Seq. ID
                  LIB3189-030-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g115492
BLAST score
                  560
E value
                  9.0e-58
Match length
                  112
% identity
                  52
NCBI Description CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)
                  calmodulin-related protein [Petunia hybrida]
Seq. No.
                  227339
Seq. ID
                  LIB3189-030-P1-K1-E12
Method
                  BLASTX
```

NCBI GI g3334115 BLAST score 163 E value 1.0e-11 Match length 48



```
% identity
 NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >qi 2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                   hirsutum]
 Seq. No.
                   227340
 Seq. ID
                   LIB3189-030-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   g1174592
BLAST score
                   659
E value
                   3.0e-69
Match length
                   123
% identity
                   99
NCBI Description TUBULIN ALPHA-1 CHAIN >gi 2119270_pir S60233 alpha-tubulin
                   - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                   sativum]
Seq. No.
                   227341
Seq. ID
                   LIB3189-030-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g2462746
BLAST score
                   279
E value
                   4.0e-25
Match length
                   74
                  72
 % identity
NCBI Description (AC002292) Similar to ATP-citrate-lyase [Arabidopsis
                   thaliana]
                   227342
Seq. No.
Seq. ID
                   LIB3189-030-P1-K1-E6
                   BLASTX
Method
NCBI GI
                   q2829204
BLAST score
                   189
E value
                   1.0e-14
Match length
                   35
 % identity
                   100
NCBI Description (AF044204) lipid transfer protein precursor [Gossypium
                   hirsutum]
Seq. No.
                   227343
Seq. ID
                   LIB3189-030-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   g3023751
BLAST score
                   470
E value
                   2.0e-47
Match length
                   110
% identity
                   31
```

NCBI Description 70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) >qi 1076772 pir S55383

peptidylprolyl isomerase (EC 5.2.1.8) - wheat

>gi\_854626\_emb\_CAA60505\_ (X86903) peptidylprolyl isomerase

[Triticum aestivum]

Seq. No. 227344

Seq. ID LIB3189-030-P1-K1-F1

Method BLASTX



```
NCBI GI
                   q3355617
BLAST score
                   216
E value
                   2.0e-17
Match length
                   56
% identity
                   75
NCBI Description (AJ000229) unnamed protein product [Hordeum vulgare]
                   227345
Seq. No.
Seq. ID
                   LIB3189-030-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   q1351408
BLAST score
                   403
E value
                   2.0e-39
Match length
                   98
% identity
                   76
                   VACUOLAR PROCESSING ENZYME PRECURSOR (VPE)
NCBI Description
                   >gi_1076563_pir__S51117 cystein proteinase - sweet orange >gi_633185_emb_CAA87720_ (Z47793) cystein proteinase (by
                   similarity) [Citrus sinensis] >gi_1588548_prf__2208463A
                   vascular processing protease [Citrus sinensis]
                   227346
Seq. No.
Seq. ID
                   LIB3189-030-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   q1703574
BLAST score
                   339
E value
                   8.0e-32
Match length
                   142
% identity
                   46
NCBI Description (U80437) C43E11.9 [Caenorhabditis elegans]
Seq. No.
                   227347
                   LIB3189-030-P1-K1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2924520
BLAST score
                   544
E value
                   8.0e-56
Match length
                   144
                   74
% identity
                   (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                   [Arabidopsis thaliana]
                   227348
Seq. No.
Seq. ID
                   LIB3189-030-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   g267082
BLAST score
                   523
E value
                   2.0e-53
                   100
Match length
                   99
% identity
                   TUBULIN BETA-8 CHAIN >gi 320189 pir JQ1592 tubulin beta-8
NCBI Description
                   chain - Arabidopsis thaliana >gi 166908 (M84705) beta-8
                   tubulin [Arabidopsis thaliana]
```

Seq. No. 227349

Seq. ID LIB3189-030-P1-K1-F7

Method BLASTX



87

61

Match length % identity

```
NCBI GI
                  g3738338
BLAST score
                  188
                  2.0e-14
E value
                  79
Match length
                  57
% identity
                  (AC005170) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  227350
Seq. ID
                  LIB3189-030-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g3184082
BLAST score
                  290
E value
                  5.0e-26
Match length
                  148
% identity
                  42
NCBI Description (AL023781) N-terminal acetyltransferase 1
                  [Schizosaccharomyces pombe]
Seq. No.
                  227351
                  LIB3189-030-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2564066
BLAST score
                  222
E value
                  3.0e-18
Match length
                  80
% identity
                  55
NCBI Description (D45900) LEDI-3 protein [Lithospermum erythrorhizon]
Seq. No.
                  227352
Seq. ID
                  LIB3189-030-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q1076738
BLAST score
                  531
E value
                  3.0e-54
Match length
                  103
                  94
% identity
NCBI Description beta-tubulin R2242 - rice
Seq. No.
                  227353
Seq. ID
                  LIB3189-030-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g3549648
BLAST score
                  386
E value
                  2.0e-37
Match length
                  120
% identity
                  62
NCBI Description (AJ010728) alpha amylase [Avena fatua]
Seq. No.
                  227354
Seq. ID
                  LIB3189-030-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g3913633
BLAST score
                  157
E value
                  3.0e-18
```



NCBI Description HYPOTHETICAL PROTEIN F8A5.25 >gi 2462742 (AC002292) Unknown protein [Arabidopsis thaliana]

Seq. No. 227355

LIB3189-030-P1-K1-H11 Seq. ID

Method BLASTX NCBI GI g2129499 BLAST score 353 E value 1.0e-41Match length 129 % identity 71

NCBI Description fiber protein E6 (clone CKE6-4A) - upland cotton

>gi 1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No. 227356

Seq. ID LIB3189-030-P1-K1-H12

Method BLASTX NCBI GI q1935912 BLAST score 161 E value 6.0e-11Match length 93 39 % identity

NCBI Description (U77346) LLS1 [Zea mays]

227357 Seq. No.

Seq. ID LIB3189-030-P1-K1-H3

Method BLASTX NCBI GI q464981 BLAST score 480 E value 3.0e-48Match length 101 % identity 92

UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN NCBI Description

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 388207 (L23762)

ubiquitin carrier protein [Lycopersicon esculentum]

227358 Seq. No.

LIB3189-030-P1-K1-H5 Seq. ID

Method BLASTX NCBI GI g2529229 BLAST score 159 E value 5.0e-11 51 Match length % identity

NCBI Description (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]

Seq. No. 227359

Seq. ID LIB3189-030-P1-K1-H6

Method BLASTX NCBI GI q2129499 BLAST score 707 E value 6.0e-75 Match length 142 93 % identity

NCBI Description fiber protein E6 (clone CKE6-4A) - upland cotton

>gi\_1000086 (U30506) E6 [Gossypium hirsutum]



```
227360
Seq. No.
Seq. ID
                   LIB3189-031-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   g1172873
BLAST score
                   444
E value
                   4.0e-44
Match length
                   147
% identity
                   56
NCBI Description CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                   precursor - Arabidopsis thaliana >gi 435619 dbj BAA02374
                   (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.
                   227361
Seq. ID
                   LIB3189-031-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   g1076316
BLAST score
                   158
E value
                   1.0e-10
Match length
                   62
                   45
% identity
NCBI Description
                   drought-induced protein Di19 - Arabidopsis thaliana
                   >gi 469110 emb CAA55321 (X78584) Di19 [Arabidopsis
                   thaliana]
                   227362
Seq. No.
Seq. ID
                   LIB3189-031-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   g267069
BLAST score
                   361
E value
                   1.0e-34
Match length
                   71
% identity
                   94
NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
                   tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                   227363
Seq. ID
                   LIB3189-031-P1-K1-A4
                   BLASTX
Method
NCBI GI
                   g3128228
BLAST score
                   144
E value
                   1.0e-09
Match length
                   40
% identity
NCBI Description
                  (AC004077) putative ribosomal protein L18A [Arabidopsis
                   thaliana] >gi 3337376 (AC004481) putative ribosomal protein
                   L18A [Arabidopsis thaliana]
Seq. No.
                   227364
                   LIB3189-031-P1-K1-A6
Seq. ID
```

Method BLASTX

Method BLASTX
NCBI GI g1619297
BLAST score 451
E value 4.0e-45
Match length 87



% identity NCBI Description (Y08490) alpha-tubulin 2 [Hordeum vulgare] 227365 Seq. No. LIB3189-031-P1-K1-A8 Seq. ID BLASTX Method NCBI GI g267069 BLAST score 296 E value 3.0e-27 Match length 56 95 % identity TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594 NCBI Description tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana] Seq. No. 227366 Seq. ID LIB3189-031-P1-K1-A9 Method BLASTX NCBI GI g4567274 BLAST score 530 E value 2.0e-54 Match length 110 % identity 85 NCBI Description (AC006841) putative cysteine proteinase precursor [Arabidopsis thaliana] 227367 Seq. No. LIB3189-031-P1-K1-B11 Seq. ID Method BLASTX NCBI GI g3047085 BLAST score 382 E value 7.0e-37 Match length 124 % identity 61 NCBI Description (AF058914) No definition line found [Arabidopsis thaliana] 227368 Seq. No. Seq. ID LIB3189-031-P1-K1-B3 BLASTX Method NCBI GI g2369766 BLAST score 294 E value 3.0e-44Match length 139 % identity NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi] 227369 Seq. No. Seq. ID LIB3189-031-P1-K1-C10 Method BLASTX NCBI GI g3135257

BLAST score 146 4.0e-09 E value

Match length 84 % identity

NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                   227370
Seq. ID
                  LIB3189-031-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  q267069
BLAST score
                  648
                  5.0e-68
E value
Match length
                  120
% identity
                  98
NCBI Description
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  227371
Seq. No.
Seq. ID
                  LIB3189-031-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q4567274
BLAST score
                  589
E value
                  3.0e-61
Match length
                  119
% identity
                  87
NCBI Description
                  (AC006841) putative cysteine proteinase precursor
                   [Arabidopsis thaliana]
                  227372
Seq. No.
Seq. ID
                  LIB3189-031-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  a267075
BLAST score
                  677
                  2.0e-71
E value
Match length
                  132
                   93
% identity
                  TUBULIN BETA-2 CHAIN >gi 388254 emb CAA38614 (X54845)
NCBI Description
                  beta-tubulin 2 [Pisum sativum]
Seq. No.
                   227373
Seq. ID
                  LIB3189-031-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q3158376
BLAST score
                   259
E value
                   2.0e-29
Match length
                  100
% identity
                   68
NCBI Description (AF035385) unknown [Arabidopsis thaliana]
Seq. No.
                   227374
Seq. ID
                  LIB3189-031-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  q112717
BLAST score
                   265
E value
                   4.0e-23
                  115
Match length
% identity
                   43
```

21 KD PROTEIN PRECURSOR (1.2 PROTEIN) >gi\_82050\_pir\_\_S10911 NCBI Description hypothetical protein precursor - carrot

>gi 18312 emb CAA36642 (X52395) precursor polypeptide (AA

-22 to 171) [Daucus carota]



```
Seq. No.
                  227375
Seq. ID
                  LIB3189-031-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g1732511
BLAST score
                  477
E value
                  6.0e-48
Match length
                  103
% identity
                  85
NCBI Description
                  (U62742) Ran binding protein 1 homolog [Arabidopsis
                  thaliana]
                  227376
Seq. No.
Seq. ID
                  LIB3189-031-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q2982322
BLAST score
                  212
E value
                  1.0e-17
Match length
                  46
% identity
                  87
NCBI Description (AF051246) probable proteasome subunit [Picea mariana]
Seq. No.
                  227377
Seq. ID
                  LIB3189-031-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  q3790102
BLAST score
                  189
E value
                  1.0e-14
Match length
                  43
% identity
                  81
                 (AF095521) pyrophosphate-dependent phosphofructokinase
NCBI Description
                  alpha subunit [Citrus X paradisi]
Seq. No.
                  227378
Seq. ID
                  LIB3189-031-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  q4049349
BLAST score
                  206
E value
                  8.0e-17
Match length
                  97
                   53
% identity
                 (AL034567) ubiquinol-cytochrome c reductase-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  227379
Seq. ID
                  LIB3189-031-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g129248
BLAST score
                  184
E value
                  1.0e-13
                  100
Match length
                  23
% identity
NCBI Description ORGAN SPECIFIC PROTEIN S2 >gi 72318 pir KNPMS2 protein S2
                  - garden pea >gi 295831 emb CAA35944 (\overline{X5}1595) S2 protein
                   [Pisum sativum]
```

227380

Seq. No.



```
LIB3189-031-P1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2129499
BLAST score
                   641
E value
                   3.0e-67
Match length
                   132
% identity
                   91
NCBI Description fiber protein E6 (clone CKE6-4A) - upland cotton
                   >gi_1000086 (U30506) E6 [Gossypium hirsutum]
Seq. No.
                   227381
Seq. ID
                   LIB3189-031-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   q464849
BLAST score
                   402
E value
                   2.0e-39
Match length
                   98
% identity
                   83
NCBI Description
                  TUBULIN ALPHA CHAIN >gi_486847_pir__$36232 tubulin alpha
                   chain - almond >gi_2041\overline{3} emb_CAA47\overline{63}5_ (X67162)
                   alpha-tubulin [Prunus dulcis]
Seq. No.
                   227382
Seq. ID
                   LIB3189-031-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   q1351856
BLAST score
                   366
E value
                   3.0e-35
Match length
                   94
                   79
% identity
NCBI Description ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
                   (ACONITASE) >gi_868003_dbj_BAA06108 (D29629) aconitase
                   [Cucurbita sp.]
Seq. No.
                   227383
Seq. ID
                  LIB3189-031-P1-K1-F6
Method
                   BLASTX
NCBI GI
                   q3348122
BLAST score
                  295
E value
                   1.0e-28
                  67
Match length
                   81
% identity
NCBI Description (AF078670) tubulin alpha chain [Artemia franciscana]
Seq. No.
                   227384
Seq. ID
                  LIB3189-031-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  q2129770
BLAST score
                  191
E value
                   2.0e-14
Match length
                   57
% identity
NCBI Description
                  xyloglucan endotransglycosylase-related protein XTR-2 -
```

Arabidopsis thaliana >gi 1244756 (U43487) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana]

>gi\_2154611\_dbj BAA20290 (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Method

NCBI GI

BLASTX

g3114901



```
Seq. No.
                   227385
Seq. ID
                   LIB3189-031-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   g267069
BLAST score
                   268
E value
                   5.0e-24
Match length
                   52
% identity
                   92
NCBI Description
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
                   tubulin alpha chain - Arabidopsis thaliana > \overline{gi}_1166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                   227386
Seq. ID
                   LIB3189-031-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   g121344
BLAST score
                   219
E value
                   1.0e-22
Match length
                   79
% identity
                   70
NCBI Description GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR
                   (GLUTAMATE-AMMONIA LIGASE) (CHLOROPLAST GS2)
                   >gi_68597_pir__AJPMQ2 glutamate--ammonia ligase (EC
                   6.3.1.2) delta precursor, chloroplast - garden pea
                   >gi 169059 (M20664) glutamine synthetase (chloroplast GS2)
                   (EC 6.3.1.2) [Pisum sativum]
Seq. No.
                   227387
Seq. ID
                   LIB3189-031-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   q2632252
BLAST score
                   273
E value
                   3.0e-24
                   74
Match length
% identity
NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor]
Seq. No.
                   227388
Seq. ID
                   LIB3189-031-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   g120674
BLAST score
                   158
E value
                   6.0e-15
Match length
                   74
% identity
                   72
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_66015_pir__DENDG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - common buttercup
                   >gi 21066 emb CAA42903 (X60345) qlyceraldehyde
                   3-phosphate dehydrogenase [Ranunculus acris]
Seq. No.
                   227389
Seq. ID
                   LIB3189-031-P1-K1-H12
```



```
BLAST score 140
E value 4.0e-09
Match length 32
% identity 81
NCBI Description (AJ0058
>gi_311
balsami

Seq. No. 227390
Seq. ID LIB3189
```

(AJ005804) pcbere [Populus balsamifera subsp. trichocarpa] >gi 3114905 emb CAA06709 (AJ005806) pceberh [Populus

balsamifera subsp. trichocarpa]

Seq. ID LIB3189-031-P1-K1-H4 Method BLASTX

NCBI GI g232024
BLAST score 718
E value 2.0e-76
Match length 134
% identity 100

NCBI Description PROTEIN E6 >gi\_421806\_pir\_\_A46130 fiber protein - upland cotton >gi\_2129498\_pir\_\_S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi\_167323 (M92051) 5' start site

is putative; putative [Gossypium hirsutum] >gi\_1000084

(U30505) E6 [Gossypium hirsutum]

Seq. No. 227391

Seq. ID LIB3189-031-P1-K1-H8

Method BLASTX
NCBI GI g2842490
BLAST score 174
E value 2.0e-12
Match length 68
% identity 46

NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No. 227392

Seq. ID LIB3189-032-P1-K1-A11

Method BLASTX
NCBI GI g120669
BLAST score 520
E value 4.0e-53
Match length 103
% identity 94

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 227393

Seq. ID LIB3189-032-P1-K1-A12

Method BLASTX
NCBI GI g2129499
BLAST score 590
E value 3.0e-61
Match length 132
% identity 83

NCBI Description fiber protein E6 (clone CKE6-4A) - upland cotton

>gi\_1000086 (U30506) E6 [Gossypium hirsutum]



```
Seq. No.
                  227394
                  LIB3189-032-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2078350
BLAST score
                  160
                  2.0e-11
E value
Match length
                  44
                  82
% identity
NCBI Description (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                  227395
                  LIB3189-032-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2465015
BLAST score
                  165
                  2.0e-11
E value
Match length
                  128
                  35
% identity
NCBI Description (AJ001449) ripening-induced protein [Fragaria vesca]
                  227396
Seq. No.
Seq. ID
                  LIB3189-032-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  q3176098
BLAST score
                  463
E value
                  2.0e-46
Match length
                  129
                  26
% identity
NCBI Description (Y15036) annexin [Medicago truncatula]
Seq. No.
                  227397
                  LIB3189-032-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334405
BLAST score
                  605
E value
                  5.0e-63
                  128
Match length
% identity
                  98
NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
                  >gi 2267583 (AF009338) vacuolar H+-ATPase subunit E
                  [Gossypium hirsutum]
                  227398
Seq. No.
                  LIB3189-032-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2497743
                  177
BLAST score
                  5.0e-13
E value
                  57
Match length
                  61
% identity
NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3)
                  >gi 999315 bbs 166991 (S78173) LTP=lipid transfer protein
                   [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa]
                   [Gossypium hirsutum]
```

Seq. No. 227399

Seq. ID LIB3189-032-P1-K1-B7

% identity

81



```
BLASTX
Method
NCBI GI
                   q2129499
BLAST score
                   611
E value
                   9.0e-64
Match length
                   130
                   88
% identity
                  fiber protein E6 (clone CKE6-4A) - upland cotton
NCBI Description
                   >gi_1000086 (U30506) E6 [Gossypium hirsutum]
                   227400
Seq. No.
Seq. ID
                   LIB3189-032-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   q4539335
BLAST score
                   179
E value
                   2.0e-13
Match length
                   97
                   35
% identity
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
Seq. No.
                   227401
                   LIB3189-032-P1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3643603
BLAST score
                   367
                   4.0e-35
E value
Match length
                   83
% identity
                   86
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
                   227402
Seq. No.
Seq. ID
                   LIB3189-032-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   g1707017
BLAST score
                   137
E value
                   1.0e-08
Match length
                   33
 % identity -
                   79
NCBI Description (U78721) RNA helicase isolog [Arabidopsis thaliana]
Seq. No.
                   227403
 Seq. ID
                   LIB3189-032-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   g3717946
BLAST score
                   279
E value
                   8.0e-25
Match length
                   92
 % identity
                   63
NCBI Description (AJ005901) vag1 [Arabidopsis thaliana]
                   227404
 Seq. No.
 Seq. ID
                   LIB3189-032-P1-K1-D12
                   BLASTX
Method
NCBI GI
                   g3450893
BLAST score
                   516
E value
                   1.0e-52
Match length
                   124
```

% identity



```
NCBI Description (AF084005) ras-like small monomeric GTP-binding protein
                  [Avena fatua]
Seq. No.
                  227405
                  LIB3189-032-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3334115
                  406
BLAST score
É value
                  1.0e-39
                  100
Match length
% identity
                  82
                  ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                  (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664
                  (AF006489) adenine nucleotide translocator 1 [Gossypium
                  hirsutum]
                  227406
Seq. No.
                  LIB3189-032-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129499
BLAST score
                  413
                  7.0e-41
E value
Match length
                  80
                  99
% identity
                 fiber protein E6 (clone CKE6-4A) - upland cotton
NCBI Description
                  >gi 1000086 (U30506) E6 [Gossypium hirsutum]
                  227407
Seq. No.
                  LIB3189-032-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2981439
BLAST score
                  267
E value
                  3.0e - 30
Match length
                  146
% identity
                  55
NCBI Description (AF051853) t-SNARE SED5 [Arabidopsis thaliana]
                  227408
Seq. No.
                  LIB3189-032-P1-K1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g464846
                  522
BLAST score
E value
                  3.0e-53
Match length
                  103
                  93
% identity
                  TUBULIN ALPHA-6 CHAIN >gi_322880_pir__S28983 tubulin
NCBI Description
                  alpha-6 chain - maize >gi 22158 emb CAA44863 (X63178)
                  alpha-tubulin #6 [Zea mays]
                  227409
Seq. No.
Seq. ID
                  LIB3189-032-P1-K1-F6
                  BLASTX
Method
NCBI GI
                  g464846
BLAST score
                  220
E value
                  3.0e-18
Match length
                  48
```



NCBI Description TUBULIN ALPHA-6 CHAIN >gi\_322880\_pir\_S28983 tubulin alpha-6 chain - maize >gi\_22158\_emb\_CAA44863\_ (X63178) alpha-tubulin #6 [Zea mays]

Seq. No. 227410

Seq. ID LIB3189-032-P1-K1-F8

Method BLASTX
NCBI GI g3763925
BLAST score 266
E value 2.0e-23
Match length 59
% identity 83

NCBI Description (AC004450) putative Af10-protein [Arabidopsis thaliana]

Seq. No. 227411

Seq. ID LIB3189-032-P1-K1-G10

Method BLASTX
NCBI GI g3122060
BLAST score 286
E value 5.0e-26
Match length 60
% identity 93

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi\_2598657\_emb\_CAA10847\_ (AJ222579) elongation factor

1-alpha (EF1-a) [Vicia faba]

Seq. No. 227412

Seq. ID LIB3189-032-P1-K1-G2

Method BLASTX
NCBI GI g1708314
BLAST score 231
E value 2.0e-27
Match length 66
% identity 98

NCBI Description HEAT SHOCK PROTEIN 83 >gi 169296 (M99431) heat shock

protein 83 [Pharbitis nil] >gi\_445625\_prf\_\_1909372A heat

shock protein 83 [Ipomoea nil]

Seq. No. 227413

Seq. ID LIB3189-032-P1-K1-G3

Method BLASTX
NCBI GI g1172874
BLAST score 254
E value 7.0e-22
Match length 59
% identity 73

NCBI Description DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR

>gi\_479589\_pir\_\_S34823 dehydration-induced protein RD22 Arabidopsis thaliana >gi\_391608\_dbj\_BAA01546\_ (D10703) rd22
[Arabidopsis thaliana] >gi\_447134\_prf\_\_1913421A rd22 gene

[Arabidopsis thaliana]

Seq. No. 227414

Seq. ID LIB3189-032-P1-K1-H1

Method BLASTX NCBI GI g3219772 BLAST score 428



```
E value
                   4.0e-47
Match length
                  104
                  93
% identity
NCBI Description ACTIN 51 >gi_1498366 (U60481) actin [Lycopersicon
                  esculentum]
Seq. No.
                  227415
Seq. ID
                  LIB3189-032-P1-K1-H10
                  BLASTX
Method
NCBI GI
                  g4406780
BLAST score
                  355
E value
                  8.0e - 34
Match length
                  68
% identity
                  94
NCBI Description (AC006532) putative multispanning membrane protein
                  [Arabidopsis thaliana]
Seq. No.
                  227416
Seq. ID
                  LIB3189-032-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g2160177
BLAST score
                  219
E value
                  6.0e-18
Match length
                  111
% identity
                  41
NCBI Description
                 (AC000132) EST gb R64758 comes from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  227417
Seq. ID
                  LIB3189-032-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g2326372
BLAST score
                  563
E value
                  4.0e-58
Match length
                  146
% identity
                  73
NCBI Description (Y14404) putative arabinose kinase [Arabidopsis thaliana]
Seq. No.
                  227418
Seq. ID
                  LIB3189-033-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g4567251
BLAST score
                  231
E value
                  3.0e-19
Match length
                  50
% identity
                  76
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
Seq. No.
                  227419
Seq. ID
                  LIB3189-033-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g3063695
BLAST score
                  278
```

E value 8.0e-25 Match length 78 67 % identity

NCBI Description (AL022537) hypothetical protein [Arabidopsis thaliana]

% identity



```
Seq. No.
                  227420
Seq. ID
                  LIB3189-033-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g2244750
BLAST score
                  542
E value
                  8.0e-56
Match length
                  111
% identity
                  95
NCBI Description (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                >qi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                  [Arabidopsis thaliana]
                  227421
Seq. No.
Seq. ID
                  LIB3189-033-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  q3128177
BLAST score
                  437
                  2.0e-43
E value
Match length
                  107
                  80
% identity
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                  227422
                  LIB3189-033-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2760830
BLAST score
                  208
E value
                  1.0e-16
Match length
                  93
                  37
% identity
NCBI Description (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
                  thaliana]
Seq. No.
                  227423
Seq. ID
                  LIB3189-033-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g477819
BLAST score
                  524
E value
                  2.0e-53
Match length
                  143
                  71
% identity
NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) beta
                  chain precursor - potato >gi 410634 bbs 136741 cytochrome c
                  reductase-processing peptidase subunit II, MPP subunit II,
                  P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,
                  530 aa]
Seq. No.
                  227424
                  LIB3189-033-P1-K1-B9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1332579
BLAST score
                  373
                  5.0e-36
E value
                  90
Match length
```

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]



47

% identity

```
227425
Seq. No.
Seq. ID
                   LIB3189-033-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   g1545805
BLAST score
                   164
E value
                   8.0e-12
Match length
                   73
% identity
                   52
NCBI Description (D64052) cytochrome P450 like TBP [Nicotiana tabacum]
                   227426
Seq. No.
                   LIB3189-033-P1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q114182
BLAST score
                   361
E value
                   8.0e-35
Match length
                   80
% identity
                   86
NCBI Description CHORISMATE SYNTHASE PRECURSOR
                    (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE)
                   >gi_99502_pir__A41197 chorismate synthase (EC 4.6.1.4) -
pink corydalis >gi_18256_emb_CAA43034_ (X60544) chorismate
                   synthase [Corydalis sempervirens]
Seq. No.
                   227427
                   LIB3189-033-P1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4006834
BLAST score
                   482
E value
                   1.0e-48
Match length
                   104
% identity
                   88
                   (AC005970) enoyl-ACP reductase (enr-A) [Arabidopsis
NCBI Description
                   thaliana]
                   227428
Seq. No.
Seq. ID
                   LIB3189-033-P1-K1-C12
                   BLASTX
Method
NCBI GI
                   g3402722
BLAST score
                   489
E value
                   1.0e-49
                   115
Match length
                   81
% identity
NCBI Description (AC004261) CPDK-related protein [Arabidopsis thaliana]
                   227429
Seq. No.
Seq. ID
                   LIB3189-033-P1-K1-C2
                   BLASTX
Method
NCBI GI
                   g115492
BLAST score
                   308
                   2.0e-49
E value
Match length
                   113
```

calmodulin-related protein [Petunia hybrida]

NCBI Description CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)



```
Seq. No.
                   227430
Seq. ID
                   LIB3189-033-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g1743354
BLAST score
                   208
E value
                   7.0e-17
Match length
                   54
                   70
% identity
NCBI Description (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
Seq. No.
                   227431
Seq. ID
                   LIB3189-033-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   q3860333
BLAST score
                   298
E value
                   4.0e-27
                   79
Match length
% identity
                   67
NCBI Description (AJ012693) basic blue copper protein [Cicer arietinum]
Seq. No.
                   227432
Seq. ID
                   LIB3189-033-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   q2231702
BLAST score
                   547
E value
                   3.0e-56
Match length
                   118
% identity
                   86
                  (U92086) clathrin assembly protein AP19 homolog [Arabidopsis thaliana] >gi_3080409_emb_CAA18728_ (AL022604)
NCBI Description
                   clathrin assembly protein AP19 homolog [Arabidopsis
                   thaliana]
Seq. No.
                   227433
Seq. ID
                   LIB3189-033-P1-K1-C9
                   BLASTX
Method
NCBI GI
                   g3128176
BLAST score
                   167
                   8.0e-12
E value
Match length
                   113
% identity
                   36
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                   227434
Seq. ID
                   LIB3189-033-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   g3776005
BLAST score
                   155
E value
                   1.0e-10
Match length
                   74
% identity
                   49
NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]
Seq. No.
                   227435
```

BLASTX NCBI GI g1619602

LIB3189-033-P1-K1-D10

Seq. ID

Method



```
BLAST score
                   414
                   9.0e-41
E value
Match length
                   112
                   39
% identity
NCBI Description (Y08726) MtN3 [Medicago truncatula]
Seq. No.
                   227436
Seq. ID
                   LIB3189-033-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   q2511594
BLAST score
                   280
E value
                   5.0e-25
                   59
Match length
% identity
                   90
                   (Y13694) multicatalytic endopeptidase complex, proteasome
NCBI Description
                   precursor, beta subunit [Arabidopsis thaliana]
                   >gi_2827525_emb_CAA16533_ (AL021633) multicatalytic
                   endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S
                   proteasome subunit PBA1 [Arabidopsis thaliana]
Seq. No.
                   227437
Seq. ID
                   LIB3189-033-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   q3122673
BLAST score
                   479
E value
                   3.0e-48
Match length
                   121
% identity
                   79
NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                   227438
Seq. No.
Seq. ID
                   LIB3189-033-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   g2791834
BLAST score
                   149
                   4.0e-15
E value
Match length
                   72
% identity
                   68
NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta]
Seq. No.
                   227439
Seq. ID
                   LIB3189-033-P1-K1-E4
Method
                   {\tt BLASTX}
NCBI GI
                   q2832696
BLAST score
                   155
                   2.0e-10
E value
                   74
Match length
                   42
% identity
NCBI Description (AL021713) putative protein [Arabidopsis thaliana]
```

Seq. No. 227440

Seq. ID LIB3189-033-P1-K1-E6

Method BLASTX
NCBI GI g2245020
BLAST score 502

Match length

% identity

147

82



```
E value
                  5.0e-51
Match length
                  137
% identity
                  69
NCBI Description
                 (Z97341) growth regulator homolog [Arabidopsis thaliana]
                  227441
Seq. No.
Seq. ID
                  LIB3189-033-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g1699370
BLAST score
                  244
                  7.0e-21
E value
Match length
                  112
% identity
                  45
                  (S82620) prolidase=peptidase D/imidopeptidase {EC 3.4.13.9}
NCBI Description
                  [mice, liver, Peptide, 493 aa] [Mus sp.]
                  227442
Seq. No.
                  LIB3189-033-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2828296
BLAST score
                  364
                  7.0e-35
E value
                  75
Match length
% identity
                  92
NCBI Description (AL021687) RNase L inhibitor [Arabidopsis thaliana]
Seq. No.
                  227443
Seq. ID
                  LIB3189-033-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g2894378
BLAST score
                  585
E value
                  1.0e-60
                  144
Match length
% identity
                  71
NCBI Description (Y14573) putative ribophorin I homologue [Hordeum vulgare]
Seq. No.
                  227444
Seq. ID
                  LIB3189-033-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g3947719
BLAST score
                  249
E value
                  3.0e-21
Match length
                  53
% identity
NCBI Description
                  (AJ012653) ribosomal protein S28 [Prunus persica]
                  >qi 3947721 emb CAA10102 (AJ012654) ribosomal protein S28
                  [Prunus persica] >gi 3947723 emb CAA10103 (AJ012655)
                  ribosomal protein S28 [Prunus persica]
Seq. No.
                  227445
Seq. ID
                  LIB3189-033-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  q1419088
BLAST score
                  651
E value
                  2.0e-68
```

Seq. No.

Seq. ID Method 227450

BLASTX

LIB3189-033-P1-K1-G4



```
NCBI Description (Z71395) calreticulin [Nicotiana plumbaginifolia]
Seq. No.
                    227446
                    LIB3189-033-P1-K1-F6
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1899188
BLAST score
                    448
E value
                    1.0e-44
Match length
                    138
                    24
% identity
NCBI Description (U90212) DNA binding protein ACBF [Nicotiana tabacum]
Seq. No.
                    227447
Seq. ID
                    LIB3189-033-P1-K1-F7
Method
                    BLASTX
NCBI GI
                    g133939
BLAST score
                    455
E value
                    2.0e-45
Match length
                    101
% identity
                    85
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70865_pir__R3NT3
                    ribosomal protein S3 - common tobacco chloroplast >gi_11865_emb_CAA77381_ (Z00044) ribosomal protein S3 [Nicotiana tabacum] >gi_225235_prf__1211235BT ribosomal
                    protein S3 [Nicotiana tabacum]
Seq. No.
                    227448
Seq. ID
                    LIB3189-033-P1-K1-G11
Method
                    BLASTX
NCBI GI
                    g136636
BLAST score
                    252
E value
                    1.0e-21
Match length
                    71
                    70
% identity
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
                    LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                    >gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 -
                    Arabidopsis thaliana >gi 442594 pdb 1AAK Ubiquitin
                    Conjugating Enzyme (E.C.\overline{6}.3.2.1\overline{9}) >\overline{q}i 29\overline{8}1894 pdb 2AAK
                    Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                    >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis
                    thaliana] >gi 431260 (L19351) ubiquitin conjugating enzyme
                    [Arabidopsis thaliana]
Seq. No.
                    227449
Seq. ID
                    LIB3189-033-P1-K1-G12
Method
                    BLASTX
NCBI GI
                    g4467151
BLAST score
                    342
E value
                    3.0e - 32
Match length
                    130
% identity
                    52
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
```

E value

1.0e-16



```
NCBI GI
                  q4158232
BLAST score
                   284
                   9.0e-26
E value
Match length
                  65
                  88
% identity
                  (Y18626) reversibly glycosylated polypeptide [Triticum
NCBI Description
                  aestivum]
Seq. No.
                  227451
                  LIB3189-033-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q267069
BLAST score
                  641
                   3.0e-67
E value
Match length
                  120
                   97
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                   227452
Seq. No.
Seq. ID
                  LIB3189-033-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q2369714
BLAST score
                   583
                   2.0e-60
E value
Match length
                  128
% identity
                   84
NCBI Description
                 (Z97178) elongation factor 2 [Beta vulgaris]
                   227453
Seq. No.
Seq. ID
                  LIB3189-033-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   g3097321
BLAST score
                   189
E value
                   3.0e-14
Match length
                  88
% identity
                   43
NCBI Description (AB013289) Bd 30K [Glycine max]
Seq. No.
                   227454
                   LIB3189-033-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1771780
BLAST score
                   404
E value
                   1.0e-39
                  112
Match length
                   72
% identity
NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]
Seq. No.
                   227455
Seq. ID
                  LIB3189-033-P1-K1-H11
Method
                  BLASTX
NCBI GI
                   g3096947
BLAST score
                  199
```

Seq. ID



```
Match length
                  92
                  52
% identity
                  (Y16327) putative cyclic nucleotide-regulated ion channel
NCBI Description
                  [Arabidopsis thaliana]
                  227456
Seq. No.
                  LIB3189-033-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2754746
BLAST score
                  385
E value
                  2.0e-37
Match length
                  97
% identity
                  70
NCBI Description (U85448) sucrose-phosphate synthase [Actinidia deliciosa]
Seq. No.
                  227457
                  LIB3189-033-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3184281
BLAST score
                  252
E value
                  1.0e-21
Match length
                  70
% identity
                  67
NCBI Description (AC004136) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                  227458
                  LIB3189-033-P1-K1-H3
Seq. ID
Method
                  BLASTX
                  g2738982
NCBI GI
BLAST score
                  180
                  3.0e-13
E value
Match length
                  57
                  58
% identity
NCBI Description (AF022157) CYP71A10 [Glycine max]
Seq. No.
                  227459
Seq. ID
                  LIB3189-0.33-P1-K1-H4
                  BLASTX
Method
NCBI GI
                  g1843527
BLAST score
                  477
                  5.0e-48
E value
                  129
Match length
                  78
% identity
NCBI Description (U73747) annexin [Gossypium hirsutum]
Seq. No.
                  227460
Seq. ID
                  LIB3189-033-P1-K1-H6
                  BLASTX
Method
NCBI GI
                  g2811278
BLAST score
                  445
E value
                  2.0e-44
Match length
                  123
                  71
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                  227461
```

LIB3189-033-P1-K1-H8



```
Method
                   BLASTX
NCBI GI
                   g2586127
BLAST score
                   329
                   8.0e-31
E value
Match length
                   106
% identity
                   61
                  (U89510) b-keto acyl reductase [Hordeum vulgare]
NCBI Description
Seq. No.
                   227462
                   LIB3189-033-P1-K1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q461736
BLAST score
                   541
E value
                   1.0e-55
Match length
                   125
% identity
                   86
                   MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR
NCBI Description
                   >gi_478786_pir__S29316 chaperonin 60 - cucurbit
>gi_12546_emb_CAA50218_ (X70868) chaperonin 60 [Cucurbita
                   sp.]
Seq. No.
                   227463
Seq. ID
                   LIB3189-034-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g2271477
BLAST score
                   375
E value
                   5.0e-36
Match length
                   100
                   75
% identity
NCBI Description (AF009631) AP47/50p [Arabidopsis thaliana]
                   227464
Seq. No.
Seq. ID
                   LIB3189-034-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   g1723176
BLAST score
                   193
                   1.0e-14
E value
Match length
                   113
                   42
% identity
                   HYPOTHETICAL 22.4 KD PROTEIN SLL0615
NCBI Description
                   >gi_1001617_dbj_BAA10348_ (D64002) transmembrane protein
                   FT27 [Synechocystis sp.] >gi_1256592 (U38892) similar to
                   Mus musculus transmembrane protein (clone pFT27); Method:
                   conceptual translation supplied by author; ORF206
                   [Synechocystis sp.]
                   227465
Seq. No.
Seq. ID
                   LIB3189-034-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   g112717
BLAST score
                   251
E value
                   2.0e-21
                   94
Match length
```

% identity 49 NCBI Description 21 KD PROTEIN PRECURSOR (1.2 PROTEIN) >gi 82050 pir S10911

hypothetical protein precursor - carrot

>gi\_18312\_emb\_CAA36642\_ (X52395) precursor polypeptide (AA



NCBI Description actin 1 - rice

## -22 to 171) [Daucus carota]

```
Seq. No.
                   227466
Seq. ID
                   LIB3189-034-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   g1914683
BLAST score
                   292
E value
                   2.0e-26
Match length
                   78
                   73
% identity
NCBI Description (Y12013) RAD23, isoform I [Daucus carota]
                   227467
Seq. No.
Seq. ID
                   LIB3189-034-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   g1657948
BLAST score
                   434
E value
                   5.0e-43
Match length
                   119
                   73
% identity
NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
                   227468
Seq. No.
Seq. ID
                   LIB3189-034-P1-K1-A4
Method
                   BLASTX
NCBI GI
                   q132866
BLAST score
                   477
                   6.0e-48
E value
Match length
                   94
                   94
% identity
                   CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi_71086_pir__R5NT2
NCBI Description
                   ribosomal protein L2 - common tobacco chloroplast
                   >gi_435269_emb_CAA77384_ (Z00044) ribosomal protein L2
[Nicotiana tabacum] >gi_1223691_emb_CAA77409_ (Z00044)
                   ribosomal protein L2 [Nicotiana tabacum]
                   >gi 225238 prf__1211235BW ribosomal protein L2 [Nicotiana
                   tabacum]
Seq. No.
                   227469
Seq. ID
                   LIB3189-034-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   g2982297
BLAST score
                   480
E value
                   2.0e-48
Match length
                   107
% identity
                   87
NCBI Description (AF051233) KIAA0107-like protein [Picea mariana]
Seq. No.
                   227470
Seq. ID
                   LIB3189-034-P1-K1-B11
                   BLASTX
Method
NCBI GI
                   g71634
BLAST score
                   689
E value
                   8.0e-73
Match length
                   136
                   97
% identity
```



```
Seq. No.
                    227471
Seq. ID
                    LIB3189-034-P1-K1-B2
                    BLASTX
Method
NCBI GI
                    g2129739
BLAST score
                    376
                    2.0e-36
E value
Match length
                    82
% identity
                    91
                    shaggy-like kinase etha - Arabidopsis thaliana
>gi_1161512_emb_CAA64409_ (X94939) shaggy-like kinase etha
[Arabidopsis thaliana] >gi_1627516_emb_CAA70144_ (Y08947)
NCBI Description
                    shaggy-like kinase etha [Arabidopsis thaliana]
                    227472
Seq. No.
                    LIB3189-034-P1-K1-B5
Seq. ID
Method
                    BLASTX
NCBI GI
                    g125051
BLAST score
                    431
E value
                    1.0e-42
Match length
                    110
% identity
                    76
                    ISOVALERYL-COA DEHYDROGENASE PRECURSOR (IVD)
NCBI Description
                    >gi_88038_pir__A37033 isovaleryl-CoA dehydrogenase (EC
                    1.3.99.10) precursor - human >gi_306897 (M34192)
                    isovaleryl-coA dehydrogenase (IVD) [Homo sapiens]
                    >gi 4504799 ref NP 002216.1 pIVD isovaleryl Coenzyme A
                    dehydrogenase
                    227473
Seq. No.
Seq. ID
                    LIB3189-034-P1-K1-B7
Method
                    BLASTX
NCBI GI
                    g2811278
BLAST score
                    555
E value
                    4.0e-57
                    141
Match length
                    74
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                    227474
Seq. ID
                    LIB3189-034-P1-K1-C1
Method
                    BLASTX
NCBI GI
                    g3876865
BLAST score
                    161
E value
                    7.0e-11
                    73
Match length
% identity
```

NCBI Description

(Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No. 227475

Seq. ID LIB3189-034-P1-K1-C2

Method BLASTX NCBI GI g3913633 BLAST score 176



```
6.0e-13
E value
Match length
                  43
% identity
                  HYPOTHETICAL PROTEIN F8A5.25 >gi_2462742 (AC002292) Unknown
NCBI Description
                  protein [Arabidopsis thaliana]
                  227476
Seq. No.
Seq. ID
                  LIB3189-034-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g832876
BLAST score
                  629
E value
                  8.0e-66
Match length
                  140
                  88
% identity
                  (L41345) ascorbate free radical reductase [Solanum
NCBI Description
                  lycopersicum] >gi 1097368 prf _2113407A ascorbate free
                  radical reductase [Lycopersicon esculentum]
                  227477
Seq. No.
Seq. ID
                  LIB3189-034-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q2431769
BLAST score
                  270
E value
                   1.0e-23
Match length
                  112
% identity
                   54
NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]
                   227478
Seq. No.
Seq. ID
                  LIB3189-034-P1-K1-D12
Method
                  BLASTX
NCBI GI
                   g2244786
BLAST score
                  202
E value
                   4.0e-28
Match length
                  104
% identity
                   47
NCBI Description (Z97335) ribonucleoprotein homolog [Arabidopsis thaliana]
                   227479
Seq. No.
Seq. ID
                   LIB3189-034-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   g2129499
BLAST score
                   783
                   8.0e-84
E value
Match length
                   156
% identity
                   94
NCBI Description fiber protein E6 (clone CKE6-4A) - upland cotton
                   >gi 1000086 (U30506) E6 [Gossypium hirsutum]
                   227480
Seq. No.
Seq. ID
                   LIB3189-034-P1-K1-D6
                  BLASTX
Method
NCBI GI
                   g4115934
BLAST score
                   604
E value
                   8.0e-63
```

133

81

Match length % identity



```
(AF118223) contains similarity to Methanobacterium
NCBI Description
                  thermoautotrophicum transcriptional regulator (GB:AE000850)
                  [Arabidopsis thaliana]
                  227481
Seq. No.
                  LIB3189-034-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244736
BLAST score
                  706
                  8.0e-75
E value
Match length
                  134
% identity
                  96
                  (D88415) expansin [Gossypium hirsutum]
NCBI Description
Seq. No.
                  227482
                  LIB3189-034-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4510354
                  261
BLAST score
E value
                  1.0e-22
                  132
Match length
                  48
% identity
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
                  227483
Seq. No.
Seq. ID
                  LIB3189-034-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q3024657
BLAST score
                  380
                  1.0e-36
E value
Match length
                  112
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi_2668740 (AF034944) translation initiation factor; GOS2
                  [Zea mays]
                  227484
Seq. No.
                  LIB3189-034-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2119014
BLAST score
                  163
                   4.0e-11
E value
Match length
                  32
                  100
% identity
NCBI Description histone H3 - African clawed frog (fragment) >gi_214274
                   (M21286) histone H3 [Xenopus laevis]
                  227485
Seq. No.
Seq. ID
                  LIB3189-034-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  q462195
BLAST score
                  195
E value
                   6.0e-15
                  107
Match length
                   47
% identity
```

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)

E value

Match length

% identity

2.0e-51

132

71



```
sativa]
                  227486
Seq. No.
Seq. ID
                  LIB3189-034-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q231660
BLAST score
                  412
                  9.0e-49
E value
Match length
                  147
% identity
                   71
                  HYPOTHETICAL 226 KD PROTEIN (ORF 1901)
NCBI Description
Seq. No.
                  227487
                  LIB3189-034-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q532530
BLAST score
                  475
E value
                  7.0e-48
Match length
                  109
                   75
% identity
NCBI Description
                  (U07953) 1-aminocyclopropane-1-carboxylate oxidase
                   [Pelargonium hortorum] >gi_1093803_prf__2104412A
                   aminocyclopropane carboxylate oxidase [Pelargonium
                  hortorum]
                  227488
Seq. No.
                  LIB3189-034-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4063751
BLAST score
                   201
E value
                   1.0e-15
Match length
                   133
% identity
                   29
                   (AC005851) putative white protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4510409 gb AAD21495.1 (AC006929) putative white
                  protein [Arabidopsis thaliana]
                   227489
Seq. No.
Seq. ID
                  LIB3189-034-P1-K1-F11
                  BLASTX
Method
NCBI GI
                   g3983663
BLAST score
                   160
E value
                   5.0e-11
                  54
Match length
% identity
                   56
NCBI Description (AB011270) importin-beta1 [Oryza sativa]
                   227490
Seq. No.
Seq. ID
                  LIB3189-034-P1-K1-F12
                  BLASTX
Method
NCBI GI
                   g1872521
BLAST score
                   507
```

>gi\_20238\_emb\_CAA36190\_ (X51910) GOS2 [Oryza sativa]

>qi 3789950 (AF094774) translation initiation factor [Oryza



```
NCBI Description (U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana]
                  >gi 1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis
                  thaliana]
Seq. No.
                  227491
Seq. ID
                  LIB3189-034-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  q4539422
BLAST score
                  490
E value
                  2.0e-49
Match length
                  140
% identity
                  70
NCBI Description (AL049171) putative protein [Arabidopsis thaliana]
Seq. No.
                  227492
Seq. ID
                  LIB3189-034-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g3421090
BLAST score
                  140
E value
                  1.0e-19
Match length
                  91
% identity
                  62
NCBI Description (AF043525) 20S proteasome subunit PAE2 [Arabidopsis
                  thalianal
Seq. No.
                  227493
Seq. ID
                  LIB3189-034-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g1170509
BLAST score
                  576
E value
                  9.0e-60
Match length
                  119
% identity
                  95
NCBI Description
                  EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)
                  >gi_478306_pir__JN0839 translation initiation factor eIF-4A
                  - wheat
Seq. No.
                  227494
Seq. ID
                  LIB3189-034-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g3152565
BLAST score
                  177
E value
                  9.0e-13
Match length
                  80
% identity
                  57
                 (AC002986) EST gb N65759 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  227495
Seq. ID
                  LIB3189-034-P1-K1-G1
Method
                  BLASTX
```

NCBI GI g1107526
BLAST score 368
E value 3.0e-35
Match length 115
% identity 63

NCBI Description (X87931) SIEP1L protein [Beta vulgaris]



```
Seq. No.
                  227496
                  LIB3189-034-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2791834
                  584
BLAST score
E value
                  1.0e-60
Match length
                  116
                  97
% identity
                  (AF041463) elongation factor 1-alpha [Manihot esculenta]
NCBI Description
Seq. No.
                  227497
Seq. ID
                  LIB3189-034-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g2979555
BLAST score
                  160
E value
                  8.0e-11
Match length
                  111
                  32
% identity
NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]
                  227498
Seq. No.
Seq. ID
                  LIB3189-034-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q730583
BLAST score
                  245
                  6.0e-21
E value
Match length
                  62
                  79
% identity
                  60S ACIDIC RIBOSOMAL PROTEIN P2 >gi 551267 emb CAA55047
NCBI Description
                   (X78213) 60s acidic ribosomal protein P2 [Parthenium
                  argentatum]
Seq. No.
                  227499
Seq. ID
                  LIB3189-034-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g1279588
BLAST score
                  437
E value
                  3.0e-43
Match length
                  129
% identity
                   65
NCBI Description
                  (Z71749) glutathione S-transferase [Nicotiana
                  plumbaginifolia]
Seq. No.
                  227500
Seq. ID
                  LIB3189-034-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g2995384
BLAST score
                  122
E value
                  6.0e-15
                  57
Match length
                  52
% identity
NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]
```

Seq. No. 227501

Seq. ID LIB3189-034-P1-K1-G8

Method BLASTX

Match length

% identity

67



```
g1209756
NCBI GI
BLAST score
                  396
E value
                  1.0e-38
Match length
                  101
                  85
% identity
                 (U43629) integral membrane protein [Beta vulgaris]
NCBI Description
                  227502
Seq. No.
Seq. ID
                  LIB3189-034-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q2160151
BLAST score
                  195
                  1.0e-15
E value
Match length
                  64
% identity
                  58
                  (AC000375) Strong similarity to Brassica aspartic protease
NCBI Description
                  (gb X77260). [Arabidopsis thaliana]
Seq. No.
                  227503
                  LIB3189-034-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g294845
BLAST score
                  552
E value
                  1.0e-56
Match length
                  152
% identity
                  70
                  (L13655) membrane protein [Saccharum hybrid cultivar
NCBI Description
                  H65-7052]
Seq. No.
                  227504
                  LIB3189-034-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2062175
BLAST score
                  578
E value
                  7.0e-60
Match length
                  141
                  82
% identity
NCBI Description (AC001645) hypothetical protein [Arabidopsis thaliana]
                  227505
Seq. No.
Seq. ID
                  LIB3189-034-P1-K1-H4
                  BLASTX
Method
NCBI GI
                  g3036807
BLAST score
                  442
E value
                  8.0e-44
Match length
                  142
                  62
% identity
NCBI Description (AL022373) putative protein [Arabidopsis thaliana]
                  227506
Seq. No.
Seq. ID
                  LIB3189-034-P1-K1-H6
                  BLASTX
Method
NCBI GI
                  g3493172
BLAST score
                  181
E value
                  6.0e-14
```

Match length

% identity

135

76



```
(U89609) fiber annexin [Gossypium hirsutum]
NCBI Description
                  227507
Seq. No.
                  LIB3189-034-P1-K1-H7
Seq. ID
Method
                  BLASTX
                  g266945
NCBI GI
                  550
BLAST score
                  2.0e-56
E value
                  131
Match length
                  84
% identity
                  60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
NCBI Description
                  >gi_100065_pir__S19978 ribosomal protein L9 - garden pea
                  >gi_20727_emb_CAA46273_ (X65155) GA [Pisum sativum]
                  >gi 1279645_emb_CAA65987_ (X97322) ribosomal protein L9
                  [Pisum sativum]
                  227508
Seq. No.
                  LIB3189-034-P1-K1-H8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1785488
BLAST score
                  215
                  3.0e-17
E value
                  120
Match length
                  37
% identity
NCBI Description (D14590) flavonoid 3',5'-hydroxylase [Campanula medium]
Seq. No.
                  227509
                  LIB3189-034-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2497743
BLAST score
                  606
                   5.0e-63
E value
Match length
                  120
                  97
% identity
NCBI Description
                  NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3)
                  >gi_999315_bbs_166991 (S78173) LTP=lipid transfer protein
                   [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa]
                   [Gossypium hirsutum]
Seq. No.
                   227510
Seq. ID
                  LIB3189-035-P1-K1-A1
Method
                  BLASTX
NCBI GI
                   g4056497
BLAST score
                  210
E value
                   7.0e-17
Match length
                  85
% identity
                   59
NCBI Description (AC005896) putative histone H2B [Arabidopsis thaliana]
                  227511
Seq. No.
Seq. ID
                  LIB3189-035-P1-K1-A11
                  BLASTX
Method
NCBI GI
                  q4262154
BLAST score
                  496
E value
                   3.0e-50
```



```
NCBI Description
                    (AC005275) putative protein phosphatase regulatory subunit
                     [Arabidopsis thaliana]
   Seq. No.
                     227512
   Seq. ID
                     LIB3189-035-P1-K1-A4
  Method
                     BLASTX
  NCBI GI
                     g4027897
  BLAST score
                     108
                     2.0e-12
  E value
  Match length
                     67
                     66
   % identity
  NCBI Description (AF049353) alpha-expansin precursor [Nicotiana tabacum]
                     227513
   Seq. No.
   Seq. ID
                     LIB3189-035-P1-K1-A5
                     BLASTX
  Method
  NCBI GI
                     g464775
  BLAST score
                     247
  E value
                     4.0e-21
  Match length
                     115
   % identity
                     55
   NCBI Description
                    SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi 542013 pir S39492
                     superoxide dismutase - Para rubber tree >gi 348137 (L11707)
                     superoxide dismutase (manganese) [Hevea brasiliensis]
                     227514
   Seq. No.
  Seq. ID
                     LIB3189-035-P1-K1-B10
  Method
                     BLASTX
  NCBI GI
                     g4539307
                     155
  BLAST score
  E value
                     1.0e-10
  Match length
                     69
   % identity
   NCBI Description
                    (AL049480) putative acidic ribosomal protein [Arabidopsis
                     thaliana]
   Seq. No.
                     227515
   Seq. ID
                     LIB3189-035-P1-K1-B2
  Method
                     BLASTX
  NCBI GI
                     g2781357
  BLAST score
                     302
  E value
                     8.0e-32
  Match length
                     107
   % identity
                     67
  NCBI Description (AC003113) F2401.13 [Arabidopsis thaliana]
  Seq. No.
                     227516
   Seq. ID
                     LIB3189-035-P1-K1-C1
  Method
                     BLASTX
  NCBI GI
                     g2462925
  BLAST score
                     644
  E value
                     1.0e-67
Match length
                     140
  % identity
                     89
  NCBI Description
                     (AJ000053) GTP cyclohydrolase II /
```

thaliana]

3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis

E value

Match length

% identity



```
Seq. No.
                   227517
Seq. ID
                   LIB3189-035-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g125887
BLAST score
                   198
E value
                   3.0e-15
Match length
                   100
% identity
                   46
NCBI Description
                   ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
                   >gi_82092_pir__S04765 LAT52 protein precursor - tomato
>gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon
                   esculentum]
Seq. No.
                   227518
Seq. ID
                   LIB3189-035-P1-K1-C7
Method
                   BLASTX
                   g3650032
NCBI GI
BLAST score
                   235
E value
                   1.0e-19
Match length
                   66
                   58
% identity
NCBI Description
                   (AC005396) gibberellin-regulated protein GAST1-like
                   [Arabidopsis thaliana]
Seq. No.
                   227519
Seq. ID
                   LIB3189-035-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   q3193301
BLAST score
                   276
E value
                   1.0e-25
Match length
                   100
% identity
                   60
NCBI Description
                   (AF069298) Arabidopsis putative chloroplast outer envelope
                   86-like protein T10P11.19 (GB: AC002330) [Arabidopsis
                   thaliana
                   227520
Seq. No.
Seq. ID
                   LIB3189-035-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   g4510378
BLAST score
                   214
E value
                   4.0e-17
Match length
                   77
% identity
NCBI Description (AC007017) hypothetical protein [Arabidopsis thaliana]
                   227521
Seq. No.
Seq. ID
                   LIB3189-035-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   g4567251
BLAST score
                   560
```

NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]

1.0e-57

141



```
Seq. No.
                  227522
Seq. ID
                  LIB3189-035-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g2281115
BLAST score
                  558
E value
                  2.0e-57
Match length
                  136
                  74
% identity
NCBI Description
                  (AC002330) putative cullin-like 1 protein [Arabidopsis
                  thaliana]
                  227523
Seq. No.
Seq. ID
                  LIB3189-035-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q886401
BLAST score
                  204
E value
                  5.0e-16
Match length
                  72
                  54
% identity
NCBI Description (L37526) MADS box protein [Oryza sativa]
Seq. No.
                  227524
Seq. ID
                  LIB3189-035-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g4467125
BLAST score
                  495
                  2.0e-53
E value
Match length
                  142
                  74
% identity
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]
Seq. No.
                  227525
                  LIB3189-035-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4559346
BLAST score
                  421
                  2.0e-41
E value
Match length
                  131
                  56
% identity
NCBI Description (AC006585) early nodulin 16 [Arabidopsis thaliana]
                  227526
Seq. No.
                  LIB3189-035-P1-K1-E3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3334138
BLAST score
                  382
E value
                  6.0e-37
Match length
                  88
% identity
                  77
NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi 669003 (U20502) calnexin
                  [Glycine max]
```

Seq. No. 227527

Seq. ID LIB3189-035-P1-K1-E9

Method BLASTX NCBI GI g1617274 BLAST score 301

NCBI Description



```
2.0e-27
E value
Match length
                  111
% identity
                  60
                  (Z72152) AMP-binding protein [Brassica napus]
NCBI Description
                  227528
Seq. No.
                  LIB3189-035-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2369714
BLAST score
                  512
E value
                  4.0e-52
Match length
                  118
% identity
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]
                  227529
Seq. No.
                  LIB3189-035-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1449179
BLAST score
                  202
                  6.0e-16
E value
Match length
                  62
% identity
                  58
NCBI Description
                  (D86506) N-ethylmaleimide sensitive fusion protein
                  [Nicotiana tabacum]
                  227530
Seq. No.
Seq. ID
                  LIB3189-035-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g4454014
BLAST score
                  186
E value
                   6.0e-14
Match length
                  122
% identity
                  34
NCBI Description (AL035396) putative protein [Arabidopsis thaliana]
                  227531
Seq. No.
Seq. ID
                  LIB3189-035-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g2702281
                  302
BLAST score
E value
                   6.0e-33
Match length
                  101
% identity
                   44
NCBI Description (AC003033) putative protein disulfide isomerase precursor
                   [Arabidopsis thaliana]
                  227532
Seq. No.
Seq. ID
                  LIB3189-035-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g2702281
BLAST score
                  157
E value
                  7.0e-11
                  55
Match length
% identity
                   64
```

[Arabidopsis thaliana]

(AC003033) putative protein disulfide isomerase precursor

% identity



```
227533
Seq. No.
Seq. ID
                  LIB3189-035-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g2497753
BLAST score
                  232
E value
                  2.0e-19
Match length
                  117
% identity
                  44
NCBI Description
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
                  >gi 1321915 emb CAA65477 (X96716) lipid transfer protein
                  [Prunus dulcis]
Seq. No.
                  227534
                  LIB3189-035-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g541951
BLAST score
                  308
E value
                  3.0e-28
Match length
                  107
% identity
                  57
NCBI Description SPCP2 protein - soybean >gi 310578 (L12258) nodulin-26
                  [Glycine max]
Seq. No.
                  227535
                  LIB3189-035-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1350720
BLAST score
                  455
E value
                  2.0e-45
Match length
                  111
                  77
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L32
Seq. No.
                  227536
Seq. ID
                  LIB3189-036-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g2497743
BLAST score
                  600
E value
                  2.0e-62
Match length
                  120
                  97
% identity
NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3)
                  >gi_999315_bbs_166991 (S78173) LTP=lipid transfer protein
                  [Gossypium hirsutum=cotton, fiber, Peptide, 120 aa]
                  [Gossypium hirsutum]
                  227537
Seq. No.
Seq. ID
                  LIB3189-036-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g3927838
BLAST score
                  224
E value
                  2.0e-18
Match length
                  68
```

NCBI Description (AC005727) unknown protein [Arabidopsis thaliana]

Method

NCBI GI

BLAST score

BLASTX

259

q3004560



```
Seq. No.
                  227538
Seq. ID
                  LIB3189-036-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q3328240
BLAST score
                  313
                  9.0e - 29
E value
Match length
                  92
                  62
% identity
NCBI Description
                  (AF064775) early nodule-specific protein [Medicago
                  truncatula]
                  227539
Seq. No.
                  LIB3189-036-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2738949
BLAST score
                  537
E value
                  4.0e-55
Match length
                  112
                  89
% identity
NCBI Description
                  (AF022213) cytosolic ascorbate peroxidase [Fragaria x
                  ananassa]
Seq. No.
                  227540
Seq. ID
                  LIB3189-036-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g1843527
BLAST score
                  671
E value
                  9.0e-71
Match length
                  138
% identity
NCBI Description (U73747) annexin [Gossypium hirsutum]
Seq. No.
                  227541
Seq. ID
                  LIB3189-036-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g3420055
BLAST score
                  504
E value
                  4.0e-51
Match length
                  120
                  80
% identity
NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]
Seq. No.
                  227542
Seq. ID
                  LIB3189-036-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g3153902
BLAST score
                  426
E value
                  4.0e-42
Match length
                  107
                  79
% identity
NCBI Description
                 (AF066076) 14-3-3-like protein [Helianthus annuus]
Seq. No.
                  227543
Seq. ID
                  LIB3189-036-P1-K1-C1
```



E value 2.0e-22 Match length 75 % identity . (AC003673) putative ATP binding protein [Arabidopsis NCBI Description thaliana] Seq. No. 227544 Seq. ID LIB3189-036-P1-K1-C2 Method BLASTX NCBI GI g3152606 BLAST score 372 E value 1.0e-35 Match length 81 77 % identity NCBI Description (AC004482) putative ring zinc finger protein [Arabidopsis thaliana] Seq. No. 227545 Seq. ID LIB3189-036-P1-K1-C3 Method BLASTX NCBI GI g267069 BLAST score 630 E value 6.0e-66 Match length 117 % identity 99 NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana] 227546 Seq. No. Seq. ID LIB3189-036-P1-K1-C5 Method BLASTX NCBI GI g3915826 BLAST score 538 E value 4.0e-55 135 Match length % identity 74 NCBI Description 60S RIBOSOMAL PROTEIN L5 Seq. No. 227547 Seq. ID LIB3189-036-P1-K1-C7 Method BLASTX NCBI GI g2829903 BLAST score 511 E value 6.0e-52 Match length 158 % identity 68 NCBI Description (AC002311) unknown protein [Arabidopsis thaliana] Seq. No. 227548

Seq. ID LIB3189-036-P1-K1-C8 Method BLASTX

NCBI GI q3688170 BLAST score 185 E value 9.0e-14 Match length 100



% identity NCBI Description (AL031804) putative protein [Arabidopsis thaliana] 227549 Seq. No. Seq. ID LIB3189-036-P1-K1-C9 Method BLASTX NCBI GI g2570515 BLAST score 365 E value 7.0e-35 Match length 119 % identity 60 NCBI Description (AF022740) glycolate oxidase [Oryza sativa] Seq. No. 227550 Seq. ID LIB3189-036-P1-K1-D3 Method BLASTX NCBI GI g2149380 BLAST score 320 E value 9.0e-30 Match length 96 % identity 67 NCBI Description (U85036) syntaxin homolog [Arabidopsis thaliana] Seq. No. 227551 Seq. ID LIB3189-036-P1-K1-D7 Method BLASTX NCBI GI g2119934 BLAST score 545 E value 6.0e-56 Match length 115 90 % identity NCBI Description translation initiation factor eIF-4A.7 - common tobacco Seq. No. 227552 Seq. ID LIB3189-036-P1-K1-D8 Method BLASTX NCBI GI q267069 BLAST score 676 E value 3.0e-71 Match length 126 % identity 99 NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_JQ1594 tubulin alpha chain - Arabidopsis thaliana >qi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana] Seq. No. 227553 Seq. ID LIB3189-036-P1-K1-E4 Method BLASTX NCBI GI q2507281 BLAST score 695 E value 1.0e-73 Match length 127

98

% identity

NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi 1668706 emb CAA66048



Seq. No. 227554

Seq. ID LIB3189-036-P1-K1-E6

Method BLASTX NCBI GI g3688170 BLAST score 180 3.0e-13E value Match length 107 44 % identity

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 227555

LIB3189-036-P1-K1-E8 Seq. ID

Method BLASTX NCBI GI q417103 BLAST score 676 3.0e-71 E value Match length 136 99 % identity

HISTONE H3.2, MINOR >gi 282871 pir S24346 histone NCBI Description

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563 (U09458) histone H3.2 [Medicago sativa] >gi 488567 ( $\overline{\text{U}}$ 09460) histone H3.2 [Medicago sativa] >gi 488569 (U09461) histone H3.2 [Medicago sativa] >gi 488575 (U09464) histone H3.2 [Medicago sativa] >gi 488577 (U09465) histone H3.2 [Medicago sativa] >gi 510911 emb CAA56153 (X79714) histone H3 [Lolium temulentum] >gi 1435157 emb CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AF093633) histone H3 [Oryza sativa] >gi 4038469 gb AAC97380 (AF109910) histone H3 [Porteresia coarctata] >gi 4490754 emb CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi 4490755 emb CAB38917.1

(AL035708) Histon H3 [Arabidopsis thaliana]

227556 Seq. No.

Seq. ID LIB3189-036-P1-K1-E9

Method BLASTX NCBI GI g4126473 BLAST score 698 E value 6.0e-74Match length 134 % identity 100

(AB014884) adenylyl cyclase associated protein [Gossypium NCBI Description

hirsutum]

227557 Seq. No.

Seq. ID LIB3189-036-P1-K1-F11

Method BLASTX NCBI GI g2191130 BLAST score 210 E value 1.0e-16 Match length 144 % identity 40

```
NCBI Description (AF007269) A IG002N01.7 gene product [Arabidopsis thaliana]
                  227558
Seq. No.
Seq. ID
                  LIB3189-036-P1-K1-F12
                  BLASTX
Method
NCBI GI
                  q1785621
BLAST score
                  263
                  6.0e-23
E value
Match length
                  136
% identity
                  43
NCBI Description
                  (Z84202) AtPK2324 [Arabidopsis thaliana] >gi 2465927
                  (AF024650) receptor-like serine/threonine kinase
                  [Arabidopsis thaliana] >gi 4249408 (AC006072) putative
                  serine/threonine protein kinase [Arabidopsis thaliana]
                  227559
Seq. No.
                  LIB3189-036-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3668089
BLAST score
                  212
                  6.0e-17
E value
                  78
Match length
                  47
% identity
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
                  227560
Seq. No.
                  LIB3189-036-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2271477
                  305
BLAST score
E value
                  6.0e-28
Match length
                  62
                  94
% identity
NCBI Description (AF009631) AP47/50p [Arabidopsis thaliana]
Seq. No.
                  227561
Seq. ID
                  LIB3189-036-P1-K1-F7
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2497743
BLAST score 555
E value 3.0e-57
Match length 113
% identity 96

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3)

>gi\_999315\_bbs\_166991 (S78173) LTP=lipid transfer protein

[Gossypium hirsutum=cotton, fiber, Peptide, 120 aa]

[Gossypium hirsutum]

Seq. No. 227562

Seq. ID LIB3189-036-P1-K1-G1

Method BLASTX
NCBI GI g1800281
BLAST score 556
E value 3.0e-57
Match length 117
% identity 21

NCBI Description (U82086) polyubiquitin [Fragaria x ananassa]



```
227563
Seq. No.
Seq. ID
                  LIB3189-036-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g2894378
BLAST score
                  249
E value
                  3.0e-21
Match length
                  126
% identity
NCBI Description (Y14573) putative ribophorin I homologue [Hordeum vulgare]
Seq. No.
                  227564
                  LIB3189-036-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2088652
BLAST score
                  544
E value
                  7.0e-56
Match length
                  129
% identity
                  78
NCBI Description
                  (AF002109) 26S proteasome regulatory subunit S12 isolog
                   [Arabidopsis thaliana] >gi_2351376 (U54561) translation
                  initiation factor eIF2 p47 subunit homolog [Arabidopsis
                  thaliana]
Seq. No.
                  227565
Seq. ID
                  LIB3189-036-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q4263779
BLAST score
                  265
E value
                  4.0e-23
                  85
Match length
% identity
                  62
NCBI Description (AC006068) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  227566
Seq. ID
                  LIB3189-036-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g3603401
BLAST score
                  370
                  1.0e-35
E value
                  100
Match length
                  69
% identity
NCBI Description (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]
Seq. No.
                  227567
Seq. ID
                  LIB3189-036-P1-K1-G6
                  BLASTX
Method
                  g131773
NCBI GI
BLAST score
                  548
                  2.0e-56
E value
Match length
                  137
% identity
                  82
NCBI Description
                 40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
                  >gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) -
```

32500

maize

227568

Seq. No.

E value

Match length

% identity

3.0e-48

113

57



```
LIB3189-036-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129499
                  437
BLAST score
E value
                  3.0e-43
Match length
                  139
                  64
% identity
NCBI Description
                  fiber protein E6 (clone CKE6-4A) - upland cotton
                  >gi 1000086 (U30506) E6 [Gossypium hirsutum]
                  227569
Seq. No.
Seq. ID
                  LIB3189-036-P1-K1-H3
                  BLASTX
Method
NCBI GI
                  q3023945
BLAST score
                  510
                  7.0e-52
E value
Match length
                  103
                  91
% identity
NCBI Description HISTONE DEACETYLASE (HD) >gi 2318131 (AF014824) histone
                  deacetylase [Arabidopsis thaliana]
Seq. No.
                  227570
                  LIB3189-036-P1-K1-H4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1174867
BLAST score
                  336
E value
                  1.0e-31
Match length
                  72
% identity
                  88
                 UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING
NCBI Description
                  PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2
                  KD PROTEIN) >gi_633687_emb_CAA55862_ (X79275)
                  ubiquinol--cytochrome c reductase [Solanum tuberosum]
                  >gi 1094912_prf__2107179A cytochrome c
                  oxidase:SUBUNIT=8.2kD [Solanum tuberosum]
Seq. No.
                  227571
Seq. ID
                  LIB3189-036-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  q2801448
BLAST score
                  306
E value
                  3.0e-28
Match length
                  74
% identity
                  73
                  (AF028341) ubiquitin-conjugating enzyme 18 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  227572
Seq. ID
                  LIB3189-036-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  q4512653
BLAST score
                  479
```

32501

NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                  227573
                  LIB3189-037-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4138137
BLAST score
                  291
E value
                  8.0e-27
Match length
                  58
                  84
% identity
NCBI Description (AJ012796) ss-galactosidase [Lycopersicon esculentum]
Seq. No.
                  227574
Seq. ID
                  LIB3189-037-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q1053047
BLAST score
                  416
                  4.0e-41
E value
Match length
                  86
                  97
% identity
                  (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)
NCBI Description
                  histone H3 [Glycine max] >gi_1053051 (U38427) histone H3
                  [Glycine max]
Seq. No.
                  227575
Seq. ID
                  LIB3189-037-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q2129946
BLAST score
                  327
E value
                   4.0e-39
Match length
                  87
                  98
% identity
NCBI Description ADP-ribosylation factor homolog GTP-binding protein NTGB1 -
                   common tobacco (fragment) >gi 1184987 (U46927) NTGB1
                   [Nicotiana tabacum]
Seq. No.
                  227576
                  LIB3189-037-P1-K1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4512699
BLAST score
                  278
E value
                  5.0e-25
                  91
Match length
                   68
% identity
NCBI Description (AC006569) putative NADH-ubiquinone oxireductase
                   [Arabidopsis thaliana]
Seq. No.
                   227577
Seq. ID
                  LIB3189-037-P1-K1-B12
                  BLASTX
Method
NCBI GI
                   g2262103
BLAST score
                  258
```

2.0e-22 E value 109 Match length

54 % identity

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 227578

LIB3189-037-P1-K1-B8 Seq. ID

BLAST score

Match length

E value

161

41

1.0e-11



```
Method
                  BLASTX
NCBI GI
                  g167367
BLAST score
                  470
                  3.0e-47
E value
Match length
                  113
% identity
                  81
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                  227579
Seq. ID
                  LIB3189-037-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g2764941
BLAST score
                  230
E value
                  4.0e-19
Match length
                  85
% identity
                  41
                  (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                  expressed in meristematic region, and style [Arabidopsis
                  thaliana]
                  227580
Seq. No.
Seq. ID
                  LIB3189-037-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g2832717
BLAST score
                  314
E value
                  2.0e-29
Match length
                  70
% identity
                  83
NCBI Description (AJ003114) alkaline/neutral invertase [Lolium temulentum]
Seq. No.
                  227581
Seq. ID
                  LIB3189-037-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g2677828
BLAST score
                  393
                  3.0e-38
E value
Match length
                  117
                  66
% identity
NCBI Description (U93166) cysteine protease [Prunus armeniaca]
                  227582
Seq. No.
Seq. ID
                  LIB3189-037-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q3395427
BLAST score
                  186
E value
                  4.0e-14
Match length
                  101
% identity
                  45
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                  227583
Seq. No.
Seq. ID
                  LIB3189-037-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g4098331
```

E value

Match length

% identity

3.0e-15 37

100



```
% identity
                  (U76896) beta-tubulin 5 [Triticum aestivum]
NCBI Description
                   227584
Seq. No.
                  LIB3189-037-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1703375
BLAST score
                  182
E value
                   8.0e-14
Match length
                   40
% identity
                   95
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 965483_dbj BAA08259_ (D45420)
                   DcARF1 [Daucus carota]
Seq. No.
                   227585
                   LIB3189-037-P1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q417154
BLAST score
                   208
E value
                   6.0e-17
Match length
                   43
                   93
% identity
NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
                   protein 82 - rice (strain Taichung Native One)
                   >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                   227586
Seq. No.
Seq. ID
                   LIB3189-037-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   g2829204
BLAST score
                   322
                   9.0e-30
E value
Match length
                   85
% identity
                   82
                  (AF044204) lipid transfer protein precursor [Gossypium
NCBI Description
                   hirsutum]
                   227587
 Seq. No.
 Seq. ID
                   LIB3189-037-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g4519507
                   264
BLAST score
                   2.0e-28
E value
Match length
                   91
                   77
 % identity
NCBI Description (D88434) protein abundantly expressed during apple fruit
                   development [Malus domestica]
                   227588
 Seq. No.
                   LIB3189-037-P1-K1-G4
 Seq. ID
                   BLASTX
Method
                   g466172
NCBI GI
 BLAST score
                   195
```

GTP-BINDING PROTEIN YPTM2 >qi 283056 pir B38202 ypt family NCBI Description - maize >gi\_287835\_emb\_CAA44919\_ (X63278) yptm2 [Zea mays] Seq. No. 227589 LIB3189-037-P1-K1-G6 Seq. ID Method BLASTX g2829204 NCBI GI BLAST score 373 E value 4.0e-36 Match length 81 88 % identity (AF044204) lipid transfer protein precursor [Gossypium NCBI Description hirsutum] 227590 Seq. No. LIB3189-037-P1-K1-G8 Seq. ID Method BLASTX NCBI GI g2511598 BLAST score 139 E value 9.0e-09 Match length 35 69 % identity (Y13696) multicatalytic endopeptidase complex, proteasome NCBI Description component, beta subunit [Arabidopsis thaliana] 227591 Seq. No. LIB3189-037-P1-K1-H8 Seq. ID BLASTX Method NCBI GI q2435518 BLAST score 220 E value 8.0e-18 Match length 114 % identity 38

% identity 38
NCBI Description (AF024504) contains similarity to C3HC4-type zinc fingers

[Arabidopsis thaliana]

Seq. No. 227592

Seq. ID LIB3189-039-P1-K1-A11

Method BLASTX
NCBI GI g3023816
BLAST score 337
E value 9.0e-32
Match length 76

Match length 76 % identity 82

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 227593

Seq. ID LIB3189-039-P1-K1-A3

Method BLASTX
NCBI GI g4102600
BLAST score 149
E value 2.0e-09
Match length 57
% identity 58

NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]



Seq. No. 227594 Seq. ID LIB3189-039-P1-K1-A5 BLASTX Method NCBI GI g2493895 BLAST score 571 E value 6.0e-59 Match length 129 % identity 88 CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE) NCBI Description (O-ACETYLSERINE (THIOL)-LYASE) (CSASE) >gi\_1071911\_pir\_\_S46438 cysteine synthase (EC 4.2.99.8) watermelon >gi\_540497\_dbj\_BAA05965\_ (D28777) cysteine synthase [Citrullus lanatus] 227595 Seq. No. Seq. ID LIB3189-039-P1-K1-A7 Method BLASTX NCBI GI g1848212

BLAST score 435 E value 3.0e-43Match length 83 % identity 47

(Y11209) protein disulfide-isomerase precursor [Nicotiana NCBI Description

tabacum]

227596 Seq. No.

Seq. ID LIB3189-039-P1-K1-A8

Method BLASTX NCBI GI g2190494 BLAST score 256 E value 4.0e-22 52 Match length % identity 98

NCBI Description (Y13646) cyclin dependent kinase [Petunia x hybrida]

227597 Seq. No.

Seq. ID LIB3189-039-P1-K1-A9

BLASTX Method NCBI GI g4154281 BLAST score 425 E value 4.0e-42 109 Match length 70 % identity

NCBI Description (AF082347) C13 endopeptidase NP1 precursor [Zea mays]

227598 Seq. No.

Seq. ID LIB3189-039-P1-K1-B11

Method BLASTX NCBI GI g3540195 BLAST score 667  $E_{\tilde{\phantom{a}}}$  value 3.0e-70 Match length 143 46 % identity

NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No. 227599

Match length

% identity

116



```
LIB3189-039-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2505940
BLAST score
                  554
E value
                  5.0e-57
Match length
                  130
% identity
                  82
NCBI Description
                  (Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]
Seq. No.
                  227600
Seq. ID
                  LIB3189-039-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q2462929
BLAST score
                  441
E value
                   6.0e-44
Match length
                  119
% identity
                   67
NCBI Description
                  (Y12295) glutathione transferase [Arabidopsis thaliana]
Seq. No.
                  227601
Seq. ID
                  LIB3189-039-P1-K1-B3
Method
                  BLASTX
NCBI GI
                   q2462929
BLAST score
                  305
E value
                   4.0e-28
Match length
                  99
% identity
                  55
NCBI Description (Y12295) glutathione transferase [Arabidopsis thaliana]
Seq. No.
                  227602
                  LIB3189-039-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4567226
BLAST score
                  189
E value
                   4.0e-14
Match length
                  73
                  55
% identity
NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]
Seq. No.
                   227603
Seq. ID
                  LIB3189-039-P1-K1-B5
                  BLASTX
Method
NCBI GI
                  g4567226
BLAST score
                  181
E value
                   3.0e-13
Match length
                  73
                   53
% identity
NCBI Description (AC007119) unknown protefn [Arabidopsis thaliana]
Seq. No.
                   227604
Seq. ID
                  LIB3189-039-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g3024017
BLAST score
                   535
E value
                  1.0e-54
```



EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) >gi\_2565421 (AF026804) eukaryotic translation

initiation factor eIF-1A [Onobrychis viciifolia]

Seq. No. 227605

NCBI Description

Seq. ID LIB3189-039-P1-K1-C11

Method BLASTX
NCBI GI g902584
BLAST score 682
E value 5.0e-72
Match length 147
% identity 14

NCBI Description (U29159) polyubiquitin containing 7 ubiquitin monomers [Zea

mays]

Seq. No. 227606

Seq. ID LIB3189-039-P1-K1-C2

Method BLASTX
NCBI GI g4512666
BLAST score 216
E value 1.0e-17
Match length 90

Match length 90 % identity 51

NCBI Description (AC006931) putative mei2 protein [Arabidopsis thaliana]

Seq. No. 227607

Seq. ID LIB3189-039-P1-K1-C8

Method BLASTX
NCBI GI g2129499
BLAST score 386
E value 2.0e-37
Match length 115
% identity 66

NCBI Description fiber protein E6 (clone CKE6-4A) - upland cotton

>gi 1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No. 227608

Seq. ID LIB3189-039-P1-K1-D1

Method BLASTX
NCBI GI 94454014
BLAST score 299
E value 4.0e-27
Match length 145
% identity 46

NCBI Description (AL035396) putative protein [Arabidopsis thaliana]

Seq. No. 227609

Seq. ID LIB3189-039-P1-K1-D11

Method BLASTX
NCBI GI g3775993
BLAST score 371
E value 2.0e-35
Match length 127
% identity 59

NCBI Description (AJ010460) RNA helicase [Arabidopsis thaliana]

Seq. No. 227610

NCBI Description

Seq. No.



```
LIB3189-039-P1-K1-D2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3879145
BLAST score
                  189
E value
                  2.0e-14
Match length
                  77
                  43
% identity
                  (Z93386) predicted using Genefinder; Similarity to Human
NCBI Description
                  placenta (DIFF33) protein (TR:Q13530); cDNA EST yk198a11.5
                  comes from this gene [Caenorhabditis elegans]
Seq. No.
                  227611
Seq. ID
                  LIB3189-039-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g559684
BLAST score
                  709
                  4.0e-75
E value
Match length
                  156
                  88
% identity
NCBI Description
                  (L36097) aquaporin [Mesembryanthemum crystallinum]
                  227612
Seq. No.
                  LIB3189-039-P1-K1-D4
Seq. ID
Method
                  BLASTX
                  g1655545
NCBI GI
BLAST score
                  328
E value
                  2.0e-30
Match length
                  142
% identity
                  46
                  (X97190) endo-beta-1,4-glucanase [Capsicum annuum]
NCBI Description
                  227613
Seq. No.
                  LIB3189-039-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2129559
BLAST score
                  238
E value
                   5.0e-20
Match length
                  120
% identity
                   46
                  cellulase homolog OR16pep - Arabidopsis thaliana
NCBI Description
                   >gi 1022807 (U37702) cellulase [Arabidopsis thaliana]
                      _3493633 (AF074092) cellulase [Arabidopsis thaliana]
                  >gi
                       3598956 (AF074375) cellulase [Arabidopsis thaliana]
                  >gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN
                   [Arabidopsis thaliana]
Seq. No.
                   227614
Seq. ID
                  LIB3189-039-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g1332579
BLAST score
                  689
E value
                   7.0e-73
                  138
Match length
% identity
                  10
```

2.0

227615

32509

(X98063) polyubiquitin [Pinus sylvestris]



```
LIB3189-039-P1-K1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3757514
BLAST score
                  438
                  1.0e-43
E value
Match length
                  103
                  80
% identity
                  (AC005167) putative plasma membrane intrinsic protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  227616
                  LIB3189-039-P1-K1-E12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1808656
BLAST score
                  199
                   1.0e-15
E value
Match length
                  84
                   54
% identity
NCBI Description (Y10804) Ubiquitin activating enzyme El [Nicotiana tabacum]
                   227617
Seq. No.
                  LIB3189-039-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3043428
                   664
BLAST score
E value
                   7.0e-70
Match length
                  144
                   90
% identity
NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
Seq. No.
                   227618
                   LIB3189-039-P1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1168735
BLAST score
                   253
E value
                   1.0e-21
                   154
Match length
                   38
% identity
NCBI Description CYTOPLASMIC AXIAL FILAMENT PROTEIN >gi_1073970_pir__F64118
                   cytoplasmic axial filament protein (cafA) homolog -
                   Haemophilus influenzae (strain Rd KW20) >gi_1574815
                   (U32814) cytoplasmic axial filament protein (cafA)
                   [Haemophilus influenzae Rd]
Seq. No.
                   227619
Seq. ID
                   LIB3189-039-P1-K1-E5
                   BLASTX
Method
NCBI GI
                   g1168735
                   206
BLAST score
E value
                   4.0e-16
Match length
                   154
                   32
% identity
NCBI Description CYTOPLASMIC AXIAL FILAMENT PROTEIN >gi 1073970 pir F64118
                   cytoplasmic axial filament protein (cafA) homolog -
```

32510

[Haemophilus influenzae Rd]

Haemophilus influenzae (strain Rd KW20) >gi\_1574815 (U32814) cytoplasmic axial filament protein (cafA)



```
227620
Seq. No.
Seq. ID
                  LIB3189-039-P1-K1-E6
Method
                  BLASTX
                  g1168735
NCBI GI
                  233
BLAST score
                  2.0e-19
E value
                  147
Match length
% identity
                  37
                  CYTOPLASMIC AXIAL FILAMENT PROTEIN >gi_1073970_pir F64118
NCBI Description
                  cytoplasmic axial filament protein (cafA) homolog -
                  Haemophilus influenzae (strain Rd KW20) >gi_1574815
                   (U32814) cytoplasmic axial filament protein (cafA)
                   [Haemophilus influenzae Rd]
                  227621
Seq. No.
                  LIB3189-039-P1-K1-F3
Seq. ID
                  BLASTX
Method
                  g3650032
NCBI GI
BLAST score
                  233
                  3.0e-19
E value
                  49
Match length
                  71
% identity
                  (AC005396) gibberellin-regulated protein GAST1-like
NCBI Description
                  [Arabidopsis thaliana]
                   227622
Seq. No.
                  LIB3189-039-P1-K1-F4
Seq. ID
                  BLASTX
Method
                  g1808656
NCBI GI
BLAST score
                  634
                   2.0e-66
E value
Match length
                  152
                   78
% identity
NCBI Description (Y10804) Ubiquitin activating enzyme E1 [Nicotiana tabacum]
                   227623
Seq. No.
                   LIB3189-039-P1-K1-F6
Seq. ID
                  BLASTX
Method
                   g1808656
NCBI GI
BLAST score
                   583
                   2.0e-60
E value
                   149
Match length
                   74
% identity
NCBI Description (Y10804) Ubiquitin activating enzyme El [Nicotiana tabacum]
                   227624
Seq. No.
                   LIB3189-039-P1-K1-F9
Seq. ID
                   BLASTX
Method
                   q3123515
NCBI GI
                   186
BLAST score
                   2.0e-14
E value
                   41
Match length
% identity
```

32511

NCBI Description (Y08761) Mago Nashi-like protein [Euphorbia lagascae]

227625

Seq. No.



```
LIB3189-039-P1-K1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3123515
                  550
BLAST score
                  1.0e-56
E value
Match length
                  115
% identity
                  90
                  (Y08761) Mago Nashi-like protein [Euphorbia lagascae]
NCBI Description
Seq. No.
                  227626
                  LIB3189-039-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2119278
BLAST score
                  703
E value
                  2.0e-74
Match length
                  133
% identity
                  96
NCBI Description tubulin beta-1 chain - rice
Seq. No.
                  227627
                  LIB3189-039-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539301
BLAST score
                  163
E value
                   2.0e-11
Match length
                  47
                  53
% identity
                  (AL049480) putative mitochondrial protein [Arabidopsis
NCBI Description
                  thaliana]
                   227628
Seq. No.
                  LIB3189-039-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g541800
BLAST score
                  708
E value
                  1.0e-81
Match length
                  159
                   92
% identity
NCBI Description protein kinase (EC 2.7.1.37) cdc2-Pa - Norway spruce
                   >gi 454980 emb CAA54746 (X77680) cdc2Pa [Picea abies]
Seq. No.
                   227629
                  LIB3189-039-P1-K1-G3
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2190494
BLAST score
                   271
E value
                   4.0e-31
                  104
Match length
                   75
% identity
NCBI Description (Y13646) cyclin dependent kinase [Petunia x hybrida]
                   227630
Seq. No.
Seq. ID
                   LIB3189-039-P1-K1-G9
```

Method BLASTX
NCBI GI g541951
BLAST score 148
E value 2.0e-09



```
63
Match length
% identity
                   51
NCBI Description
```

SPCP2 protein - soybean >gi 310578 (L12258) nodulin-26

[Glycine max]

227631 Seq. No.

LIB3189-039-P1-K1-H1 Seq. ID

Method BLASTX NCBI GI g1946371 BLAST score 209 E value 2.0e-16 Match length 67 % identity 60

NCBI Description (U93215) regulatory protein Viviparous-1 isolog

[Arabidopsis thaliana]

Seq. No. 227632

LIB3189-039-P1-K1-H11 Seq. ID

Method BLASTX NCBI GI g4544443 BLAST score 521 E value 4.0e-53 Match length 151 % identity 51

(AC006592) putative mitochondrial uncoupling protein NCBI Description

[Arabidopsis thaliana]

227633 Seq. No.

LIB3189-039-P1-K1-H2 Seq. ID

Method BLASTX NCBI GI g2829871 BLAST score 114 1.0e-12 E value Match length 66

% identity 59

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

227634 Seq. No.

Seq. ID LIB3189-039-P1-K1-H3

BLASTX Method NCBI GI g3650032 BLAST score 237 E value 8.0e-20 49 Match length % identity 73

NCBI Description (AC005396) gibberellin-regulated protein GAST1-like

[Arabidopsis thaliana]

227635 Seq. No.

Seq. ID LIB3189-039-P1-K1-H5

BLASTX Method NCBI GI g2829204 BLAST score 190 E value 1.0e-14 Match length 92 % identity

NCBI Description (AF044204) lipid transfer protein precursor [Gossypium

Seq. No.

Seq. ID Method

227641

BLASTX

LIB3189-040-P1-K1-A12



## hirsutum]

```
227636
Seq. No.
Seq. ID
                  LIB3189-039-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g285636
BLAST score
                  268
E value
                  2.0e-23
Match length
                  129
% identity
                  51
NCBI Description (D14161) ORF [Hordeum vulgare]
                  227637
Seq. No.
Seq. ID
                  LIB3189-039-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g992706
BLAST score
                  572
E value
                  4.0e-59
Match length
                  122
% identity
                  84
NCBI Description (U33758) UBC13 [Arabidopsis thaliana]
                  227638
Seq. No.
Seq. ID
                  LIB3189-039-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  q4262250
BLAST score
                  495
E value
                  4.0e-50
Match length
                  144
                  73
% identity
NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]
Seq. No.
                  227639
Seq. ID
                  LIB3189-040-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g1843527
BLAST score
                  248
                  2.0e-21
E value
Match length
                  55
% identity
                  91
NCBI Description (U73747) annexin [Gossypium hirsutum]
Seq. No.
                  227640
Seq. ID
                  LIB3189-040-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  q1888357
BLAST score
                  238
                  4.0e-20
E value
Match length
                  120
% identity
                  45
                  (X98130) alpha-mannosidase [Arabidopsis thaliana]
NCBI Description
                  >gi_1890154_emb CAA72432 (Y11767) alpha-mannosidase
                  precursor [Arabidopsis thaliana]
```



```
q4006829
NCBI GI
BLAST score
                  375
E value
                  4.0e-36
Match length
                  123
                  59
% identity
                  (AC005970) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  227642
Seq. No.
Seq. ID
                  LIB3189-040-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q2501850
                  203
BLAST score
                  2.0e-16
E value
Match length
                  39
% identity
                  100
NCBI Description
                 (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]
                  227643
Seq. No.
                  LIB3189-040-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3980396
BLAST score
                  462
E value
                  3.0e-52
Match length
                  114
% identity
                  81
NCBI Description
                  (AC004561) putative C-4 sterol methyl oxidase [Arabidopsis
                  thaliana]
                  227644
Seq. No.
Seq. ID
                  LIB3189-040-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g1173209
BLAST score
                  394
E value
                  1.0e-38
Match length
                  81
% identity
                  94
                  40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal
NCBI Description
                  protein S16 protein - upland cotton
                  >gi 439654 emb CAA53567 (X75954) RS16 protein, 40S subunit
                   [Gossypium hirsutum]
Seq. No.
                  227645
Seq. ID
                  LIB3189-040-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g480450
BLAST score
                  442
E value
                  7.0e-44
Match length
                  122
                  75
% identity
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
NCBI Description
```

thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid

reductoisomerase [Arabidopsis thaliana]

227646 Seq. No.

Seq. ID LIB3189-040-P1-K1-B11

Method BLASTX NCBI GI g586004



```
BLAST score
                   632
E value
                   4.0e-66
Match length
                   128
                   90
% identity
                   SUPEROXIDE DISMUTASE [CU-ZN] >gi 421962 pir S34267
NCBI Description
                   superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato
                   >gi_542090_pir__S40404 superoxide dismutase (EC 1.15.1.1)
(Cu-Zn) - sweet potato >gi_311971_emb_CAA51654_ (X73139)
                   superoxide dismutase [Ipomoea batatas]
                   227647
Seq. No.
Seq. ID
                   LIB3189-040-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   q2129473
BLAST score
                   237
E value
                   8.0e-20
                   92
Match length
                   50
% identity
NCBI Description
                   arabinogalactan-like protein - loblolly pine >gi 607774
                   (U09556) arabinogalactan-like protein [Pinus taeda]
Seq. No.
                   227648
Seq. ID
                   LIB3189-040-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   g1173209
BLAST score
                   150
E value
                   3.0e-10
Match length
                   51
% identity
                   67
NCBI Description
                   40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal
                   protein S16 protein - upland cotton
                   >gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit
                   [Gossypium hirsutum]
Seq. No.
                   227649
Seq. ID
                   LIB3189-040-P1-K1-B8
Method
                 BLASTX
NCBI GI
                   g1172872
BLAST score
                   547
E value
                   3.0e-56
Match length
                   125
                   82
% identity
NCBI Description
                  CYSTEINE PROTEINASE RD19A PRECURSOR >gi 541856 pir JN0718
                   drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
                   precursor - Arabidopsis thaliana >gi 435618 dbj BAA02373
                   (D13042) thiol protease [Arabidopsis thaliana]
                   >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible
                   cysteine proteinase RD19A precursor [Arabidopsis thaliana]
Seq. No.
                   227650
```

 Seq. No.
 227650

 Seq. ID
 LIB3189-040-P1-K1-C10

 Method
 BLASTX

 NCBI GI
 g3334113

 BLAST score
 466

E value 1.0e-46 Match length 89 % identity 100



NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >gi\_1006831 (U35015) acyl-CoA-binding protein [Gossypium hirsutum]

Seq. No. 227651

Seq. ID LIB3189-040-P1-K1-C11

Method BLASTX
NCBI GI g2970051
BLAST score 223
E value 2.0e-18
Match length 60
% identity 67

NCBI Description (AB012110) ARG10 [Vigna radiata]

Seq. No. 227652

Seq. ID LIB3189-040-P1-K1-C12

Method BLASTX
NCBI GI g3493172
BLAST score 411
E value 2.0e-40
Match length 91
% identity 89

NCBI Description (U89609) fiber annexin [Gossypium hirsutum]

Seq. No. 227653

Seq. ID LIB3189-040-P1-K1-C5

Method BLASTX
NCBI GI g3805845
BLAST score 240
E value 5.0e-20
Match length 86
% identity 56

NCBI Description (AL031986) putative protein [Arabidopsis thaliana]

Seq. No. 227654

Seq. ID LIB3189-040-P1-K1-C6

Method BLASTX
NCBI GI g3493172
BLAST score 275
E value 8.0e-25
Match length 64
% identity 84

NCBI Description (U89609) fiber annexin [Gossypium hirsutum]

Seq. No. 227655

Seq. ID LIB3189-040-P1-K1-C7

Method BLASTX
NCBI GI g1168257
BLAST score 579
E value 5.0e-60
Match length 137
% identity 82

NCBI Description ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC ISOZYME 1

(TRANSAMINASE A)  $>gi_693690$  (U15033) aspartate

aminotransferase [Arabidopsis thaliana]

Seq. No. 227656

Seq. ID LIB3189-040-P1-K1-D10



```
Method
                  BLASTX
NCBI GI
                  q3341681
BLAST score
                  657
E value
                  4.0e-69
Match length
                  140
% identity
                  (AC003672) small GTP-binding protein [Arabidopsis thaliana]
NCBI Description
                  >gi_741994_prf__2008312A GTP-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  227657
Seq. ID
                  LIB3189-040-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  q1173104
BLAST score
                  584
                  2.0e-60
E value
Match length
                  125
                  76
% identity
NCBI Description RIBONUCLEASE 2 PRECURSOR >gi_289210 (M98336) ribonuclease
                   [Arabidopsis thaliana] >gi_2642160 (AC003000) ribonuclease,
                  RNS2 [Arabidopsis thaliana]
Seq. No.
                  227658
Seq. ID
                  LIB3189-040-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q2811278
BLAST score
                  727
E value
                  3.0e-77
Match length
                  149
                  89
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                  227659
Seq. ID
                  LIB3189-040-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g3461820
BLAST score
                  237
E value
                  9.0e-20
                  59
Match length
                  63
% identity
NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.
                  227660
Seq. ID
                  LIB3189-040-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g464707
BLAST score
                  692
E value
                  4.0e-73
                  152
Match length
                  88
% identity
                 40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal
NCBI Description
                  protein S18.A - Arabidopsis thaliana
```

>gi\_405613\_emb\_CAA80684\_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273 (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi 434345\_emb\_CAA82274\_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi\_434906\_emb\_CAA82275\_ (Z28962)

BLAST score

E value

223

7.0e-19



S18 ribosomal protein [Arabidopsis thaliana] >gi\_2505871\_emb\_CAA72909\_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi\_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb\_Z28701, DNA gb\_Z23165 from A. thaliana. ESTs gb\_T21121, gb\_Z17755, gb\_R64776 and gb\_R30430 come from this gene. [Arabidopsis thaliana] >gi\_4538910\_emb\_CAB39647.1\_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

```
227661
Seq. No.
                  LIB3189-040-P1-K1-F2
Seq. ID
                  BLASTX
Method
                  g113240
NCBI GI
                  427
BLAST score
                  2.0e-50
E value
Match length
                  102
                  98
% identity
NCBI Description ACTIN 2 >gi_71636_pir__ATRZ2 actin 2 - rice
                  >gi_20329_emb_CAA33873_ (X15864) actin [Oryza sativa]
                  227662
Seq. No.
                  LIB3189-040-P1-K1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3702368
BLAST score
                  644
                  2.0e-67
E value
Match length
                  159
                  74
% identity
NCBI Description (AJ001855) alpha subunit of F-actin capping protein
                   [Arabidopsis thaliana]
                  227663
Seq. No.
                  LIB3189-040-P1-K1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3063698
BLAST score
                  148
E value
                   1.0e-09
Match length
                   44
                   66
% identity
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]
                   227664
Seq. No.
                   LIB3189-040-P1-K1-G10
Seq. ID
                  BLASTX
Method
                   g1084358
NCBI GI
BLAST score
                   498
E value
                   2.0e-50
Match length
                   143
                   69
% identity
NCBI Description ATP synthase - soybean
Seq. No.
                   227665
                   LIB3189-040-P1-K1-G12
Seq. ID
                   BLASTX
Method
                   q1350988
NCBI GI
```



56 Match length 84 % identity 40S RIBOSOMAL PROTEIN S3B (S1B) >gi 2119058 pir I51635 NCBI Description ribosomal protein S1 - African clawed frog >gi\_587600\_emb\_CAA84291\_ (Z34530) ribosomal protein S1 [Xenopus laevis] >gi 587602\_emb\_CAA84290\_ (Z34529) ribosomal protein [Xenopus laevis] Seq. No. 227666 LIB3189-040-P1-K1-G3 Seq. ID Method BLASTX NCBI GI g3757514 BLAST score 487 3.0e-49E value Match length 106 86 % identity (AC005167) putative plasma membrane intrinsic protein NCBI Description [Arabidopsis thaliana] Seq. No. 227667 LIB3189-040-P1-K1-G4 Seq. ID BLASTX Method NCBI GI g4204300 BLAST score 200 2.0e-15 E value Match length 79 51 % identity NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana] Seq. No. 227668 LIB3189-040-P1-K1-G6 Seq. ID BLASTX Method g3643603 NCBI GI BLAST score 571 E value 4.0e-59 130 Match length 84 % identity NCBI Description (AC005395) unknown protein [Arabidopsis thaliana] 227669 Seq. No. LIB3189-040-P1-K1-G9 Seq. ID BLASTX Method g2129499 NCBI GI BLAST score 717 E value 4.0e-76 Match length 145 92 % identity NCBI Description fiber protein E6 (clone CKE6-4A) - upland cotton >gi 1000086 (U30506) E6 [Gossypium hirsutum] 227670 Seq. No. LIB3189-040-P1-K1-H3

Seq. ID

BLASTX Method NCBI GI q3098571 BLAST score 174 2.0e-12 E value Match length 151



% identity (AF049028) BURP domain containing protein [Brassica napus] NCBI Description 227671 Seq. No. LIB3189-040-P1-K1-H4 Seq. ID BLASTX Method q4580395 NCBI GI 224 BLAST score E value 3.0e-18 121 Match length 45 % identity (AC007171) putative kinesin-related protein [Arabidopsis NCBI Description thaliana] 227672 Seq. No. LIB3189-040-P1-K1-H5 Seq. ID BLASTX Method g2982268 NCBI GI 547 BLAST score E value 3.0e-56 Match length 115 93 % identity NCBI Description (AF051217) probable 40S ribosomal protein S15 [Picea mariana] 227673 Seq. No. LIB3189-040-P1-K1-H7 Seq. ID BLASTX Method NCBI GI g730645 BLAST score 226 E value 9.0e-19 Match length 72 67 % identity 40S RIBOSOMAL PROTEIN S15 >gi\_629556\_pir\_\_S43412 ribosomal NCBI Description protein S15 - Arabidopsis thaliana >gi 313152 emb CAA80679 (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >qi 313188 emb CAA80681 (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi\_1903366\_gb\_AAB70449\_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb R29788,gb\_ATTS0365 come from this gene. [Arabidopsis thaliana] 227674 Seq. No. LIB3189-040-P1-K1-H9 Seq. ID BLASTX Method NCBI GI g1928981 242 BLAST score 1.0e-20 E value 72 Match length 74 % identity NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis]

Seq. No. 227675

Seq. ID LIB3189-041-P1-K1-A2

Method BLASTX NCBI GI g4204300

NCBI GI

E value

BLAST score

Match length

314

68

7.0e-29



```
BLAST score
                   187
                   5.0e-14
E value
                   72
Match length
                   53
% identity
                   (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   227676
Seq. No.
                   LIB3189-041-P1-K1-A8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1708152
BLAST score
                   143
                   8.0e-09
E value
                   97
Match length
                   44
% identity
                   PROBABLE ATP-DEPENDENT RNA HELICASE DBP5 (HELICASE CA5/6)
NCBI Description
                   >gi_2133053_pir__S66920 probable RNA helicase CA5/6 - yeast
                   (Saccharomyces cerevisiae) >gi_1353268 (U28135) Dbp5p [Saccharomyces cerevisiae] >gi_1420175_emb_CAA99237_
                    (Z74954) ORF YOR046c [Saccharomyces cerevisiae]
Seq. No.
                   227677
                   LIB3189-041-P1-K1-B11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4324967
BLAST score
                    541
                    2.0e-55
E value
Match length
                   103
                    100
% identity
NCBI Description (AF114796) ADP-ribosylation factor [Glycine max]
                    227678
Seq. No.
                    LIB3189-041-P1-K1-B6
Seq. ID
Method
                    BLASTX
                    q4210948
NCBI GI
                    341
BLAST score
E value
                    3.0e - 32
Match length
                    77
% identity
NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]
                    227679
Seq. No.
                    LIB3189-041-P1-K1-B7
Seq. ID
Method
                    BLASTX
NCBI GI
                    g4210948
BLAST score
                    599
E value
                    3.0e-62
Match length
                    147
% identity
                    82
NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]
                    227680
Seq. No.
                    LIB3189-041-P1-K1-B9
Seq. ID
                    BLASTX
Method
                    g1173187
```

Match length

% identity

136

63



```
% identity
                  40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673
NCBI Description
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                  strawberry >gi_643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
                  227681
Seq. No.
                  LIB3189-041-P1-K1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2832717
                  304
BLAST score
                  1.0e-27
E value
                  93
Match length
% identity
                  63
NCBI Description (AJ003114) alkaline/neutral invertase [Lolium temulentum]
                  227682
Seq. No.
                  LIB3189-041-P1-K1-C11
Seq. ID
Method
                  BLASTX
                  g1332579
NCBI GI
BLAST score
                  616
E value
                  3.0e-64
                  125
Match length
                  10
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
                   227683
Seq. No.
                  LIB3189-041-P1-K1-C12
Seq. ID
                  {\tt BLASTX}
Method
                   g464621
NCBI GI
BLAST score
                  376
                   4.0e-36
E value
                   97
Match length
                   78
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir S28586
                   ribosomal protein ML16 - common ice plant
                   >qi 19539 emb CAA49175 (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
                   227684
Seq. No.
Seq. ID
                   LIB3189-041-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   q70644
BLAST score
                   593
                   1.0e-61
E value
                   124
Match length
% identity
                   18
NCBI Description ubiquitin precursor - common sunflower (fragment)
                   227685
Seq. No.
                   LIB3189-041-P1-K1-C7
Seq. ID
Method
                   BLASTX
                   q232202
NCBI GI
BLAST score
                   446
E value
                   3.0e-44
```



NCBI Description GLUTATHIONE S-TRANSFERASE PARB (CLASS-PHI)

>gi\_285295\_pir\_\_A41789 glutathione transferase (EC
2.5.1.18) - common tobacco >gi\_218294\_dbj\_BAA01394\_
(D10524) glutathione S-transferase [Nicotiana tabacum]

Seq. No. 227686

Seq. ID LIB3189-041-P1-K1-D10

Method BLASTX
NCBI GI g2367392
BLAST score 180
E value 1.0e-13
Match length 82
% identity 40

NCBI Description (U82513) random slug cDNA25 protein [Dictyostelium

discoideum]

Seq. No. 227687

Seq. ID LIB3189-041-P1-K1-D12

Method BLASTX
NCBI GI g3080401
BLAST score 419
E value 3.0e-41
Match length 108
% identity 73

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

>gi 4455265 emb CAB36801.1 (AL035527) putative protein

[Arabidopsis thaliana]

Seq. No. 227688

Seq. ID LIB3189-041-P1-K1-D2

Method BLASTX
NCBI GI g3548818
BLAST score 179
E value 2.0e-13
Match length 41
% identity 83

NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 227689

Seq. ID LIB3189-041-P1-K1-D6

Method BLASTX
NCBI GI g3914394
BLAST score 183
E value 1.0e-13
Match length 42
% identity 83

NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE

(PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi\_2118335\_pir\_\_S60473 phosphoglycerate mutase (EC 5.4.2.1) - common ice plant >gi 602426 (U16021)

phosphoglyceromutase [Mesembryanthemum crystallinum]

Seq. No. 227690

Seq. ID LIB3189-041-P1-K1-D7

Method BLASTX NCBI GI g2959322 BLAST score 684



E value 3.0e-72 Match length 154 84

NCBI Description (Y14616) Importin alpha-like protein [Arabidopsis thaliana]

Seq. No. 227691

Seq. ID LIB3189-041-P1-K1-D8

Method BLASTX
NCBI GI g136739
BLAST score 449
E value 1.0e-60
Match length 139
% identity 88

NCBI Description UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE

PYROPHOSPHORYLASE) (UDPGP) >gi 67061\_pir\_\_XNPOU

UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -

potato >gi 218001 dbj BAA00570 (D00667) UDP-glucose

pyrophosphorylase precursor [Solanum tuberosum]

Seq. No. 227692

Seq. ID LIB3189-041-P1-K1-D9

Method BLASTX
NCBI GI g130720
BLAST score 269
E value 1.0e-23
Match length 123
% identity 42

NCBI Description PROTEOLIPID PROTEIN PPA1 >gi\_101508\_pir\_\_A34633 probable

H+-transporting ATPase (EC 3.6.1.35) lipid-binding protein - yeast (Saccharomyces cerevisiae) >gi\_172221 (M35294) proteolipid protein of proton ATPase [Saccharomyces

cerevisiae] >gi\_500700 (U10399) Ppa1p: Proteolipid protein

of proton ATPase [Saccharomyces cerevisiae]

Seq. No. 227693

Seq. ID LIB3189-041-P1-K1-E10

Method BLASTX
NCBI GI 94337175
BLAST score 485
E value 7.0e-49
Match length 138
% identity 68

NCBI Description (AC006416) ESTs gb T20589, gb T04648, gb AA597906,

gb\_T04111, gb\_R841\overline{80}, gb\_R654\overline{28}, gb\_T4\overline{439}, gb\_T76570, gb\_R90004, gb\_T45020, gb\_T42457, gb\_T20921, gb\_AA042762 and gb\_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No. 227694

Seq. ID LIB3189-041-P1-K1-E11

Method BLASTX
NCBI GI g1703375
BLAST score 509
E value 9.0e-52
Match length 99
% identity 99

NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi\_965483\_dbj\_BAA08259\_ (D45420)

DcARF1 [Daucus carota]

% identity

92



```
227695
Seq. No.
                   LIB3189-041-P1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2129630
BLAST score
                   415
E value
                   1.0e-40
Match length
                   106
% identity
                   67
                   lamin - Arabidopsis thaliana >gi 1262754 emb CAA65750
NCBI Description
                   (X97023) lamin [Arabidopsis thal\overline{i}ana] >g\overline{i}_33\overline{9}5760 (U7\overline{7}721)
                   unknown [Arabidopsis thaliana]
Seq. No.
                   227696
Seq. ID
                   LIB3189-041-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g3702349
BLAST score
                   445
E value
                   3.0e-44
Match length
                   110
% identity
                   80
NCBI Description (AC005397) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   227697
Seq. ID
                   LIB3189-041-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   g126896
BLAST score
                   606
E value
                   4.0e-63
Match length
                   138
% identity
                   86
                  MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                   >gi 319831_pir__DEPUMW malate dehydrogenase (EC 1.1.1.37)
                   precursor, mitochondrial - watermelon
                   >gi 18297 emb CAA35239 (X17362) precursor protein (AA -27
                   to 320) [Citrullus lanatus]
                   227698
Seq. No.
Seq. ID
                   LIB3189-041-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   g3264759
BLAST score
                   512
E value
                   4.0e-52
                   120
Match length
% identity
                   83
NCBI Description (AF071889) 40S ribosomal protein S8 [Prunus armeniaca]
                   227699
Seq. No.
Seq. ID
                   LIB3189-041-P1-K1-F6
Method
                   BLASTX
NCBI GI
                   g1346675
BLAST score
                   529
                   5.0e-54
E value
Match length
                   107
```

>gi 499112 (U10283) nucleoside diphosphate kinase [Flaveria

NCBI Description NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B)



## bidentis]

227700 Seq. No. Seq. ID LIB3189-041-P1-K1-F7 Method BLASTX NCBI GI g3123161 BLAST score 135 1.0e-10 E value Match length 99 22 % identity NCBI Description HYPOTHETICAL 77.0 KD TRP-ASP REPEATS CONTAINING PROTEIN

F35G12.4 IN CHROMOSOME III >gi\_3876723\_emb\_CAA86335\_(Z46242) similar to beta-transducin; cDNA EST EMBL:Z14703 comes from this gene; cDNA EST EMBL:D67532 comes from this gene; cDNA EST EMBL:D69055 comes from this gene; cDNA EST

EMBL:D64515 comes from this gene; cDNA EST EMBL:D655

 Seq. No.
 227701

 Seq. ID
 LIB3189-041-P1-K1-F8

 Method
 BLASTX

 NCBI GI
 g1616659

 BLAST score
 678

 E value
 2.0e-71

E value 2.0e
Match length 150
% identity 85

NCBI Description (U49387) adenylosuccinate synthetase [Triticum aestivum]

Seq. No. 227702

Seq. ID LIB3189-041-P1-K1-F9

Method BLASTX
NCBI GI 94204300
BLAST score 195
E value 6.0e-15
Match length 75
% identity 52

NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No. 227703

Seq. ID LIB3189-041-P1-K1-G10

Method BLASTX
NCBI GI g231586
BLAST score 760
E value 4.0e-81
Match length 155
% identity 97

NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR

>gi\_82027\_pir\_\_S20504 H+-transporting ATP synthase (EC
3.6.1.34) beta chain, mitochondrial - Para rubber tree
>gi\_18831\_emb\_CAA41401\_ (X58498) mitochondrial ATP synthase

beta-subunit [Hevea brasiliensis]

Seq. No. 227704

Seq. ID LIB3189-041-P1-K1-G11

Method BLASTX
NCBI GI g1174592
BLAST score 709
E value 4.0e-75



```
Match length
                  134
                  98
% identity
                  TUBULIN ALPHA-1 CHAIN >qi 2119270 pir S60233 alpha-tubulin
NCBI Description
                  - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                  sativum]
                  227705
Seq. No.
                  LIB3189-041-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2935416
BLAST score
                  662
                  1.0e-69
E value
Match length
                  157
                  81
% identity
NCBI Description (AF047896) isoflavone reductase homolog [Betula pendula]
                  227706
Seq. No.
                  LIB3189-041-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2384758
BLAST score
                  412
                  2.0e-40
E value
Match length
                  86
% identity
                  92
NCBI Description (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza
                  sativa]
                  227707
Seq. No.
                  LIB3189-041-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4008159
BLAST score
                  631
E value
                  5.0e-66
Match length
                  154
% identity
                  79
NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]
                  227708
Seq. No.
Seq. ID
                  LIB3189-041-P1-K1-G5
                  BLASTX
Method
NCBI GI
                  g1353516
BLAST score
                  314
E value
                  7.0e-29
                  109
Match length
% identity
                   60
NCBI Description (U38651) sugar transporter [Medicago truncatula]
                  227709
Seq. No.
Seq. ID
                  LIB3189-041-P1-K1-G6
                  BLASTX
Method
NCBI GI
                  g1351974
BLAST score
                  548
```

2.0e-56 E value 112 Match length % identity 96

NCBI Description ADP-RIBOSYLATION FACTOR >gi 1076788 pir S49325

ADP-ribosylation factor - maize >gi 1076789 pir S53486



ADP-ribosylation factor - maize >gi\_556686\_emb\_CAA56351\_ (X80042) ADP-ribosylation factor [Zea mays]

 Seq. No.
 227710

 Seq. ID
 LIB3189-041-P1-K1-G7

 Method
 BLASTX

 NCBI GI
 g2662343

 BLAST score
 583

 E value
 2.0e-60

113 98

% identity 98
NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 227711

Match length

Seq. ID LIB3189-041-P1-K1-G9

Method BLASTX
NCBI GI g3367534
BLAST score 505
E value 3.0e-59
Match length 125
% identity 81

NCBI Description (AC004392) Strong similarity to coatamer alpha subunit

(HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis

thaliana]

Seq. No. 227712

Seq. ID LIB3189-041-P1-K1-H1

Method BLASTX
NCBI GI g2754860
BLAST score 199
E value 5.0e-16
Match length 46
% identity 83

NCBI Description (AF039953) cytosolic ascorbate peroxidase [Fragaria x

ananassa]

Seq. No. 227713

Seq. ID LIB3189-041-P1-K1-H10

Method BLASTX
NCBI GI g3482967
BLAST score 279
E value 1.0e-24
Match length 70
% identity 77

NCBI Description (AL031369) Protein phosphatase 2C-like protein [Arabidopsis

thaliana] >gi\_4559345\_gb\_AAD23006.1\_AC006585\_1 (AC006585)

protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 227714

Seq. ID LIB3189-041-P1-K1-H11

Method BLASTX
NCBI GI g2498885
BLAST score 219
E value 7.0e-18
Match length 121
% identity 41

NCBI Description PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM A





```
>gi_1296664_emb_CAA65774_ (X97064) Sec23 protein [Homo
sapiens]
```

Seq. No. 227715

Seq. ID LIB3189-041-P1-K1-H12

Method BLASTX
NCBI GI g2231702
BLAST score 605
E value 5.0e-63
Match length 118
% identity 93

NCBI Description (U92086) clathrin assembly protein AP19 homolog

[Arabidopsis thaliana] >gi 3080409\_emb CAA18728\_ (AL022604)

clathrin assembly protein AP19 homolog [Arabidopsis

thaliana]

Seq. No. 227716

Seq. ID LIB3189-041-P1-K1-H2

Method BLASTX
NCBI GI g4056488
BLAST score 326
E value 3.0e-30
Match length 76
% identity 75

NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 227717

Seq. ID LIB3189-041-P1-K1-H3

Method BLASTX
NCBI GI g1246403
BLAST score 286
E value 1.0e-25
Match length 88
% identity 66

NCBI Description (X94698) TINY [Arabidopsis thaliana] >gi\_3406035 (AC005405)

TINY [Arabidopsis thaliana]

Seq. No. 227718

Seq. ID LIB3189-041-P1-K1-H7

Method BLASTX
NCBI GI g3075398
BLAST score 238
E value 6.0e-20
Match length 89
% identity 51

NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]

Seq. No. 227719

Seq. ID LIB3189-042-P1-K1-A11

Method BLASTX
NCBI GI g3702333
BLAST score 200
E value 2.0e-15
Match length 109
% identity 44

NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]



```
227720
Seq. No.
Seq. ID
                  LIB3189-042-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g3367534
                  677
BLAST score
E value
                  2.0e-71
Match length
                  155
% identity
                  81
NCBI Description
                  (AC004392) Strong similarity to coatamer alpha subunit
                  (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis
                  thaliana]
                  227721
Seq. No.
                  LIB3189-042-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3869088
                  528
BLAST score
E value
                  5.0e-54
Match length
                  105
% identity
                  97
NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
                  227722
Seq. No.
Seq. ID
                  LIB3189-042-P1-K1-A8
Method
                  BLASTX
                  g2811278
NCBI GI
BLAST score
                  565
E value
                  2.0e-58
Match length
                  119
% identity
                  87
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                  227723
Seq. ID
                  LIB3189-042-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  q2244732
BLAST score
                  328
E value
                  6.0e-47
                  109
Match length
                  93
% identity
NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
                  227724
Seq. No.
Seq. ID
                  LIB3189-042-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  q2497753
BLAST score
                  376
E value
                  4.0e-36
Match length
                  123
% identity
                  55
NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
```

>gi 1321915\_emb\_CAA65477\_ (X96716) lipid transfer protein

[Prunus dulcis]

Seq. No. 227725

LIB3189-042-P1-K1-B12 Seq. ID

Method BLASTX



```
q1203832
NCBI GI
                  670
BLAST score
E value
                  1.0e-70
Match length
                  149
% identity
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
NCBI Description
                  [Hordeum vulgare] >gi_1588407_prf 2208395A beta-D-glucan
                  exohydrolase [Hordeum vulgare]
Seq. No.
                  227726
                  LIB3189-042-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2673912
BLAST score
                  427
E value
                  4.0e-42
Match length
                  125
% identity
                  65
NCBI Description (AC002561) unknown protein [Arabidopsis thaliana]
Seq. No.
                  227727
Seq. ID
                  LIB3189-042-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g2244931
BLAST score
                  169
E value
                  8.0e-12
Match length
                  130
                  35
% identity
                  (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3426058 emb CAA07572_ (AJ007585) IB1P8-4 protein
                  [Arabidopsis thaliana]
                  227728
Seq. No.
Seq. ID
                  LIB3189-042-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g3395426
BLAST score
                  225
                  1.0e-18
E value
                  90
Match length
                  49
% identity
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                  227729
Seq. No.
Seq. ID
                  LIB3189-042-P1-K1-B6
                  BLASTX
Method
NCBI GI
                  g267069
BLAST score
                  377
                  4.0e-65
E value
                  124
Match length
                  99
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
```

Seq. No. 227730

Seq. ID LIB3189-042-P1-K1-B8

Method BLASTX



```
q2505879
NCBI GI
BLAST score
                     246
E value
                     3.0e-21
Match length
                     55
% identity
                     85
                    (Y12776) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                     227731
Seq. ID
                     LIB3189-042-P1-K1-C2
Method
                     BLASTX
NCBI GI
                     q4539404
BLAST score
                     194
E value
                     9.0e-15
Match length
                     101
% identity
                     45
NCBI Description
                     (AL049524) putative protein [Arabidopsis thaliana]
                     227732
Seq. No.
                     LIB3189-042-P1-K1-C3
Seq. ID
Method
                     BLASTX
NCBI GI
                     q3319921
BLAST score
                     275
E value
                     2.0e-24
Match length
                     99
                     60
% identity
NCBI Description
                     (AJ223388) Hev b 3 [Hevea brasiliensis]
                     >gi_3319923_emb_CAA11304_ (AJ223389) Hev b 3 [Hevea
brasiliensis] >gi_3319925_emb_CAA11305_ (AJ223390) Hev b 3
[Hevea brasiliensis] >gi_3818475 (AF051317) small rubber
                     particle protein [Hevea brasiliensis]
Seq. No.
                     227733
                     LIB3189-042-P1-K1-C7
                     BLASTX
                     g2392772
                     162
                     4.0e-11
                     86
                     48
```

```
Seq. ID
Method
NCBI GI
BLAST score
E value
```

Match length % identity

(AC002534) putative chloroplast prephenate dehydratase NCBI Description [Arabidopsis thaliana]

Seq. No. 227734

Seq. ID LIB3189-042-P1-K1-C8

Method BLASTX NCBI GI q2129499 BLAST score 628 E value 1.0e-65 130 Match length 90 % identity

NCBI Description fiber protein E6 (clone CKE6-4A) - upland cotton

>gi 1000086 (U30506) E6 [Gossypium hirsutum]

227735 Seq. No.

Seq. ID LIB3189-042-P1-K1-D11

Method BLASTXNCBI GI g3269288



```
BLAST score
                   350
E value
                   4.0e-33
                  79
Match length
% identity
                   84
                  (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                   227736
Seq. No.
                  LIB3189-042-P1-K1-D2
Seq. ID
Method
                   BLASTX
                   g2117168
NCBI GI
BLAST score
                   407
                   9.0e-40
E value
                   77
Match length
                   100
% identity
                  (Z73961) RAC1 [Lotus japonicus]
NCBI Description
                   227737
Seq. No.
                   LIB3189-042-P1-K1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2735550
                   214
BLAST score
                   4.0e-17
E value
Match length
                   89
% identity
                   47
NCBI Description (U96638) unc-50 related protein; URP [Rattus norvegicus]
                   227738
Seq. No.
                   LIB3189-042-P1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3482967
BLAST score
                   410
E value
                   4.0e-40
                   96
Match length
                   79
% identity
                   (AL031369) Protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                   thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585)
                   protein phosphatase 2C [Arabidopsis thaliana]
                   227739
Seq. No.
                   LIB3189-042-P1-K1-D6
Seq. ID
                   BLASTX
Method
                   g1246403
NCBI GI
BLAST score
                   294
                   1.0e-26
E value
Match length
                   93
% identity
                   66
                   (X94698) TINY [Arabidopsis thaliana] >gi_3406035 (AC005405)
NCBI Description
                   TINY [Arabidopsis thaliana]
                   227740
Seq. No.
                   LIB3189-042-P1-K1-E4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q401213
.BLAST score
                   225
E value
                   2.0e-18
```

87

61

Match length

% identity



```
ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE PRECURSOR >gi 166792
NCBI Description
                  (M96073) phosphoribosylanthranilate transferase
                  [Arabidopsis thaliana] >gi 445600 prf 1909347A
                  phosphoribosylanthranilate transferase [Arabidopsis
                  thaliana]
                  227741
Seq. No.
                  LIB3189-042-P1-K1-E6
Seq. ID
                  BLASTX
Method
                  q2459417
NCBI GI
                  404
BLAST score
                  2.0e-39
E value
                  103
Match length
                   77
% identity
                   (AC002332) putative pre-mRNA splicing factor PRP19
NCBI Description
                   [Arabidopsis thaliana]
                   227742
Seq. No.
                  LIB3189-042-P1-K1-E7
Seq. ID
                  BLASTX
Method
                   g167367
NCBI GI
                   617
BLAST score
                   2.0e-64
E value
                   153
Match length
                   79
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                   227743
Seq. No.
                   LIB3189-042-P1-K1-F10
Seq. ID
                   BLASTX
Method
                   q1402833
NCBI GI
                   225
BLAST score
                   2.0e-18
E value
                   81
Match length
                   57
 % identity
                  (U60147) plasma membrane major intrinsic protein 1 [Beta
NCBI Description
                   vulgaris]
                   227744
 Seq. No.
                   LIB3189-042-P1-K1-F4
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g3925363
                   456
 BLAST score
                   1.0e-45
 E value
                   138
 Match length
 % identity
                   66
 NCBI Description (AF067961) homeodomain protein [Malus domestica]
                   227745
 Seq. No.
                   LIB3189-042-P1-K1-F5
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                    g3158476
 BLAST score
                    451
                    5.0e-45
 E value
                   121
 Match length
                    83
 % identity
 NCBI Description (AF067185) aquaporin 2 [Samanea saman]
```

Seq. No.

227751



```
227746
Seq. No.
                  LIB3189-042-P1-K1-F7
Seq. ID
Method
                  BLASTX
                  g2765240
NCBI GI
                  212
BLAST score
                  6.0e-17
E value
                  119
Match length
% identity
                  40
                  (Y12805) invertase inhibitor [Nicotiana tabacum]
NCBI Description
                  227747
Seq. No.
                  LIB3189-042-P1-K1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  a2829204
BLAST score
                  502
                   7.0e-51
E value
Match length
                  120
                   85
% identity
                  (AF044204) lipid transfer protein precursor [Gossypium
NCBI Description
                  hirsutum]
                   227748
Seq. No.
                  LIB3189-042-P1-K1-G11
Seq. ID
Method
                  BLASTX
                  g3445200
NCBI GI
                  147
BLAST score
                   2.0e-09
E value
                   106
Match length
                   40
% identity
                  (AC004786) putative squalene epoxidase [Arabidopsis
NCBI Description
                   thaliana]
                   227749
Seq. No.
Seq. ID
                   LIB3189-042-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   q3876865
BLAST score
                   172
                   3.0e-12
E value
                   96
Match length
% identity
                   36
                   (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177
NCBI Description
                   comes from this gene; cDNA EST EMBL: C09822 comes from this
                   gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST
                   yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co
Seq. No.
                   227750
                   LIB3189-042-P1-K1-G6
Seq. ID
Method
                   BLASTX
                   g1350930
NCBI GI
BLAST score
                   468
E value
                   6.0e-47
                   100
Match length
                   92
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S13
```

NCBI GI

E value

BLAST score

g3493172

9.0e-52

508



```
LIB3189-042-P1-K1-H2
Seq. ID
Method
                   BLASTX
                   g3150415
NCBI GI
BLAST score
                   262
                   3.0e-38
E value
Match length
                   112
                   49
% identity
                   (AC004165) sec13-related protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3420046 (AC004680) sec13-related protein [Arabidopsis
                   thaliana]
                   227752
Seq. No.
                   LIB3189-042-P1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   a1170507
                   477
BLAST score
                   6.0e-48
E value
Match length
                   114
                   80
% identity
                   EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3)
NCBI Description
                   >gi_100276_pir__S22579 translation initiation factor eIF-4A
- curled-leaved tobacco >gi_19699_emb_CAA43514_ (X61206)
                   nicotiana eukaryotic translation initiation factor 4A
                   [Nicotiana plumbaginifolia]
                   227753
Seq. No.
                   LIB3189-042-P1-K1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1345643
                   438
BLAST score
E value
                   2.0e-43
                   134
Match length
% identity
                   66
                   FLAVONOID 3',5'-HYDROXYLASE 2 (F3'5'H) (CYTOCHROME P450
NCBI Description
                   75A3) (CYPLXXVA3) >gi_629709_pir__S38984 flavonoid
                    3',5'-hydroxylase Hf2 - garden petunia
                   >gi_311654_emb_CAA80265_ (Z22544) flavonoid
                    3',5'-hydroxylase [Petunia x hybrida]
                   >gi 738771_prf__2001426A flavonoid 3',5'-hydroxylase
                    [Petunia x hybrida]
Seq. No.
                   227754
                   LIB3189-042-P1-K1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                    g4115376
BLAST score
                   199
E value
                    2.0e-15
                   138
Match length
                    16
% identity
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
                    227755
Seq. No.
                   LIB3189-042-P1-K1-H7
Seq. ID
                   BLASTX
Method
```



```
111
Match length
                  90
% identity
NCBI Description (U89609) fiber annexin [Gossypium hirsutum]
Seq. No.
                  227756
                  LIB3189-042-P1-K1-H8
Seq. ID
                  BLASTX
Method
                  g1800281
NCBI GI
                  709
BLAST score
                  4.0e-75
E value
                  147
Match length
                  22
% identity
NCBI Description (U82086) polyubiquitin [Fragaria x ananassa]
                  227757
Seq. No.
                  LIB3189-043-P1-K1-A11
Seq. ID
                  BLASTX
Method
                  g3688188
NCBI GI
                  488
BLAST score
                  3.0e-49
E value
                  117
Match length
                  80
% identity
                  (AL031804) pyruvate decarboxylase-1 (Pdc1) [Arabidopsis
NCBI Description
                  thaliana]
                  227758
Seq. No.
                  LIB3189-043-P1-K1-A12
Seq. ID
Method
                  BLASTX
                  g1856971
NCBI GI
                  193
BLAST score
                   1.0e-21
E value
Match length
                   67
                   87
% identity
                  (D26058) This gene is specifically expressed at the S phase
NCBI Description
                   during the cell cycle in the synchronous culture of
                   periwinkle cells. [Catharanthus roseus]
                   227759
Seq. No.
                   LIB3189-043-P1-K1-A3
Seq. ID
Method
                   BLASTX
                   q1350944
NCBI GI
BLAST score
                   172
                   8.0e-13
E value
                   42
Match length
% identity
                   83
NCBI Description 40S RIBOSOMAL PROTEIN S17
Seq. No.
                   227760
                   LIB3189-043-P1-K1-A4
Seq. ID
                   BLASTX
Method
                   g2879867
NCBI GI
BLAST score
                   234
                   1.0e-19
E value
                   99
Match length
 % identity
                   48
                  (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces
NCBI Description
```

32538

pombe]



```
227761
Seq. No.
                  LIB3189-043-P1-K1-A7
Seq. ID
                  BLASTX
Method
                  g2497753
NCBI GI
                  323
BLAST score
                  5.0e-30
E value
                  115
Match length
                  53
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
NCBI Description
                  >gi 1321915 emb_CAA65477_ (X96716) lipid transfer protein
                  [Prunus dulcis]
                  227762
Seq. No.
                  LIB3189-043-P1-K1-A8
Seq. ID
Method
                  BLASTX
                  q3334661
NCBI GI
BLAST score
                  356
                  9.0e-34
E value
                  117
Match length
                  56
% identity
                  (Y10490) putative cytochrome P450 [Glycine max]
NCBI Description
                  227763
Seq. No.
                  LIB3189-043-P1-K1-B1
Seq. ID
                  BLASTX
Method
                   g3914430
NCBI GI
BLAST score
                   479
                   3.0e-48
E value
                   113
Match length
                   83
% identity
                  PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON
NCBI Description
                   CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)
                   >gi_2285800_dbj_BAA21650_ (D78172) 26S proteasome beta
                   subunit [Spinacia oleracea]
                   227764
Seq. No.
                   LIB3189-043-P1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4337175
                   490
BLAST score
                   2.0e-49
E value
                   138
Match length
% identity
                   (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
NCBI Description
                   gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                   gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
                   gb AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   LIB3189-043-P1-K1-B2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3935150
BLAST score
                   382
```

32539

8.0e-37

148

55

E value

Match length % identity



NCBI Description (AC005106) T25N20.14 [Arabidopsis thaliana] Seq. No. 227766

Seq. ID LIB3189-043-P1-K1-B6

Method BLASTX
NCBI GI g2501494
BLAST score 160
E value 7.0e-11
Match length 76
% identity 47

NCBI Description FLAVONOL 3-O-GLUCOSYLTRANSFERASE 5 (UDP-GLUCOSE FLAVONOID

3-O-GLUCOSYLTRANSFERASE 5) >gi\_542015\_pir\_\_S41951

UTP-glucose glucosyltransferase - cassava >gi\_453249\_emb\_CAA54612\_ (X77462) UTP-glucose

glucosyltransferase [Manihot esculenta]

Seq. No. 227767

Seq. ID LIB3189-043-P1-K1-B7

Method BLASTX
NCBI GI g2443751
BLAST score 710
E value 3.0e-75
Match length 153
% identity 89

NCBI Description (AF020303) fumarase [Arabidopsis thaliana] >gi\_2529676

(AC002535) putative fumarase [Arabidopsis thaliana]

Seq. No. 227768

Seq. ID LIB3189-043-P1-K1-C11

Method BLASTX
NCBI GI g1694976
BLAST score 450
E value 9.0e-45
Match length 129
% identity 68

NCBI Description (Y09482) HMG1 [Arabidopsis thaliana]

>gi\_2832361\_emb\_CAA74402 (Y14073) HMG protein [Arabidopsis

thaliana]

Seq. No. 227769

Seq. ID LIB3189-043-P1-K1-C2

Method BLASTX
NCBI GI g2842424
BLAST score 493
E value 7.0e-50
Match length 141
% identity 67

NCBI Description (AJ223948) RNA helicase [Homo sapiens]

Seq. No. 227770

Seq. ID LIB3189-043-P1-K1-C3

Method BLASTX
NCBI GI g4105269
BLAST score 237
E value 8.0e-20
Match length 148
% identity 39



(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase NCBI Description [Rattus norvegicus] 227771 Seq. No.

LIB3189-043-P1-K1-C5 Seq. ID Method BLASTX NCBI GI q1771162 BLAST score 237 E value 7.0e-20 Match length 141 % identity 60

(X98930) SBT2 [Lycopersicon esculentum] NCBI Description

>gi\_3687307\_emb\_CAA07000\_ (AJ006379) subtilisin-like

protease [Lycopersicon esculentum]

227772 Seq. No.

Seq. ID LIB3189-043-P1-K1-C8

Method BLASTX NCBI GI q1854386 BLAST score 269 E value 1.0e-30 Match length 146 % identity 53

NCBI Description (AB001375) similar to soluble NSF attachment protein [Vitis

vinifera]

Seq. No. 227773

LIB3189-043-P1-K1-C9 Seq. ID

Method BLASTX NCBI GI g3334115 BLAST score 334 E value 3.0e - 31Match length 96 71 % identity

NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)

(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium

hirsutum]

227774 Seq. No.

Seq. ID LIB3189-043-P1-K1-D10

BLASTX Method NCBI GI g3202042 BLAST score 550 E value 2.0e-56 Match length 133 80

NCBI Description (AF069324) 26S proteasome regulatory subunit S5A

[Mesembryanthemum crystallinum]

227775 Seq. No.

% identity

Seq. ID LIB3189-043-P1-K1-D12

Method BLASTX NCBI GI g2662415 BLAST score 141 1.0e-08 E value 48 Match length

Match length

% identity

136



```
% identity
NCBI Description (U97494) metallothionein-like protein [Prunus armeniaca]
                  227776
Seq. No.
Seq. ID
                  LIB3189-043-P1-K1-D2
                  BLASTX
Method
NCBI GI
                  g4240116
BLAST score
                  494
E value
                  5.0e-50
Match length
                  126
                  74
% identity
                  (AB007799) NADH-cytochrome b5 reductase [Arabidopsis
NCBI Description
                  thaliana] >gi 4240118 dbj BAA74838 (AB007800)
                  NADH-cytochrome b5 reductase [Arabidopsis thaliana]
Seq. No.
                  227777
Seq. ID
                  LIB3189-043-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q3461835
BLAST score
                  702
E value
                  2.0e-74
Match length
                  147
% identity
                  87
NCBI Description
                  (AC005315) putative protein kinase [Arabidopsis thaliana]
                  >gi 3927840 (AC005727) putative protein kinase [Arabidopsis
                  thaliana]
                  227778
Seq. No.
Seq. ID
                  LIB3189-043-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g2623199
BLAST score
                  525
E value
                  1.0e-53
Match length
                  112
% identity
                  89
                 (AF030290) protein phosphatase X isoform 2 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  227779
Seq. ID
                  LIB3189-043-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g3128175
BLAST score
                  155
E value
                  2.0e-10
Match length
                  119
% identity
                  33
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                  227780
Seq. ID
                  LIB3189-043-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g1332579
BLAST score
                  677
E value
                  2.0e-71
```

32542

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Method

NCBI GI

BLAST score

BLASTX

183

g4105696



```
Seq. No.
                  227781
Seq. ID
                  LIB3189-043-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g2982465
BLAST score
                  215
E value
                  3.0e-17
Match length
                  123
% identity
                  42
NCBI Description (AL022223) putative protein [Arabidopsis thaliana]
Seq. No.
                  227782
Seq. ID
                  LIB3189-043-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g2062167
BLAST score
                  572
E value
                  4.0e-59
Match length
                  153
                  71
% identity
NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis
                  thaliana]
                  227783
Seq. No.
Seq. ID
                  LIB3189-043-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g2811278
BLAST score
                  764
E value
                  1.0e-81
Match length
                  154
                  90
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                  227784
Seq. ID
                  LIB3189-043-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g2982465
BLAST score
                  178
E value
                  2.0e-13
Match length
                  75
% identity
NCBI Description (AL022223) putative protein [Arabidopsis thaliana]
Seq. No.
                  227785
Seq. ID
                  LIB3189-043-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  q167367
BLAST score
                  477
E value
                  5.0e-48
Match length
                  130
% identity
                  77
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                  227786
Seq. ID
                  LIB3189-043-P1-K1-E7
```

BLAST score

Match length

E value

523

152

2.0e-53



```
E value
                    4.0e-14
Match length
                   41
% identity
                   80
NCBI Description
                  (AF049870) beta tubulin 1 [Arabidopsis thaliana]
                   227787
Seq. No.
Seq. ID
                   LIB3189-043-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   g1170507
BLAST score
                   471
E value
                   3.0e-47
Match length
                   114
% identity
                   79
NCBI Description EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3)
                   >gi_100276_pir__S22579 translation initiation factor eIF-4A - curled-leaved tobacco >gi_19699_emb_CAA43514_ (X61206)
                   nicotiana eukaryotic translation initiation factor 4A
                   [Nicotiana plumbaginifolia]
Seq. No.
                   227788
Seq. ID
                   LIB3189-043-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   q4235430
BLAST score
                   618
E value
                   2.0e-64
Match length
                   143
                   81
% identity
NCBI Description (AF098458) latex-abundant protein [Hevea brasiliensis]
Seq. No.
                   227789
Seq. ID
                   LIB3189-043-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   g4097579
BLAST score
                   499
E value
                   2.0e-50
Match length
                   105
% identity
                   87
NCBI Description (U64922) NTGP1 [Nicotiana tabacum]
                   227790
Seq. No.
Seq. ID
                   LIB3189-043-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   g567893
BLAST score
                   173
E value
                   3.0e-12
Match length
                   66
% identity
                   52
NCBI Description
                  (L37382) beta-galactosidase-complementation protein
                   [Cloning vector]
Seq. No.
                   227791
Seq. ID
                   LIB3189-043-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   q4580460
```

% identity NCBI Description (AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana] Seq. No. 227792 Seq. ID LIB3189-043-P1-K1-F7 Method BLASTX g2072986 NCBI GI BLAST score 720 E value 2.0e-76 Match length 152 % identity 84 NCBI Description (U95142) putative G-protein-coupled receptor [Arabidopsis thaliana] >gi\_2072988 (U95143) putative G-protein-coupled receptor [Arabidopsis thaliana] Seq. No. 227793 Seq. ID LIB3189-043-P1-K1-F9 Method BLASTX NCBI GI g2119937 BLAST score 437 E value 3.0e-4390 Match length % identity 93 NCBI Description translation initiation factor eIF-4A.13 - common tobacco (fragment) Seq. No. 227794

Seq. ID LIB3189-043-P1-K1-G1

Method BLASTX NCBI GI g498038 BLAST score 509 E value 1.0e-58 Match length 150 % identity 81

NCBI Description (L33792) lipid transfer protein [Senecio odorus]

Seq. No. 227795

Seq. ID LIB3189-043-P1-K1-G3

Method BLASTX NCBI GI g1710780 BLAST score 502 E value 6.0e-51 Match length 132 % identity 74

NCBI Description 40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433

(X96613) cytoplasmic ribosomal protein S7 [Podospora

anserina]

Seq. No. 227796

Seq. ID LIB3189-043-P1-K1-G4

Method BLASTX NCBI GI g4544399 BLAST score 546 E value 5.0e-56 Match length 148 % identity 70

32545 \*

Match length

NCBI Description

% identity

60

55



```
NCBI Description
                  (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
                  thaliana]
                   227797
Seq. No.
Seq. ID
                  LIB3189-043-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g1362105
BLAST score
                  379
E value
                  2.0e-36
Match length
                  141
% identity
                  51
NCBI Description alcohol dehydrogenase (EC 1.1.1.1) - common tobacco
                   (fragment) >gi_551257_emb_CAA57446_ (X81853) alcohol
                  dehydrogenase [Nicotiana tabacum]
Seq. No.
                  227798
Seq. ID
                  LIB3189-043-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g4115925
BLAST score
                  305
E value
                  7.0e-28
Match length
                  137
                  36
% identity
NCBI Description
                  (AF118222) contains similarity to RNA recognition motifs
                   (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
                  >gi_4539439 emb CAB40027.1 (AL049523) RNA-binding protein
                   [Arabidopsis thaliana]
Seq. No.
                  227799
Seq. ID
                  LIB3189-043-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g3068704
BLAST score
                  619
E value
                  1.0e-64
Match length
                  149
% identity
                  79
NCBI Description (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                  227800
Seq. ID
                  LIB3189-043-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  q3868853
BLAST score
                  183
E value
                  1.0e-13
Match length
                  60
% identity
                  63
NCBI Description (AB013853) GPI-anchored protein [Vigna radiata]
Seq. No.
                  227801
Seq. ID
                  LIB3189-043-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g3237190
BLAST score
                  170
E value
                  6.0e-12
```

32546

(AB014760) cystein proteinase inhibitor [Cucumis sativus]



227802 Seq. No. Seq. ID LIB3189-043-P1-K1-H9 Method BLASTX NCBI GI g1944518 BLAST score 530 E value 3.0e-54Match length 128 % identity 77 NCBI Description

(Y07822) Shaqqy-like kinase tetha [Arabidopsis thaliana]

>gi 3047105 (AF058919) protein kinase [Arabidopsis

thaliana]

Seq. No. 227803

Seq. ID LIB3189-044-P1-K1-A4

Method BLASTX NCBI GI g2497743 BLAST score 606 E value 4.0e-63 Match length 120 % identity 97

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3)

>gi\_999315\_bbs\_166991 (S78173) LTP=lipid transfer protein

[Gossypium hirsutum=cotton, fiber, Peptide, 120 aa]

[Gossypium hirsutum]

Seq. No. 227804

Seq. ID LIB3189-044-P1-K1-A5

Method BLASTX NCBI GI g3876865 BLAST score 185 E value 9.0e-14 Match length 109 % identity 37

NCBI Description (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177

comes from this gene; cDNA EST EMBL:C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co

Seq. No. 227805

Seq. ID LIB3189-044-P1-K1-A8

Method BLASTX NCBI GI g3522937 BLAST score 351 E value 3.0e - 33Match length 133 % identity

NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]

Seq. No. 227806

Seq. ID LIB3189-044-P1-K1-B1

Method BLASTX NCBI GI g3759184 BLAST score 372 E value 1.0e-35 Match length 150

% identity 53



```
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
  Seq. No.
                    227807
  Seq. ID
                    LIB3189-044-P1-K1-B11
  Method
                    BLASTX
  NCBI GI
                    g82620
 BLAST score
                    526
                    8.0e-54
 E value
 Match length
                    127
  % identity
                    73
 NCBI Description probable serine-type carboxypeptidase (EC 3.4.16.1) - wheat
  Seq. No.
                    227808
  Seq. ID
                    LIB3189-044-P1-K1-B12
 Method
                    BLASTX
 NCBI GI
                    q4006829
 BLAST score
                    238
 E value
                    6.0e-20
 Match length
                    97
  % identity
                    53
 NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]
 Seq. No.
                    227809
 Seq. ID
                    LIB3189-044-P1-K1-B3
 Method
                    BLASTX
 NCBI GI
                    g729470
 BLAST score
                    360
 E value
                    3.0e-34
 Match length
                    99
 % identity
                    72
 NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
                    (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
                    >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2)
                    precursor, mitochondrial - potato >gi 297798 emb CAA79702
                    (Z21493) mitochondrial formate dehydrogenase precursor
                    [Solanum tuberosum]
 Seq. No.
                    227810
 Seq. ID
                    LIB3189-044-P1-K1-B7
 Method
                    BLASTX
 NCBI GI
                    g4204281
 BLAST score
                    231
 E value
                    4.0e-19
 Match length
                    133
 % identity
 NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                    227811
 Seq. ID
                    LIB3189-044-P1-K1-B8
 Method
                    BLASTX
 NCBI GI
                    q2811031
 BLAST score
                    485
 E value
                    6.0e-49
 Match length
                    143
 % identity
                    68
 NCBI Description
                    BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (BADH)
```

>gi\_2109299\_gb\_AAB58165.1\_ (AF000132) betaine aldehyde

Seq. No.

227817



## dehydrogenase [Amaranthus hypochondriacus]

```
Seq. No.
                   227812
Seq. ID
                  LIB3189-044-P1-K1-C11
Method
                  BLASTX
NCBI GI
                   g2454182
BLAST score
                   355
E value
                   1.0e-33
Match length
                   131
% identity
                   60
NCBI Description
                  (U80185) pyruvate dehydrogenase E1 alpha subunit
                   [Arabidopsis thaliana]
Seq. No.
                   227813
Seq. ID
                  LIB3189-044-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g3650032
BLAST score
                  237
E value
                  7.0e-20
Match length
                  49
% identity
                  73
                  (AC005396) gibberellin-regulated protein GAST1-like
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  227814
Seq. ID
                  LIB3189-044-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g3152576
BLAST score
                  177
E value
                  2.0e-13
Match length
                  65
% identity
                   63
                  (AC002986) Similar to liver-specific transport protein
NCBI Description
                  gb_L27651 from Rattus norviegicus. [Arabidopsis thaliana]
Seq. No.
                  227815
Seq. ID
                  LIB3189-044-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g4580460
BLAST score
                  165
                  5.0e-12
E value
Match length
                  45
% identity
                  78
NCBI Description
                  (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
                  thaliana]
Seq. No.
                  227816
                  LIB3189-044-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3861068
BLAST score
                  155
E value
                  3.0e-10
                  52
Match length
% identity
                  54
NCBI Description
                  (AJ235272) unknown [Rickettsia prowazekii]
```



```
LIB3189-044-P1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g728938
BLAST score
                   659
                   2.0e-69
E value
Match length
                   142
% identity
                   92
NCBI Description PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP
                   (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE)
                   (H+-PPASE) >gi_322841_pir__JC1466 inorganic pyrophosphatase (EC 3.6.1.1) - barley >gi_285638_dbj_BAA02717_ (D13472)
                   inorganic pyrophosphatse ase' [Hordeum vulgare]
                   227818
Seq. No.
Seq. ID
                   LIB3189-044-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   g3757514
BLAST score
                   217
E value
                   7.0e-18
                   74
Match length
% identity
                   64
NCBI Description (AC005167) putative plasma membrane intrinsic protein
                   [Arabidopsis thaliana]
                   227819
Seq. No.
Seq. ID
                   LIB3189-044-P1-K1-D3
                   BLASTX
Method
NCBI GI
                   g3182981
BLAST score
                   547
E value
                   3.0e-56
Match length
                   132
% identity
                   80
NCBI Description CELL ELONGATION PROTEIN DIMINUTO >gi 1695692 dbj BAA13096
                   (D86494) diminuto [Pisum sativum]
Seq. No.
                   227820
                   LIB3189-044-P1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2245131
BLAST score
                   173
                   2.0e-12
E value
Match length
                   110
% identity
NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]
                   227821
Seq. No.
Seq. ID
                   LIB3189-044-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   q124224
BLAST score
                   427
E value
                   3.0e-42
Match length
                   93
% identity
                   87
NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)
                   >gi 100345 pir S21060 translation initiation factor eIF-5A
                   - common tobacco >gi 19887 emb CAA45105 (X63543)
```

eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Match length

% identity

78 45



```
227822
Seq. No.
                  LIB3189-044-P1-K1-E11
Seq. ID
Method
                  BLASTX
                  q4185139
NCBI GI
                  188
BLAST score
                  2.0e-24
E value
                  79
Match length
                  63
% identity
                  (AC005724) putative diacylglycerol kinase [Arabidopsis
NCBI Description
                  thaliana]
                  227823
Seq. No.
                  LIB3189-044-P1-K1-E7
Seq. ID
Method
                  BLASTX
                  g586076
NCBI GI
                  321
BLAST score
                  4.0e-30
E value
                  60
Match length
% identity
                  TUBULIN BETA-1 CHAIN >gi_486734 pir _S35142 tubulin beta
NCBI Description
                   chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta
                  tubulin 1 [Lupinus albus]
                   227824
Seq. No.
                   LIB3189-044-P1-K1-F11
Seq. ID
                   BLASTX
Method
                   q3600033
NCBI GI
                   397
BLAST score
                   1.0e-38
E value
Match length
                   140
% identity
                   (AF080119) contains similarity to the N terminal domain of
NCBI Description
                   the E1 protein (Pfam: E1_N.hmm, score: 12.36) [Arabidopsis
                   thaliana]
                   227825
Seq. No.
                   LIB3189-044-P1-K1-F12
Seq. ID
                   BLASTX
Method
                   g267069
NCBI GI
BLAST score
                   610
                   1.0e-63
E value
                   114
Match length
                   98
% identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                   227826
Seq. No.
                   LIB3189-044-P1-K1-F5
Seq. ID
                   BLASTX
Method
                   g531829
NCBI GI
                   160
BLAST score
                   7.0e-11
E value
```



```
(U12390) beta-galactosidase alpha peptide [cloning vector
NCBI Description
                  pSport1]
                  227827
Seq. No.
                  LIB3189-044-P1-K1-H1
Seq. ID
                  BLASTX
Method
                  q1703380
NCBI GI
                  479
BLAST score
                  3.0e-48
E value
                  93
Match length
                  99
% identity
                  ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)
NCBI Description
                  ADP-ribosylation factor [Oryza sativa]
                   227828
Seq. No.
                  LIB3189-044-P1-K1-H11
Seq. ID
                  BLASTX
Method
                   g3582328
NCBI GI
                   158
BLAST score
                   1.0e-10
E value
                   118
Match length
                   14
% identity
NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]
                   227829
Seq. No.
                   LIB3189-044-P1-K1-H5
Seq. ID
                   BLASTX
Method
                   a3702333
NCBI GI
                   157
BLAST score
                   1.0e-10
E value
Match length
                   96
                   44
% identity
NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]
                   227830
Seq. No.
                   LIB3189-044-P1-K1-H8
Seq. ID
Method
                   BLASTX
                   g3646340
NCBI GI
                   695
BLAST score
                   2.0e-73
E value
Match length
                   149
 % identity
                   91
NCBI Description (AJ000763) MADS-box protein [Malus domestica]
                   227831
 Seq. No.
                   LIB3189-044-P1-K1-H9
 Seq. ID
Method
                   BLASTX
                   q4455208
 NCBI GI
                   534
 BLAST score
                   9.0e-55
 E value
                   132
 Match length
 % identity
                   75
 NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
                   227832
 Seq. No.
                   LIB3189-045-P1-K1-A11
 Seq. ID
```

32552

BLASTX

Method

NCBI GI

BLAST score

297



```
g2191145
NCBI GI
                  254
BLAST score
                  6.0e-22
E value
Match length
                  115
                  50
% identity
                  (AF007269) A_IG002N01.4 gene product [Arabidopsis thaliana]
NCBI Description
                  227833
Seq. No.
                  LIB3189-045-P1-K1-A12
Seq. ID
                  BLASTX
Method
                  g123650
NCBI GI
                  503
BLAST score
                  4.0e-60
E value
                  142
Match length
                  85
% identity
                  HEAT SHOCK COGNATE 70 KD PROTEIN >gi_82245_pir__S03250 heat
NCBI Description
                   shock protein 70 (clone pMON9743) - garden petunia
                   >gi_20557_emb_CAA30018_ (X06932) heat shock protein 70
                   [Petunia x hybrida]
                  227834
Seq. No.
                  LIB3189-045-P1-K1-A9
Seq. ID
                  BLASTX
Method
                   g2213626
NCBI GI
                  197
BLAST score
                   2.0e-15
E value
                   97
Match length
                   44
% identity
NCBI Description (AC000103) F21J9.18 [Arabidopsis thaliana]
                   227835
Seq. No.
                   LIB3189-045-P1-K1-B11
Seq. ID
Method
                   BLASTX
                   q1173218
NCBI GI
BLAST score
                   664
E value
                   7.0e-70
Match length
                   130
                   98
% identity
                   40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal
NCBI Description
                   protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412)
                   cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                   227836
Seq. No.
                   LIB3189-045-P1-K1-B3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q508304
BLAST score
                   238
E value
                   6.0e-20
Match length
                   75
                   67
 % identity
                  (L22305) corC [Medicago sativa]
NCBI Description
                   227837
Seq. No.
                   LIB3189-045-P1-K1-B8
Seq. ID
                   BLASTX
Method
                   g1370198
```



```
7.0e-27
E value
                   83
Match length
                   76
% identity
                   (Z73948) RAB8E [Lotus japonicus]
NCBI Description
                   227838
Seq. No.
                   LIB3189-045-P1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g122007
BLAST score
                   452
                   5.0e-45
E value
                   117
Match length
                   79
% identity
                   HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley
NCBI Description
                   >gi 20448 emb \overline{\text{CAA}}37828 (X\overline{53}831) H2A histone protein (AA 1
                   - 149) [Petroselinum crispum]
                   227839
Seq. No.
                   LIB3189-045-P1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2739044
BLAST score
                   581
E value
                   3.0e-60
Match length
                   145
                   73
% identity
                   (AF024651) polyphosphoinositide binding protein Ssh1p
NCBI Description
                   [Glycine max]
                   227840
Seq. No.
                   LIB3189-045-P1-K1-C12
Seq. ID
                   BLASTX
Method
                   g4115925
NCBI GI
BLAST score
                   453
                   4.0e-45
E value
                   99
Match length
% identity
                   (AF118222) contains similarity to RNA recognition motifs
NCBI Description
                    (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
                   >qi 4539439 emb CAB40027.1_ (AL049523) RNA-binding protein
                   [Arabidopsis thaliana]
                   227841
Seq. No.
                   LIB3189-045-P1-K1-C3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q99737
                   515
BLAST score
                   2.0e-67
E value
                   154
Match length
                   85
% identity
                   NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -
NCBI Description
                   Arabidopsis thaliana >gi_16189_emb_CAA46815_ (X66017)
                   NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]
                    227842
Seq. No.
 Seq. ID
                   LIB3189-045-P1-K1-C7
                    BLASTX
Method
```

32554

q3914935

NCBI GI

Method

NCBI GI

BLASTX

q2760837



```
BLAST score
                  8.0e-43
E value
                  152
Match length
                  60
% identity
                  40S RIBOSOMAL PROTEIN SA (P40) >gi_3204099_emb_CAA07226_
NCBI Description
                   (AJ006759) ribosome-associated protein p40 [Cicer
                  arietinum]
                  227843
Seq. No.
                  LIB3189-045-P1-K1-D10
Seq. ID
Method
                  BLASTX
                  g3790102
NCBI GI
                  747
BLAST score
E value
                   1.0e-79
                   155
Match length
% identity
                   (AF095521) pyrophosphate-dependent phosphofructokinase
NCBI Description
                   alpha subunit [Citrus X paradisi]
                   227844
Seq. No.
                   LIB3189-045-P1-K1-D11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1703115
BLAST score
                   504
                   3.0e-51
E value
                   95
Match length
                   97
% identity
                   ACTIN 3 >gi_2129526_pir__S68112 actin 3 - Arabidopsis
NCBI Description
                   thaliana >gi 1145695 (U39480) actin [Arabidopsis thaliana]
                   >qi 3236244 (AC004684) actin 3 protein [Arabidopsis
                   thaliana]
                   227845
Seq. No.
                   LIB3189-045-P1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3924823
                   254
BLAST score
                   7.0e-22
E value
                   118
Match length
                   46
% identity
                   (Z83113) cDNA EST yk491a11.5 comes from this gene; cDNA EST
NCBI Description
                   yk491a11.3 comes from this gene [Caenorhabditis elegans]
                   227846
 Seq. No.
                   LIB3189-045-P1-K1-E11
 Seq. ID
                   BLASTX
Method
                   q3694872
NCBI GI
                   488
 BLAST score
                   3.0e-49
 E value
                   116
 Match length
                   79
 % identity
                   (AF092547) profilin [Ricinus communis]
 NCBI Description
                   227847
 Seq. No.
 Seq. ID
                   LIB3189-045-P1-K1-E12
```

NCBI Description

thaliana]



```
BLAST score
                   697
                   9.0e-74
E value
Match length
                  155
% identity
                  83
NCBI Description (AC003105) putative cytochrome P450 [Arabidopsis thaliana]
                   227848
Seq. No.
                   LIB3189-045-P1-K1-E3
Seq. ID
Method
                  BLASTX
                   q4457219
NCBI GI
BLAST score
                   161
                   6.0e-11
E value
                   83
Match length
% identity
                   47
NCBI Description (AF127796) acyl carrier protein [Capsicum chinense]
Seq. No.
                   227849
                   LIB3189-045-P1-K1-E6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1350956
                   511
BLAST score
                   5.0e-52
E value
Match length
                   108
                   93
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)
                   227850
Seq. No.
                   LIB3189-045-P1-K1-E8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2462929
BLAST score
                   173
                   7.0e-13
E value
Match length
                   63
                   51
% identity
                  (Y12295) glutathione transferase [Arabidopsis thaliana]
NCBI Description
                   227851
Seq. No.
                   LIB3189-045-P1-K1-E9
Seq. ID
                   BLASTX
Method
                   g2811278
NCBI GI
                   196
BLAST score
                   1.0e-15
E value
                   36
Match length
                   94
 % identity
                   (AF043284) expansin [Gossypium hirsutum]
 NCBI Description
                   227852
 Seq. No.
                   LIB3189-045-P1-K1-F10
 Seq. ID
                   BLASTX
 Method
                   q4008006
 NCBI GI
                   450
 BLAST score
                    9.0e-45
 E value
 Match length
                   155
                    57
 % identity
                   (AF084034) receptor-like protein kinase [Arabidopsis
```



```
227853
Seq. No.
                   LIB3189-045-P1-K1-F12
Seq. ID
                   BLASTX
Method
                   g3894158
NCBI GI
                   326
BLAST score
                   3.0e - 30
E value
                   119
Match length
                   48
% identity
                   (AC005312) similar to phloem-specific lectin [Arabidopsis
NCBI Description
                   thaliana]
                   227854
Seq. No.
                   LIB3189-045-P1-K1-F3
Seq. ID
                   BLASTX
Method
                   g1173187
NCBI GI
                   607
BLAST score
                   3.0e-63
E value
                   120
Match length
                   96
% identity
                   40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673
NCBI Description
                   ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                    strawberry >gi_643074 (U19940) putative 40S ribosomal
                    protein s12 [Fragaria x ananassa]
                    227855
Seq. No.
                   LIB3189-045-P1-K1-F4
Seq. ID
                   BLASTX
Method
                    g464986
NCBI GI
                    336
BLAST score
                    8.0e-32
E value
                    62
Match length
                    98
% identity
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                    LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                    >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana
                    >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                    enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                    ubiquitin conjugating enzyme [Arabidopsis thaliana]
                    >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana]
                    >gi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein
                    ligase UBC9 [Arabidopsis thaliana]
                    227856
 Seq. No.
                    LIB3189-045-P1-K1-F5
 Seq. ID
Method
                    BLASTX
 NCBI GI
                    q548847
 BLAST score
                    168
                    3.0e-13
 E value
 Match length
                    46
                    96
 % identity
                    CHLOROPLAST 30S RIBOSOMAL PROTEIN S12
 NCBI Description
                    >gi 1086182_pir__S39501 ribosomal protein S12 -
```

protein S12 [Nicotiana tabacum]

curled-leaved tobacco >gi\_225248 prf\_1211235CG ribosomal



```
227857
Seq. No.
                  LIB3189-045-P1-K1-F9
Seq. ID
                  BLASTX
Method
                  g3169182
NCBI GI
                  328
BLAST score
                  1.0e-30
E value
                  72
Match length
                  83
% identity
NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]
                   227858
Seq. No.
                  LIB3189-045-P1-K1-G1
Seq. ID
Method
                  BLASTX
                   q1553133
NCBI GI
                   150
BLAST score
                   1.0e-09
E value
                   153
Match length
                   12
% identity
NCBI Description (U64722) actin-fragmin kinase [Physarum polycephalum]
                   227859
Seq. No.
                   LIB3189-045-P1-K1-G10
Seq. ID
                   BLASTX
Method
                   g3451069
NCBI GI
BLAST score
                   290
                   4.0e-26
E value
                   122
Match length
                   44
% identity
NCBI Description (AL031326) hypothetical protein [Arabidopsis thaliana]
                   227860
Seq. No.
                   LIB3189-045-P1-K1-G11
Seq. ID
                   BLASTX
Method
                   g4490733
NCBI GI
                   210
BLAST score
E value
                   5.0e-17
Match length
                   98
                   46
% identity
NCBI Description (AL035709) putative protein [Arabidopsis thaliana]
                   227861
Seq. No.
                   LIB3189-045-P1-K1-G12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4467151
BLAST score
                   413
                   2.0e-40
E value
Match length
                   144
                   60
 % identity
 NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
                   227862
 Seq. No.
                   LIB3189-045-P1-K1-G6
 Seq. ID
                   BLASTX
 Method
                   g3860272
 NCBI GI
                   329
 BLAST score
```

32558

4.0e-31

76

E value

Match length

BLAST score

% identity

E value Match length 189 1.0e-14

35

100



```
% identity
NCBI Description
                  (AC005824) putative suppressor protein [Arabidopsis
                  thaliana] >gi 4314399 gb AAD15609 (AC006232) putative skd1
                  protein [Arabidopsis thaliana]
Seq. No.
                  227863
Seq. ID
                  LIB3189-045-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q4337210
BLAST score
                  159
                  5.0e-11
E value
Match length
                  57
% identity
                  56
NCBI Description (AC006403) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  227864
                  LIB3189-045-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2815246
BLAST score
                  218
E value
                  1.0e-17
Match length
                  55
                  71
% identity
NCBI Description (X95709) class I type 2 metallothionein [Cicer arietinum]
Seq. No.
                  227865
                  LIB3189-045-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1703275
BLAST score
                  272
E value
                  6.0e-24
Match length
                  54
% identity
                  89
NCBI Description METHIONINE AMINOPEPTIDASE 2 (METAP 2) (PEPTIDASE M 2)
                  (INITIATION FACTOR 2 ASSOCIATED 67 KD GLYCOPROTEIN) (P67)
Seq. No.
                  227866
Seq. ID
                  LIB3189-045-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g123650
BLAST score
                  513
E value
                  2.0e-52
Match length
                  102
% identity
                  96
NCBI Description
                 HEAT SHOCK COGNATE 70 KD PROTEIN >qi 82245 pir S03250 heat
                  shock protein 70 (clone pMON9743) - garden petunia
                  >gi 20557 emb CAA30018 (X06932) heat shock protein 70
                  [Petunia x hybrida]
                  227867
Seq. No.
                  LIB3189-045-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2497742
```



```
NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
                  >gi_995907 (U15153) nonspecific lipid transfer protein
                  precursor [Gossypium hirsutum]
                  227868
Seq. No.
                  LIB3189-045-P1-K1-H6
Seq. ID
                  BLASTX
Method
                  g3176669
NCBI GI
                  178
BLAST score
                  6.0e-13
E value
                  118
Match length
                   38
% identity
```

NCBI Description (AC004393) End is cut off. [Arabidopsis thaliana] 227869

Seq. No. LIB3189-045-P1-K1-H7 Seq. ID BLASTX Method g2253583 NCBI GI 160 BLAST score 7.0e-11 E value

74 Match length 53 % identity

NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]

227870 Seq. No. LIB3189-046-P1-K1-A2 Seq. ID Method BLASTX q1408471 NCBI GI

521 BLAST score 4.0e-53 E value 136 Match length 74 % identity

(U48938) actin depolymerizing factor 1 [Arabidopsis NCBI Description thaliana] >gi\_3851707 (AF102173) actin depolymerizing

factor 1 [Arabidopsis thaliana]

Seq. No. 227871

LIB3189-046-P1-K1-A4 Seq. ID

BLASTX Method q3668082 NCBI GI 451 BLAST score E value 7.0e-45129 Match length % identity

(AC004667) putative DAL1 protein [Arabidopsis thaliana] NCBI Description

227872 Seq. No.

LIB3189-046-P1-K1-A7 Seq. ID

Method BLASTX NCBI GI g3599491 BLAST score 651 2.0e-68 E value 152 Match length 79 % identity

(AF085149) putative aminotransferase [Capsicum chinense] NCBI Description

Seq. No. 227873



LIB3189-046-P1-K1-A8 Seq. ID Method BLASTX NCBI GI q4165550 BLAST score 191 E value 8.0e-25 Match length 73 70 % identity (AJ004915) apgm [Malus domestica] NCBI Description 227874 Seq. No. Seq. ID LIB3189-046-P1-K1-B11 Method BLASTX NCBI GI q3876865 BLAST score 171 E value 3.0e-12 Match length 99 % identity 36 (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177 NCBI Description comes from this gene; cDNA EST EMBL: C09822 comes from this gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co 227875 Seq. No. Seq. ID LIB3189-046-P1-K1-B12 Method BLASTX NCBI GI g4567285 BLAST score 150 E value 3.0e-10 Match length 38 % identity 82 NCBI Description (AC006841) hypothetical protein [Arabidopsis thaliana] Seq. No. 227876 LIB3189-046-P1-K1-B2 Seq. ID Method BLASTX NCBI GI g2443878 BLAST score 255 E value 6.0e-22 Match length 126 % identity 49 NCBI Description (AC002294) Unknown protein [Arabidopsis thaliana] Seq. No. 227877 LIB3189-046-P1-K1-B8 Seq. ID Method BLASTX NCBI GI q3924596 BLAST score 278 E value 1.0e-24 Match length 78 % identity 73 (AF069442) putative phospho-ser/thr phosphatase NCBI Description [Arabidopsis thaliana]

Seq. No. 227878

Seq. ID LIB3189-046-P1-K1-C5

Method BLASTX NCBI GI g1617036



```
BLAST score
                  2.0e-21
E value
                  70
Match length
                  74
% identity
NCBI Description (Y08624) Ted2 [Vigna unguiculata]
                  227879
Seq. No.
                  LIB3189-046-P1-K1-D1
Seq. ID
                  BLASTX
Method
                  q2660664
NCBI GI
                  532
BLAST score
                  2.0e-54
E value
                  151
Match length
% identity
NCBI Description (AC002342) unknown protein [Arabidopsis thaliana]
                   227880
Seq. No.
                  LIB3189-046-P1-K1-D11
Seq. ID
                   BLASTX
Method
                   q267069
NCBI GI
                   643
BLAST score
                   2.0e-67
E value
                   123
Match length
                   97
% identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                   227881
Seq. No.
                   LIB3189-046-P1-K1-D12
Seq. ID
                   BLASTX
Method
                   g2244971
NCBI GI
                   261
BLAST score
                   3.0e-23
E value
Match length
                   65
% identity
                  (Z97340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   227882
Seq. No.
                   LIB3189-046-P1-K1-D3
Seq. ID
                   BLASTX
Method
                   q3851636
NCBI GI
 BLAST score
                   460
                   3.0e-46
E value
Match length
                   108
 % identity
                   81
                   (AF098519) unknown [Avicennia marina] >gi_4128206
 NCBI Description
                    (AF056316) 40S ribosome protein S7 [Avicennia marina]
                   227883
 Seq. No.
                   LIB3189-046-P1-K1-D4
 Seq. ID
                   BLASTX
 Method
                   g2894596
 NCBI GI
                   213
 BLAST score
```

32562

2.0e-17

58

E value

Match length



% identity (AL021889) putative protein [Arabidopsis thaliana] NCBI Description 227884 Seq. No. LIB3189-046-P1-K1-D7 Seq. ID BLASTX Method g2149051 NCBI GI 259 BLAST score 4.0e-27 E value 85 Match length 78 % identity (U73810) small Ras-like GTP-binding protein [Arabidopsis NCBI Description thaliana] 227885 Seq. No. LIB3189-046-P1-K1-D8 Seq. ID BLASTX Method g2149051 NCBI GI 252 BLAST score 4.0e-22 E value 49 Match length 98 % identity (U73810) small Ras-like GTP-binding protein [Arabidopsis NCBI Description thaliana] 227886 Seq. No. LIB3189-046-P1-K1-E1 Seq. ID Method BLASTX g464621 NCBI GI 151 BLAST score 8.0e-10 E value 38 Match length 76 % identity 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir S28586 NCBI Description ribosomal protein ML16 - common ice plant >gi\_19539\_emb\_CAA49175\_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum] 227887 Seq. No. LIB3189-046-P1-K1-E12 Seq. ID BLASTX Method g303750 NCBI GI 263 BLAST score 3.0e-37 E value 95 Match length % identity (D12548) GTP-binding protein [Pisum sativum] NCBI Description >gi 738940 prf 2001457H GTP-binding protein [Pisum sativum] 227888 Seq. No. LIB3189-046-P1-K1-E7 Seq. ID Method BLASTX NCBI GI g2911050 BLAST score 182

32563

2.0e-13

106

E value Match length

NCBI Description



```
% identity
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
                  227889
Seq. No.
                  LIB3189-046-P1-K1-E9
Seq. ID
                  BLASTX
Method
                  g2511689
NCBI GI
                  337
BLAST score
                  1.0e-31
E value
                  97
Match length
                  61
% identity
NCBI Description (Z99952) cysteine proteinase precursor [Phaseolus vulgaris]
                  227890
Seq. No.
                  LIB3189-046-P1-K1-F11
Seq. ID
                  BLASTX
Method
                   q232024
NCBI GI
                   705
BLAST score
                   9.0e-75
E value
                   136
Match length
                   96
% identity
                   PROTEIN E6 >gi 421806 pir A46130 fiber protein - upland
NCBI Description
                   cotton >gi_2129498_pir__S65061 fiber protein E6 (clone
                   CKE6-1A) - upland cotton >gi 167323 (M92051) 5' start site
                   is putative; putative [Gossypium hirsutum] >gi_1000084
                   (U30505) E6 [Gossypium hirsutum]
                   227891
Seq. No.
                   LIB3189-046-P1-K1-F12
Seq. ID
                   BLASTX
Method
                   g2924520
NCBI GI
                   501
BLAST score
                   7.0e-51
E value
                   106
Match length
                   92
% identity
                   (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                   [Arabidopsis thaliana]
                   227892
Seq. No.
                   LIB3189-046-P1-K1-F2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2811278
                   401
BLAST score
                   3.0e-39
E value
                   121
Match length
                   68
 % identity
                   (AF043284) expansin [Gossypium hirsutum]
 NCBI Description
 Seq. No.
                   227893
                   LIB3189-046-P1-K1-F5
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g2662343
                   357
 BLAST score
                    3.0e - 34
 E value
                   74
 Match length
                    93
 % identity
```

32564

(D63581) EF-1 alpha [Oryza sativa]



```
227894
Seq. No.
                   LIB3189-046-P1-K1-F6
Seq. ID
                   BLASTX
Method
                   g1256771
NCBI GI
                   186
BLAST score
                   4.0e-15
E value
                   68
Match length
                   68
% identity
                   (U51270) COP9 [Spinacia oleracea]
NCBI Description
                   227895
Seq. No.
                   LIB3189-046-P1-K1-F7
Seq. ID
                   BLASTX
Method
                   g4204313
NCBI GI
                   331
BLAST score
                   5.0e-31
E value
                   73
Match length
                   88
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                    [Arabidopsis thaliana]
                   227896
Seq. No.
                   LIB3189-046-P1-K1-F9
Seq. ID
                   BLASTX
Method
                   g559005
NCBI GI
                    406
BLAST score
                    9.0e-40
E value
                    106
Match length
                    75
% identity
                   (U15933) ascorbate peroxidase [Nicotiana tabacum]
NCBI Description
                    227897
Seq. No.
                    LIB3189-046-P1-K1-G1
 Seq. ID
                    BLASTX
Method
                    q399940
NCBI GI
 BLAST score
                    140
                    4.0e-09
 E value
                    56
 Match length
                    59
 % identity
                    MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR
 NCBI Description
                    >gi_100004_pir__S25005 heat shock protein, 70K - kidney
                    bean >gi_22636_emb_CAA47345_ (X66874) 70 kDa heat shock protein [Phaseolus vulgaris]
                    227898
Seq. No.
                    LIB3189-046-P1-K1-G11
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q3128228
                    589
 BLAST score
                    4.0e-61
 E value
 Match length
                    128
                    87
 % identity
                    (AC004077) putative ribosomal protein L18A [Arabidopsis
 NCBI Description
                    thaliana] >gi_3337376 (AC004481) putative ribosomal protein
```

L18A [Arabidopsis thaliana]



```
227899
Seq. No.
                  LIB3189-046-P1-K1-G3
Seq. ID
                  BLASTX
Method
                  q3158376
NCBI GI
                  479
BLAST score
                  3.0e-48
E value
                  131
Match length
                  74
% identity
NCBI Description (AF035385) unknown [Arabidopsis thaliana]
                  227900
Seq. No.
                  LIB3189-046-P1-K1-G5
Seq. ID
                  BLASTX
Method
                   g1632831
NCBI GI
                   531
BLAST score
                   2.0e-54
E value
                   114
Match length
                   91
% identity
NCBI Description (Z49698) orf [Ricinus communis]
                   227901
Seq. No.
                   LIB3189-046-P1-K1-G6
Seq. ID
                   BLASTX
Method
                   g2832649
NCBI GI
                   603
BLAST score
                   1.0e-62
E value
Match length
                   154
                   73
% identity
                   (AL021710) adenylosuccinate lyase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   227902
Seq. No.
                   LIB3189-046-P1-K1-G7
Seq. ID
                   BLASTX
Method
                   q399940
NCBI GI
                   339
BLAST score
E value
                   5.0e-33
                   100
Match length
                   82
 % identity
                   MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR
NCBI Description
                   >gi 100004 pir S25005 heat shock protein, 70K - kidney
                   bean >gi 22636_emb_CAA47345_ (X66874) 70 kDa heat shock
                   protein [Phaseolus vulgaris]
                   227903
 Seq. No.
                   LIB3189-046-P1-K1-G8
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g3913925
                   196
 BLAST score
                   5.0e-15
 E value
                   117
 Match length
                    41
 % identity
 NCBI Description ACID BETA-FRUCTOFURANOSIDASE AIV-18 (ACID
                   SUCROSE-6-PHOSPHATE HYDROLASE) (ACID INVERTASE) >gi 1857714
```

Seq. No. 227904

(U87849) acid beta-fructosidase [Capsicum annuum]

NCBI GI



```
LIB3189-046-P1-K1-H5
Seq. ID
                  BLASTX
Method
                  g1743354
NCBI GI
                   177
BLAST score
                   5.0e-13
E value
                   39
Match length
                   82
% identity
NCBI Description (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
                   227905
Seq. No.
                   LIB3189-046-P1-K1-H6
Seq. ID
                   BLASTX
Method
                   g3915031
NCBI GI
                   271
BLAST score
                   3.0e-24
E value
Match length
                   80
                   66
% identity
                   ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
NCBI Description
                   (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232
                   (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase
                   [Gossypium hirsutum]
                   227906
Seq. No.
                   LIB3189-046-P1-K1-H7
Seq. ID
                   BLASTX
Method
                   g3395436
NCBI GI
                   261
BLAST score
                   1.0e-22
E value
                   128
Match length
                   39
% identity
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                   227907
 Seq. No.
                   LIB3189-047-P1-K1-A12
 Seq. ID
                   BLASTX
 Method
                   q169459
 NCBI GI
 BLAST score
                   247
                   6.0e-21
 E value
 Match length
                   96
                   51
 % identity
                   (M18538) pop3 peptide [Populus balsamifera subsp.
 NCBI Description
                   trichocarpa X Populus deltoides]
                    227908
 Seq. No.
                   LIB3189-047-P1-K1-A3
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                    g2811278
 BLAST score
                    500
 E value
                    1.0e-50
                    110
 Match length
                    83
 % identity
 NCBI Description (AF043284) expansin [Gossypium hirsutum]
                    227909
 Seq. No.
                    LIB3189-047-P1-K1-A4
 Seq. ID
                    BLASTX
 Method
```

g2129473

% identity

83



```
259
BLAST score
                  2.0e-22
E value
                  94
Match length
                  52
% identity
                  arabinogalactan-like protein - loblolly pine >gi_607774
NCBI Description
                   (U09556) arabinogalactan-like protein [Pinus taeda]
                  227910
Seq. No.
                  LIB3189-047-P1-K1-A6
Seq. ID
                  BLASTX
Method
                   g1173018
NCBI GI
BLAST score
                   260
                   1.0e-22
E value
                   84
Match length
                   67
% identity
                   60S RIBOSOMAL PROTEIN L2 >gi_1076399_pir__S54250 ribosomal
NCBI Description
                   protein L2 - Arabidopsis thaliana >gi 798818_emb_CAA60445_
                   (X86765) 60S ribosomal protein L2 [Arabidopsis thaliana]
                   227911
Seq. No.
                   LIB3189-047-P1-K1-A7
Seq. ID
                   BLASTX
Method
                   g1431629
NCBI GI
                   267
BLAST score
                   6.0e-24
E value
Match length
                   69
% identity
                   71
                  (X99348) pectinacetylesterase precursor [Vigna radiata]
NCBI Description
                   227912
Seq. No.
                   LIB3189-047-P1-K1-B11
Seq. ID
                   BLASTX
Method
                   q3169182
NCBI GI
                   357
BLAST score
                   3.0e - 34
E value
Match length
                   78
% identity
                   (AC004401) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   227913
                   LIB3189-047-P1-K1-B2
Seq. ID
Method
                   BLASTX
                   g2811278
NCBI GI
BLAST score
                   263
                   1.0e-24
E value
Match length
                   78
% identity
                   79
                   (AF043284) expansin [Gossypium hirsutum]
NCBI Description
                   227914
Seq. No.
                   LIB3189-047-P1-K1-B3
Seq. ID
Method
                   BLASTX
                   g3860323
NCBI GI
                   355
 BLAST score
                   8.0e-34
E value
                   78
Match length
```

NCBI Description



```
NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]
                    227915
 Seq. No.
                    LIB3189-047-P1-K1-B5
 Seq. ID
                    BLASTX
Method
                    g507275
 NCBI GI
 BLAST score
                    178
 E value
                    6.0e-13
                    105
 Match length
 % identity
                    40
                   (L34159) NADPH:quinone oxidoreductase/zeta crystallin [Lama
 NCBI Description
                    quanicoe]
                    227916
 Seq. No.
                    LIB3189-047-P1-K1-C10
 Seq. ID
                    BLASTX
 Method
                    g1174592
 NCBI GI
 BLAST score
                    611
                    1.0e-63
 E value
                    118
 Match length
                    96
 % identity
                    TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
 NCBI Description
                    - garden pea >gi_525332 (\overline{U}12589) \overline{alpha-tubulin} [Pisum
                    sativum]
                    227917
 Seq. No.
                    LIB3189-047-P1-K1-C12
 Seq. ID
                    BLASTX
 Method
                    g3426039
 NCBI GI
                    344
  BLAST score
                     2.0e-32
  E value
                    127
 Match length
                     58
  % identity
  NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]
                    227918
  Seq. No. Seq. ID
                    LIB3189-047-P1-K1-C4
                    BLASTX
  Method
  NCBI GI
                     g1174592
  BLAST score
                     655
                     2.0e-78
  E value
                     157
  Match length
                     99
  % identity
                     TUBULIN ALPHA-1 CHAIN >gi 2119270_pir__S60233 alpha-tubulin
  NCBI Description
                     - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
                     sativum]
                     227919
  Seq. No.
  Seq. ID
                     LIB3189-047-P1-K1-C7
  Method
                     BLASTX
                     q136739
  NCBI GI
                     379
  BLAST score
                     3.0e-46
  E value
  Match length
                     120
  % identity
                    UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
```

PYROPHOSPHORYLASE) (UDPGP) >gi\_67061\_pir\_\_XNPOU

NCBI Description



UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi\_218001\_dbj\_BAA00570\_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

```
227920
Seq. No.
                  LIB3189-047-P1-K1-C9
Seq. ID
                  BLASTX
Method
                  g3924823
NCBI GI
                  219
BLAST score
                  9.0e-18
E value
                  71
Match length
                   54
% identity
                  (Z83113) cDNA EST yk491a11.5 comes from this gene; cDNA EST
NCBI Description
                   yk491a11.3 comes from this gene [Caenorhabditis elegans]
                   227921
Seq. No.
                   LIB3189-047-P1-K1-D12
Seq. ID
                   BLASTX
Method
                   g1352316
NCBI GI
                   212
BLAST score
                   5.0e-25
E value
                   79
Match length
                   62
% identity
                  DR1 PROTEIN HOMOLOG >gi_633026_dbj_BAA07288_ (D38110) Dr1
NCBI Description
                   [Arabidopsis thaliana]
                   227922
Seq. No.
                   LIB3189-047-P1-K1-D2
Seq. ID
                   BLASTX
Method
                   g3894191
NCBI GI
                   174
BLAST score
                   2.0e-12
E value
                   66
Match length
                   50
% identity
                  (AC005662) unknown protein [Arabidopsis thaliana]
NCBI Description
                   227923
Seq. No.
                   LIB3189-047-P1-K1-D3
Seq. ID
                   BLASTX
Method
                   q3080417
NCBI GI
BLAST score
                   212
                   4.0e-17
E value
                   55
Match length
% identity
                  (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
                   227924
 Seq. No.
                   LIB3189-047-P1-K1-D4
 Seq. ID
                   BLASTX
Method
                   g1086249
NCBI GI
                   273
BLAST score
                   5.0e-24
E value
Match length
                   123
                   45
 % identity
```

subtilisin-like protease - Alnus glutinosa

[Alnus glutinosa]

>gi 757522\_emb\_CAA59964\_ (X85975) subtilisin-like protease



```
227925
Seq. No.
                  LIB3189-047-P1-K1-E10
Seq. ID
                  BLASTX
Method
                  q4185153
NCBI GI
                  238
BLAST score
                  5.0e-20
E value
                  103
Match length
                  50
% identity
                  (AC005724) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  227926
Seq. No.
                  LIB3189-047-P1-K1-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                   g71634
                   716
BLAST score
                   5.0e-76
E value
Match length
                   135
                   99
% identity
                   actin 1 - rice
NCBI Description
                   227927
Seq. No.
                   LIB3189-047-P1-K1-E12
Seq. ID
                   BLASTX
Method
                   g4538920
NCBI GI
                   324
BLAST score
                   4.0e-30
E value
Match length
                   107
% identity
                   46
                   (AL049483) nitrogen fixation like protein [Arabidopsis
NCBI Description
                   thaliana]
                   227928
Seq. No.
                   LIB3189-047-P1-K1-E2
Seq. ID
                   BLASTX
Method
                   g1168728
NCBI GI
                   358
BLAST score
                   4.0e-34
E value
                   77
Match length
                   90
 % identity
                   CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883)
NCBI Description
                   cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]
                   227929
 Seq. No.
                   LIB3189-047-P1-K1-E3
 Seq. ID
                   BLASTX
 Method
                   q729974
 NCBI GI
                   468
 BLAST score
                   7.0e-47
 E value
                   121
 Match length
                   71
 % identity
                   FLORAL HOMEOTIC PROTEIN PMADS1 (GREEN PETAL HOMEOTIC
 NCBI Description
                   PROTEIN) >gi_322773_pir__S31693 transcription factor gp -
                    garden petunia >gi_22665_emb_CAA49567_ (X69946) GP (green
                   petal) [Petunia x hybrida]
```

227930

Seq. No.

Seq. ID

Method



```
LIB3189-047-P1-K1-E4
Seq. ID
                  BLASTX
Method
                  q132944
NCBI GI
                  524
BLAST score
                   2.0e-53
E value
                  115
Match length
                   84
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal
NCBI Description
                  protein L3 (ARP2) - Arabidopsis thaliana >gi_806279
                   (M32655) ribosomal protein [Arabidopsis thaliana]
                   227931
Seq. No.
                   LIB3189-047-P1-K1-E5
Seq. ID
                   BLASTX
Method
                   g3805845
NCBI GI
BLAST score
                   233
                   2.0e-19
E value
                   83
Match length
% identity
                   60
                   (AL031986) putative protein [Arabidopsis thaliana]
NCBI Description
                   227932
Seq. No.
                   LIB3189-047-P1-K1-E6
Seq. ID
                   BLASTX
Method
                   q4406774
NCBI GI
                   192
BLAST score
                   1.0e-14
E value
                   55
Match length
% identity
                   67
                   (AC006836) putative nonsense-mediated mRNA decay protein,
NCBI Description
                   5' partial [Arabidopsis thaliana]
                   227933
Seq. No.
                   LIB3189-047-P1-K1-F1
 Seq. ID
                   BLASTX
Method
                   g3668089
 NCBI GI
                   374
 BLAST score
                   4.0e-38
 E value
                   132
 Match length
                   59
 % identity
                   (AC004667) unknown protein [Arabidopsis thaliana]
 NCBI Description
                   227934
 Seq. No.
                   LIB3189-047-P1-K1-F10
 Seq. ID
                   BLASTX
 Method
                   q3024017
 NCBI GI
                                         ---
                    380
 BLAST score
                    9.0e-40
 E value
                    94
 Match length
                    91
 % identity
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)
 NCBI Description
                    (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation
                    initiation factor eIF-1A [Onobrychis viciifolia]
                    227935
 Seq. No.
```

32572

LIB3189-047-P1-K1-F2

BLASTX

```
q2811278
NCBI GI
                   756
BLAST score
                   1.0e-80
E value
                  155
Match length
% identity
                  (AF043284) expansin [Gossypium hirsutum]
NCBI Description
                   227936
Seq. No.
                  LIB3189-047-P1-K1-F6
Seq. ID
                  BLASTX
Method
                   g231586
NCBI GI
BLAST score
                   462
                   2.0e-46
E value
                   108
Match length
                   86
% identity
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                   >gi_82027_pir__S20504 H+-transporting ATP synthase (EC
                   3.6.1.34) beta chain, mitochondrial - Para rubber tree
                   >gi_18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase
                   beta-subunit [Hevea brasiliensis]
                   227937
Seq. No.
                   LIB3189-047-P1-K1-F7
Seq. ID
                   BLASTX
Method
                   g2995384
NCBI GI
                   142
BLAST score
                   2.0e-09
E value
Match length
                   41
                   68
% identity
                   (AJ004810) cytochrome P450 monooxygenase [Zea mays]
NCBI Description
                   227938
Seq. No.
                   LIB3189-047-P1-K1-F8
Seq. ID
                   BLASTX
Method
                   q3600032
NCBI GI
BLAST score
                   208
E value
                   1.0e-16
                   59
Match length
% identity
                   68
                   (AF080119) contains similarity to tropomyosin (Pfam:
NCBI Description
                   Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam:
                   ATP-synt_B.hmm, score: 10.89) [Arabidopsis thaliana]
                   227939
Seq. No.
                   LIB3189-047-P1-K1-F9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1176658
BLAST score
                   256
E value
                   3.0e-24
Match length
                   139
                   41
 % identity
                   HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II
 NCBI Description
                   >gi 726363 (U23168) No definition line found
                   [Caenorhabditis elegans]
```

227940

LIB3189-047-P1-K1-G5

Seq. No.

Seq. ID



```
BLASTX
Method
                  q4337175
NCBI GI
                  266
BLAST score
                  1.0e-23
E value
                  82
Match length
                  62
% identity
                  (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
NCBI Description
                  gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                  gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
                  gb_AA720210 come from this gene. [Arabidopsis thaliana]
                  227941
Seq. No.
                  LIB3189-047-P1-K1-G7
Seq. ID
                  BLASTX
Method
                  q3334113
NCBI GI
                  300
BLAST score
                  2.0e-27
E value
                   63
Match length
                   90
% identity
                  ACYL-COA-BINDING PROTEIN (ACBP) >gi_1006831 (U35015)
NCBI Description
                   acyl-CoA-binding protein [Gossypium hirsutum]
                   227942
Seq. No.
                   LIB3189-047-P1-K1-G9
Seq. ID
                   BLASTX
Method
                   q1703375
NCBI GI
BLAST score
                   405
                   8.0e-40
E value
Match length
                   84
                   93
% identity
                  ADP-RIBOSYLATION FACTOR 1 >gi 965483 dbj_BAA08259 (D45420)
NCBI Description
                   DcARF1 [Daucus carota]
                   227943
Seq. No.
                   LIB3189-047-P1-K1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1213629
                   660
BLAST score
                   2.0e-69
E value
                   153
Match length
                   78
 % identity
NCBI Description (X95991) pectinesterase [Prunus persica]
                   227944
 Seq. No.
                   LIB3189-047-P1-K1-H2
 Seq. ID
                   BLASTX
Method
 NCBI GI
                   q3264828
                   721
 BLAST score
                   1.0e-76
 E value
                   149
 Match length
                   93
 % identity
                   (AF072404) cotton fiber expressed protein 1 [Gossypium
 NCBI Description
                   hirsutum]
```

Seq: No. 227945

Seq. ID LIB3189-047-P1-K1-H3

Method BLASTX

NCBI GI

g464986



```
q2702281
NCBI GI
                  251
BLAST score
                   8.0e-22
E value
                  58
Match length
                   43
% identity
                   (AC003033) putative protein disulfide isomerase precursor
NCBI Description
                   [Arabidopsis thaliana]
                   227946
Seq. No.
                   LIB3189-047-P1-K1-H5
Seq. ID
                   BLASTX
Method
                   g1173218
NCBI GI
                   271
BLAST score
                   3.0e-24
E value
                   55
Match length
                   96
% identity
                   40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal
NCBI Description
                   protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412)
                   cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                   227947
Seq. No.
                   LIB3189-047-P1-K1-H6
Seq. ID
                   BLASTX
Method
                   g2244826
NCBI GI
                   357
BLAST score
                   5.0e - 34
E value
                   100
Match length
                   72
% identity
                   (Z97336) replication control protein homolog [Arabidopsis
NCBI Description
                   thaliana]
                   227948
Seq. No.
                   LIB3189-047-P1-K1-H8
Seq. ID
                   BLASTX
Method
                   q3264832
NCBI GI
BLAST score
                   326
E value
                   9.0e-31
                   76
Match length
% identity
                   (AF072406) cotton fiber expressed protein 3 [Gossypium
NCBI Description
                   hirsutum]
                   227949
Seq. No.
                   LIB3189-047-P1-K1-H9
Seq. ID
                   BLASTX
Method
                   g2702281
NCBI GI
BLAST score
                   183
                   6.0e-14
E value
                   49
Match length
                   43
 % identity
                   (AC003033) putative protein disulfide isomerase precursor
NCBI Description
                   [Arabidopsis thaliana]
                   227950
 Seq. No.
                   LIB3189-048-P1-K1-A1
 Seq. ID
                   BLASTX
 Method
```

32575



242 BLAST score E value 4.0e-39 82 Match length % identity 95 UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN NCBI Description LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi\_421857\_pir\_\_S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi 297884 emb CAA78714 (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi 349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi 600391 emb CAA51201 (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi\_4455355\_emb\_CAB36765.1 (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana] Seq. No. 227951 LIB3189-048-P1-K1-A11 Seq. ID Method BLASTX g131773 NCBI GI BLAST score 568 1.0e-58 E value 143 Match length 80 % identity NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH2) >gi\_82724\_pir\_\_B30097 ribosomal protein S14 (clone MCH2) maize Seq. No. 227952 Seq. ID LIB3189-048-P1-K1-A2 Method BLASTX NCBI GI g2244847 BLAST score 171 1.0e-12 E value Match length 58 55 % identity NCBI Description (Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana] Seq. No. 227953 LIB3189-048-P1-K1-A5 Seq. ID Method BLASTX NCBI GI q4559358

Method BLASTX
NCBI GI g4559358
BLAST score 122
E value 1.0e-10
Match length 73
% identity 48

NCBI Description (AC006585) putative steroid binding protein [Arabidopsis

thaliana]

Seq. No. 227954

Seq. ID LIB3189-048-P1-K1-A6

Method BLASTX
NCBI GI g3377797
BLAST score 592
E value 2.0e-61
Match length 146



```
% identity
                   (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                   by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                   H36046; coded for by A. thaliana cDNA T44067; coded for by
                   A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                   R90691 [Ara
                   227955
Seq. No.
                   LIB3189-048-P1-K1-A8
Seq. ID
                   BLASTX
Method
                   g120669
NCBI GI
                   557
BLAST score
                   2.0e-57
E value
                   120
Match length
                   88
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi 19566_emb_CAA42905_ (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
                   227956
Seq. No.
                   LIB3189-048-P1-K1-A9
Seq. ID
                   BLASTX
Method
                   g3668089
NCBI GI
                   230
BLAST score
                   4.0e-19
E value
Match length
                   85
                   48
% identity
                  (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
                   227957
Seq. No.
                   LIB3189-048-P1-K1-B4
Seq. ID
                   BLASTX
Method
                   q267069
NCBI GI
                   182
BLAST score
                   2.0e-13
E value
                   42
Match length
                   79
% identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183 pir _JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi 166914
                    (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                    (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                    227958
Seq. No.
                   LIB3189-048-P1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                    g2462825
                    266
BLAST score
                    3.0e-23
E value
Match length
                   91
                    59
 % identity
                   (AF000657) contains Procite 'RNP1' putative RNA-binding
NCBI Description
                    region [Arabidopsis thaliana]
```

Seq. No. 227959

Seq. ID LIB3189-048-P1-K1-C10



```
BLASTX
Method
                  a3876865
NCBI GI
BLAST score
                  168
                  1.0e-11
E value
Match length
                  91
                  37
% identity
                  (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177
NCBI Description
                  comes from this gene; cDNA EST EMBL: C09822 comes from this
                  gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST
                  yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co
                  227960
Seq. No.
                  LIB3189-048-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q465820
BLAST score
                   477
                   6.0e-48
E value
                  127
Match length
                   66
% identity
                  HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III
NCBI Description
                   >gi_280536_pir__S28301 hypothetical protein C40H1.6 -
                   Caenorhabditis elegans >gi_3874819_emb_CAA79557_ (Z19154)
                   C40H1.6 [Caenorhabditis elegans]
Seq. No.
                   227961
                   LIB3189-048-P1-K1-D10
Seq. ID
Method
                   BLASTX
                   g4371290
NCBI GI
                   139
BLAST score
                   1.0e-08
E value
                   83
Match length
% identity
                   41
                  (AC006260) unknown protein [Arabidopsis thaliana]
NCBI Description
                   227962
Seq. No.
Seq. ID
                   LIB3189-048-P1-K1-D11
Method
                   BLASTX
                   q1702986
NCBI GI
                   502
BLAST score
                   7.0e-51
E value
                   129
Match length
                   81
% identity
                   14-3-3-LIKE PROTEIN GF14 CHI >gi_1255987 (U09377) GF14chi
NCBI Description
                   isoform [Arabidopsis thaliana] >gi 1256534 (L09112) GF14
                   chi chain [Arabidopsis thaliana]
Seq. No.
                   227963
                   LIB3189-048-P1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2129769
BLAST score
                   497
```

E value 2.0e-50 110 Match length % identity

xyloglucan endo-transglycosylase precursor - Arabidopsis NCBI Description thaliana >gi\_944810\_dbj\_BAA09783\_ (D63508) endo-xyloglucan

transferase [Arabidopsis thaliana]



```
227964
Seq. No.
                  LIB3189-048-P1-K1-D6
Seq. ID
                  BLASTX
Method
                  g400054
NCBI GI
                  172
BLAST score
                  9.0e-13
E value
                  59
Match length
                  58
% identity
                  DIHYDROXY-ACID DEHYDRATASE (DAD) >gi_486729_pir__S35137
NCBI Description
                  probable phosphogluconate dehydratase (EC 4.2.1.12) -
                  Lactococcus lactis subsp. lactis >gi_2565156 (U92974) IlvD
                   [Lactococcus lactis]
                   227965
Seq. No.
                  LIB3189-048-P1-K1-D9
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3876865
                   161
BLAST score
                   5.0e-11
E value
Match length
                   73
                   40
% identity
                   (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177
NCBI Description
                   comes from this gene; cDNA EST EMBL: C09822 comes from this
                   gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST
                   yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co
                   227966
Seq. No.
                   LIB3189-048-P1-K1-E11
Seq. ID
Method
                   BLASTX
                   g2499710
NCBI GI
                   270
BLAST score
                   4.0e-24
E value
                   82
Match length
                   44
% identity
                  PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
NCBI Description
                   (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                   >gi 1438075 (L33686) phospholipase D [Ricinus communis]
                   227967
Seq. No.
                   LIB3189-048-P1-K1-E12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1346735
                   665
BLAST score
                   6.0e-70
E value
                   149
Match length
                   81
% identity
                   2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
NCBI Description
                   (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
                   >gi_1076562_pir__S49647 phosphoglycerate mutase (EC
                   5.4.2.1) - castor bean >gi_474170 emb CAA49995_ (X70652)
                   phosphoglycerate mutase [Ricinus communis]
```

Seq. No. 227968

Seq. ID LIB3189-048-P1-K1-E2

Method BLASTX NCBI GI g2833386



BLAST score 211 5.0e-17 E value Match length 71 66 % identity RIBULOSE-PHOSPHATE 3-EPIMERASE PRECURSOR NCBI Description (PENTOSE-5-PHOSPHATE 3-EPIMERASE) (PPE) (RPE) (R5P3E) >gi\_2129493\_pir\_\_S62724 ribulose-phosphate 3-epimerase (EC 5.1.3.1) precursor - spinach >gi\_1162980 (L42328) ribulose-5-phosphate 3-epimerase [Spinacia oleracea] >gi\_3264788 (AF070941) ribulose-phosphate 3-epimerase [Spinacia oleracea] >gi\_1587969\_prf\_2207382A D-ribulose-5-phosphate 3-epimerase [Sorghum bicolor] 227969

Seq. No. LIB3189-048-P1-K1-E3 Seq. ID BLASTX Method g2642238 NCBI GI BLAST score 211 4.0e-17 E value 66 Match length

67 % identity (AF031241) endoplasmic reticulum HSC70-cognate binding NCBI Description protein precursor [Glycine max]

227970 Seq. No. -LIB3189-048-P1-K1-E8 Seq. ID BLASTX Method NCBI GI g729618 BLAST score 552

1.0e-62 E value 143 Match length 81 % identity

78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 2 (GRP 78-2) NCBI Description

(IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG 2) (BIP 2) >gi\_82172\_pir\_\_PQ0262 luminal binding protein BLP-2 common tobacco (fragment) >gi\_100338\_pir\_\_S21878 heat shock protein BiP homolog blp2 - common tobacco (fragment)

>gi\_19807\_emb\_CAA42661\_ (X60059) luminal binding protein

(BiP) [Nicotiana tabacum]

227971 Seq. No.

LIB3189-048-P1-K1-F1 Seq. ID

BLASTX Method NCBI GI q267069 695 BLAST score 1.0e-73E value 130 Match length % identity

TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594 NCBI Description tubulin alpha chain - Arabidopsis thaliana >gi\_166914

(M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

227972 Seq. No.

LIB3189-048-P1-K1-F3 Seq. ID

BLASTX Method g541951 NCBI GI



```
BLAST score
                  169
                   4.0e-12
E value
Match length
                  86
                   42
% identity
                  SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26
NCBI Description
                   [Glycine max]
                   227973
Seq. No.
                  LIB3189-048-P1-K1-F4
Seq. ID
                   BLASTX
Method
                   g4510347
NCBI GI
BLAST score
                   221
                   5.0e-18
E value
                   77
Match length
                   60
% identity
                   (AC006921) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   227974
Seq. No.
                   LIB3189-048-P1-K1-F5
Seq. ID
                   BLASTX
Method
                   g4510347
NCBI GI
BLAST score
                   144
                   1.0e-16
E value
Match length
                   98
                   56
% identity
                   (AC006921) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   227975
Seq. No.
                   LIB3189-048-P1-K1-G11
Seq. ID
                   BLASTX
Method
                   q3123271
NCBI GI
                   477
BLAST score
                   3.0e-49
E value
                   106
Match length
                   87
% identity
                   40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052)
NCBI Description
                   ribosomal protein S6 [Arabidopsis thaliana]
                   227976
Seq. No.
                   LIB3189-048-P1-K1-G3
Seq. ID
                   BLASTX
Method
                   g231660
NCBI GI
                   370
BLAST score
                   2.0e-35
E value
                   150
Match length
                   53
%.identity
                  HYPOTHETICAL 226 KD PROTEIN (ORF 1901)
NCBI Description
                   227977
Seq. No.
                   LIB3189-048-P1-K1-G6
Seq. ID
                   BLASTX
Method
                   q3650032
NCBI GI
BLAST score
                   219
                   4.0e-18
E value
                   52
Match length
                   63
 % identity
                   (AC005396) gibberellin-regulated protein GAST1-like
 NCBI Description
```



## [Arabidopsis thaliana]

```
227978
Seq. No.
                   LIB3189-048-P1-K1-G7
Seq. ID
                   BLASTX
Method
                   q3122060
NCBI GI
BLAST score
                   175
                   4.0e-13
E value
                   46
Match length
                   76
% identity
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                   >gi 2598657_emb_CAA10847_ (AJ222579) elongation factor
                   1-alpha (EF1-a) [Vicia faba]
                   227979
Seq. No.
                   LIB3189-048-P1-K1-G8
Seq. ID
                   BLASTX
Method
                   g3834307
NCBI GI
                   415
BLAST score
                   1.0e-40
E value
                   149
Match length
                   57
% identity
                   (AC005679) Strong similarity to gene T10I14.120 gi_2832679
NCBI Description
                   putative protein from Arabidopsis thaliana BAC gb_AL021712.
                   ESTs gb_N65887 and gb_N65627 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   227980
                   LIB3189-048-P1-K1-H3
Seq. ID
                   BLASTX
Method
                   g3299896
NCBI GI
                   436
BLAST score
                   3.0e-43
E value
                   102
Match length
                    74
% identity
                   (AF020390) beta-galactosidase [Lycopersicon esculentum]
NCBI Description
Seq. No.
                    227981
                   LIB3189-048-P1-K1-H6
Seq. ID
                   BLASTX
Method
                    g2851508
NCBI GI
                    237
BLAST score
                    2.0e-20
E value
                    56
Match length
                    75
 % identity
                   60S RIBOSOMAL PROTEIN L21 >gi 2160162 (AC000132) Similar to
NCBI Description
                    ribosomal protein L21 (gb_L38826). ESTs
                    gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein
                    L21 [Arabidopsis thaliana]
                    227982
 Seq. No.
                    LIB3189-048-P1-K1-H9
 Seq. ID
                    BLASTX
 Method
                    g1332579
 NCBI GI
```

522

3.0e-53

BLAST score

E value



```
Match length
                   113
% identity
                   10
                   (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
                   227983
Seq. No.
                   LIB3189-049-P1-K1-A11
Seq. ID
Method
                   BLASTX
                   g2651310
NCBI GI
                   358
BLAST score
                   5.0e - 34
E value
                   145
Match length
                   46
% identity
                   (ACO02336) putative PTR2-B peptide transporter [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   227984
                   LIB3189-049-P1-K1-A12
Seq. ID
Method
                   BLASTX
                   q2244888
NCBI GI
                   194
BLAST score
                   5.0e-15
E value
Match length
                   83
                    46
% identity
                   (Z97338) similarity to cytochrome P450 [Arabidopsis
NGBI Description
                   thaliana]
                    227985
Seq. No.
                   LIB3189-049-P1-K1-A2
Seq. ID
                    BLASTX
Method
                    q3522929
NCBI GI
                    681
BLAST score
                    5.0e-72
E value
Match length
                    150
                    89
% identity
                    (AC002535) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                    [Arabidopsis thaliana] >gi_3738279 (AC005309) putative
                    dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
                    227986
Seq. No.
                    LIB3189-049-P1-K1-A3
Seq. ID
                    BLASTX
Method
NCBI GI
                    q2493144
BLAST score
                    248
                    1.0e-21
E value
                    66
Match length
                    79
% identity
                    VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE
NCBI Description
                    16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
                    (clone AVA-P2) - Arabidopsis thaliana >gi 926937 (L44585)
                    vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
```

Seq. No. 227987

Seq. ID LIB3189-049-P1-K1-A6

thaliana]

Method BLASTX NCBI GI g1545805

BLAST score

145



```
208
BLAST score
                  9.0e-17
E value
                  76
Match length
                  57
% identity
                  (D64052) cytochrome P450 like TBP [Nicotiana tabacum]
NCBI Description
                  227988
Seq. No.
                  LIB3189-049-P1-K1-A7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g549061
                  405
BLAST score
                  2.0e-39
E value
                  112
Match length
                  71
% identity
                  T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA)
NCBI Description
                  (CCT-ZETA-1) >gi_631655_pir__S43063 CCT (chaperonin
                  containing TCP-1) zeta chain - mouse
                  >gi 468554_emb_CAA83432_ (Z31557) CCT (chaperonin
                  containing TCP-1) zeta subunit [Mus musculus]
                  227989
Seq. No.
                  LIB3189-049-P1-K1-A8
Seq. ID
Method
                  BLASTX
                  g1703318
NCBI GI
                  536
BLAST score
                  7.0e-55
E value
Match length
                  148
                  30
% identity
                  ANNEXIN-LIKE PROTEIN RJ4 >gi 1362037 pir S56674 annexin
NCBI Description
                  homolog RJ4 (clone RJ4) - garden strawberry (fragment)
                  >gi 643076 (U19941) annexin [Fragaria x ananassa]
                  227990
Seq. No.
                  LIB3189-049-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2245000
BLAST score
                  148
E value
                   2.0e-09
                   125
Match length
                   30
% identity
                  (Z97341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   227991
Seq. No.
Seq. ID
                   LIB3189-049-P1-K1-B12
                  BLASTX
Method
NCBI GI
                   q71498
BLAST score
                   391
E value
                   6.0e - 38
Match length
                   113
                   67
% identity
NCBI Description heat shock protein 17.7 - garden pea
Seq. No.
                   227992
                   LIB3189-049-P1-K1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4337175
```

32584

Seq. ID



```
1.0e-09
E value
                    49
Match length
                    61
% identity
                    (AC006416) ESTs gb T20589, gb T04648, gb_AA597906,
NCBI Description
                    gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                    gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
                    227993
Seq. No.
                    LIB3189-049-P1-K1-B6
Seq. ID
                    BLASTX
Method
NCBI GI
                    q267070
BLAST score
                    661
                    1.0e-69
E value
Match length
                    135
                    95
% identity
                    TUBULIN ALPHA-6 CHAIN >gi_282852_pir__JQ1597 tubulin
NCBI Description
                    alpha-6 chain - Arabidopsis thaliana >gi_166920 (M84699)
                    TUĀ6 [Arabidopsis thaliana] >gi_2244853_emb_CAB10275_ (Z97337) tubulin alpha-6 chain (TUA6) [Arabidopsis
                    thaliana]
                    227994
Seq. No.
                    LIB3189-049-P1-K1-B8
Seq. ID
                    BLASTX
Method
                    g2695861
NCBI GI
BLAST score
                    139
                    6.0e-09
E value
                    42
Match length
                    67
% identity
                    (Y14272) 3-deoxy-D-manno-2-octulosonate-8-phosphate
NCBI Description
                    synthase [Pisum sativum] >gi_2695863_emb_CAA74645_ (Y14273)
                    3-deoxy-D-manno-2-octulosonate-8-phosphate synthase [Pisum
                    sativum]
                    227995
Seq. No.
Seq. ID
                    LIB3189-049-P1-K1-C10
                    BLASTX
Method
                    q2642215
NCBI GI
                    254
BLAST score
                    8.0e-22
E value
Match length
                    75
% identity
                     69
NCBI Description (AF030386) NOI protein [Arabidopsis thaliana]
                     227996
Seq. No.
Seq. ID
                     LIB3189-049-P1-K1-C6
Method
                     BLASTX
NCBI GI
                     g3367576
BLAST score
                     497
E value
                     3.0e-50
Match length
                     127
                     70
 % identity
NCBI Description (AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]
                     227997
 Seq. No.
```

LIB3189-049-P1-K1-C7

Seq. ID

Method

1



```
Method
                   BLASTX
                   g1931639
NCBI GI
BLAST score
                   277
                   1.0e-24
E value
                   120
Match length
                   42
% identity
                   (U95973) lysophospholipase isolog [Arabidopsis thaliana]
NCBI Description
                   227998
Seq. No.
                   LIB3189-049-P1-K1-C8
Seq. ID
                   BLASTX
Method
                   g586076
NCBI GI
                    375
BLAST score
                    2.0e-36
E value
Match length
                    73
                    93
% identity
                   TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta
NCBI Description
                    tubulin 1 [Lupinus albus]
                    227999
Seq. No.
                    LIB3189-049-P1-K1-D1
Seq. ID
Method
                    BLASTX
                    g3915031
NCBI GI
                    659
BLAST score
                    1.0e-77
E value
                    147
Match length
                    96
% identity
                    ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
NCBI Description
                    (STEAROYL-ACP DESATURASE) >gi 1217628_emb_CAA65232
                    (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase
                    [Gossypium hirsutum]
                    228000
Seq. No.
                    LIB3189-049-P1-K1-D8
Seq. ID
                    BLASTX
Method
                    g542157
NCBI GI
                    642
BLAST score
                    3.0e-67
E value
                    148
Match length
                    80
% identity
NCBI Description ribosomal 5S RNA-binding protein - Rice
                    228001
Seq. No.
                    LIB3189-049-P1-K1-E11
Seq. ID
                    BLASTX
Method
                    g2982318
NCBI GI
BLAST score
                    311
                    5.0e-29
E value
Match length
                    66
 % identity
                    86
                    (AF051244) probable 60S ribosomal protein L15 [Picea
NCBI Description
                    mariana]
                    228002
 Seq. No.
```

32586

LIB3189-049-P1-K1-E2

BLASTX,

Match length

NCBI Description

% identity



g1702983 NCBI GI 328 BLAST score 1.0e-30 E value 104 Match length 58 % identity AUXIN-REPRESSED 12.5 KD PROTEIN >gi 99855 pir S11850 NCBI Description hypothetical protein - garden strawberry >gi\_22573\_emb\_CAA36676\_ (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi\_927034 (L44142) auxin-repressed protein [Fragaria ananassa] 228003 Seq. No. LIB3189-049-P1-K1-E7 Seq. ID Method BLASTX q586076 NCBI GI BLAST score 615 3.0e-64 E value 120 Match length 95 % identity TUBULIN BETA-1 CHAIN >gi\_486734\_pir\_\_S35142 tubulin beta chain - white lupine >gi\_402636\_emb\_CAA49736\_ (X70184) Beta NCBI Description tubulin 1 [Lupinus albus] 228004 Seq. No. LIB3189-049-P1-K1-F10 Seq. ID Method BLASTX NCBI GI q2341034 286 BLAST score 5.0e-26 E value 59 Match length 95 % identity (AC000104) F19P19.13 [Arabidopsis thaliana] NCBI Description 228005 Seq. No. LIB3189-049-P1-K1-F6 Seq. ID BLASTX Method NCBI GI q2498076 BLAST score 446 2.0e-44E value 94 Match length % identity 91 NUCLEOSIDE DIPHOSPHATE KINASE (NDK) (NDP KINASE) NCBI Description >qi 1619958 (U72142) nucleoside diphosphate kinase [Helianthus annuus] 228006 Seq. No. Seq. ID LIB3189-049-P1-K1-F7 Method BLASTX NCBI GI q3075394 BLAST score 350 E value 3.0e-33

protein [Arabidopsis thaliana]

106

69

(ACOO4484) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana] >gi 3559809 emb CAA09311 (AJ010713) fiddlehead



```
228007
Seq. No.
                  LIB3189-049-P1-K1-G11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3668097
BLAST score
                  159
                  5.0e-11
E value
                  34
Match length
                  82
% identity
                  (AC004667) putative glycine cleavage system protein H
NCBI Description
                  precursor [Arabidopsis thaliana]
                  228008
Seq. No.
                  LIB3189-049-P1-K1-G2
Seq. ID
Method
                  BLASTX
                  g3493172
NCBI GI
BLAST score
                  219
                  2.0e-18
E value
                  57
Match length
                  75
% identity
                  (U89609) fiber annexin [Gossypium hirsutum]
NCBI Description
                  228009
Seq. No.
                  LIB3189-049-P1-K1-G3
Seq. ID
                  BLASTX
Method
                   q2499488
NCBI GI
BLAST score
                   342
                   1.0e-32
E value
Match length
                   71
                   90
% identity
                  PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
NCBI Description
                   ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                   (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                   (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849)
                   pyrophosphate-dependent phosphofructokinase alpha subunit
                   [Ricinus communis]
Seq. No.
                   228010
                   LIB3189-049-P1-K1-G6
Seq. ID
                   BLASTX
Method
                   q3668097
NCBI GI
                   266
BLAST score
E value
                   2.0e-23
                   74
Match length
                   74
% identity
                  (AC004667) putative glycine cleavage system protein H
NCBI Description
                   precursor [Arabidopsis thaliana]
Seq. No.
                   228011
                   LIB3189-049-P1-K1-H11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1345673
BLAST score
                   270
E value
                   6.0e-24
Match length
                   65
% identity
                   78
```

NCBI Description CATALASE ISOZYME 1 >gi\_862452\_dbj\_BAA09506\_ (D55645)

catalase [Cucurbita pepo]



71 NCBI Description 60S RIBOSOMAL PROTEIN L5

Match length % identity

```
228012
Seq. No.
                  LIB3189-049-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1710151
BLAST score
                  608
E value
                  2.0e-63
Match length
                  127
% identity
                  87
                 (U72711) proline iminopeptidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  228013
                  LIB3189-050-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3850571
BLAST score
                  436
E value
                  3.0e-43
Match length
                  94
                  89
% identity
                  (AC005278) Similar to gb U85207 snRNP core Sm protein
NCBI Description
                  homolog Sm-X5 from Mus musculus. EST gb AA612141 comes
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                  228014
Seq. ID
                  LIB3189-050-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q4454051
BLAST score
                  469
E value
                  4.0e-47
Match length
                  98
% identity
                  (AL035394) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   228015
Seq. ID
                  LIB3189-050-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g1169494
BLAST score
                  ~239
E value
                   4.0e-20
                  85
Match length
                   58
% identity
NCBI Description ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
                   >gi 2119915 pir S60659 EF-Tu protein precursor - soybean
                   >gi 949873 emb CAA61444 (X89058) EF-Tu protein [Glycine
                  max]
                   228016
Seq. No.
Seq. ID
                  LIB3189-050-P1-K1-A4
                  BLASTX
Method
NCBI GI
                   g3915826
BLAST score
                   373
                   5.0e-52
E value
```



[Arabidopsis thaliana]

% identity

NCBI Description

```
Seq. No.
                  228017
Seq. ID
                  LIB3189-050-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g3738257
                  500
BLAST score
                  9.0e-51
E value
                  105
Match length
% identity
                  93
                  (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
NCBI Description
                  nigra]
                  228018
Seq. No.
                  LIB3189-050-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2267567
BLAST score
                  394
E value
                  2.0e-38
Match length
                  85
% identity
                  87
                  (AF009003) glycine-rich RNA binding protein 1 [Pelargonium
NCBI Description
                  x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding
                  protein 2 [Pelargonium x hortorum]
Seq. No.
                  228019
Seq. ID
                  LIB3189-050-P1-K1-A9
Method
                BLASTX
NCBI GI
                  q2864614
BLAST score
                  187
E value
                  5.0e-14
Match length
                  80
% identity
                  51
NCBI Description (AL021811) putative protein [Arabidopsis thaliana]
Seq. No.
                  228020
Seq. ID
                  LIB3189-050-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g3913791
BLAST score
                  161
E value
                   5.0e-19
                  56
Match length
                   89
% identity
NCBI Description GLUTAMATE--CYSTEINE LIGASE PRECURSOR
                   (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS)
                   >gi 2407615 (AF017983) gamma-glutamylcysteine synthetase
                   [Lycopersicon esculentum]
                   228021
Seq. No.
                  LIB3189-050-P1-K1-B4
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2244994
BLAST score
                  707
E value
                   6.0e-75
Match length
                  144
```

(Z97341) similarity to isp4 protein - fission yeast



```
228022
Seq. No.
                  LIB3189-050-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4210948
BLAST score
                  239
E value
                  5.0e-30
Match length
                  74
                  87
% identity
NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]
Seq. No.
                  228023
Seq. ID
                  LIB3189-050-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                  590
                  3.0e-61
E value
Match length
                  112
                  100
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  228024
Seq. No.
                  LIB3189-050-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3876865
BLAST score
                  150
E value
                   9.0e-10
Match length
                  66
                   41
% identity
                  (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177
NCBI Description
                   comes from this gene; cDNA EST EMBL: C09822 comes from this
                   gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST
                   yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co
                   228025
Seq. No.
Seq. ID
                  LIB3189-050-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g2244931
BLAST score
                   153
                   5.0e-10
E value
Match length
                   118
                   33
% identity
                  (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3426058 emb CAA07572 (AJ007585) IB1P8-4 protein
                   [Arabidopsis thaliana]
Seq. No.
                   228026
                   LIB3189-050-P1-K1-C10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3334115
BLAST score
                   573
                   3.0e-59
E value
                   118
Match length
                   97
% identity
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
```

hirsutum]

(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi\_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium



```
228027
Seq. No.
                  LIB3189-050-P1-K1-C12
Seq. ID
                  BLASTX
Method
                  g4191778
NCBI GI
                  359
BLAST score
                  4.0e - 34
E value
                  95
Match length
                  76
% identity
                   (AC005917) putative nucleosome assembly protein I
NCBI Description
                   [Arabidopsis thaliana]
                  228028
Seq. No.
                  LIB3189-050-P1-K1-C4
Seq. ID
Method
                  BLASTX
                   g3668089
NCBI GI
BLAST score
                   140
                   4.0e-10
E value
                   88
Match length
                   43
% identity
                  (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
                   228029
Seq. No.
                  LIB3189-050-P1-K1-C6
Seq. ID
Method
                   BLASTX
                   g120669
NCBI GI
BLAST score
                   450
                   8.0e-45
E value
Match length
                   102
                   83
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                   228030
                   LIB3189-050-P1-K1-C7
Seq. ID
Method
                   BLASTX
                   q401322
NCBI GI
                   331
BLAST score
E value
                   7.0e-31
                   80
Match length
                   82
% identity
                   VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
NCBI Description
                   SUBUNIT) >gi 167313 (L03186) vacuolar H+-ATPase catalytic
                   subunit [Gossypium hirsutum]
Seq. No.
                   228031
                   LIB3189-050-P1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3759184
BLAST score
                   264
E value
                   5.0e-23
Match length
                   111
```

53

NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

% identity

Match length

NCBI Description

% identity

66



```
228032
Seq. No.
                    LIB3189-050-P1-K1-C9
Seq. ID
                    BLASTX
Method
                    g2245082
NCBI GI
BLAST score
                    389
                    8.0e-38
E value
                    117
Match length
                    63
% identity
                    (Z97343) SCARECROW homolog [Arabidopsis thaliana]
NCBI Description
                    228033
Seq. No.
                    LIB3189-050-P1-K1-D10
Seq. ID
                    BLASTX
Method
                    g586076
NCBI GI
                    281
BLAST score
                    1.0e-25
E value
                    52
Match length
                    96
% identity
                    TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta
NCBI Description
                    tubulin 1 [Lupinus albus]
                    228034
Seq. No.
                    LIB3189-050-P1-K1-D12
Seq. ID
                    BLASTX
Method
NCBI GI
                    g2980770
BLAST score
                    417
                    5.0e-41
E value
                    137
Match length
                    56
% identity
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]
                    228035
Seq. No.
                    LIB3189-050-P1-K1-D2
Seq. ID
                    BLASTX
Method
NCBI GI
                    q2500380
                    565
BLAST score
E value
                    2.0e-58
                    105
Match length
% identity
                     99
                    60S RIBOSOMAL PROTEIN L44 >gi_2119128_pir__JC4923 ribosomal protein RL44 - upland cotton >gi_1553129 (U64677) ribosomal
NCBI Description
                     protein L44 isoform a [Gossypium hirsutum] >gi 1553131
                     (U64678) ribosomal protein L44 isoform b [Gossypium
                    hirsutum]
Seq. No.
                     228036
Seq. ID
                    LIB3189-050-P1-K1-E11
Method
                    BLASTX
NCBI GI
                     q1688296
BLAST score
                     295
E value
                     3.0e-27
```

32593

[Arabidopsis thaliana]

(U78297) plasma membrane intrinsic protein PIP3

Seq. ID

Method



```
228037
 Seq. No.
                    LIB3189-050-P1-K1-E3
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4455208
 BLAST score
                    596
 E value
                    6.0e-62
 Match length
                    138
                    84
 % identity
                   (AL035440) putative protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    228038
                    LIB3189-050-P1-K1-E4
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q4467359
                    596
 BLAST score
                    8.0e-69
 E value
 Match length
                    145
                    88
 % identity
                    (AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    228039
                    LIB3189-050-P1-K1-E9
 Seq. ID
 Method
                    BLASTX
- NCBI GI
                    q3420006
 BLAST score
                    312
 E value
                    1.0e-28
                    93
 Match length
                    61
 % identity
 NCBI Description (AF000306) steroid sulfotransferase 2 [Brassica napus]
                    228040
 Seq. No.
                    LIB3189-050-P1-K1-F3
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1213450
 BLAST score
                    535
 E value
                    9.0e-55
 Match length
                    141
 % identity
                    76
 NCBI Description
                    (U48963) isopentenyl pyrophosphate isomerase [Clarkia
                    breweri]
                    228041
 Seq. No.
                    LIB3189-050-P1-K1-F5
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    -g3327868
 BLAST score
                    152
                    7.0e-10
 E value
 Match length
                    68
                    56
 % identity
                    (AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis
 NCBI Description
                    thaliana]
                    228042
 Seq. No.
```

LIB3189-050-P1-K1-F7

BLASTX



```
g267069
NCBI GI
BLAST score
                  574
                  2.0e-59
E value
Match length
                  112
% identity
                  95
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  228043
Seq. No.
                  LIB3189-050-P1-K1-F8
Seq. ID
Method
                  BLASTX
                  g4038034
NCBI GI
BLAST score
                  344
E value
                  2.0e-32
Match length
                  87
                  75
% identity
NCBI Description (AC005936) unknown protein [Arabidopsis thaliana]
Seq. No.
                  228044
                  LIB3189-050-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706102
BLAST score
                  199
E value
                  1.0e-15
Match length
                  90
                  46
% identity
                  CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 160 KD
NCBI Description
                  SUBUNIT (CPSF 160 KD SUBUNIT) >gi_1045574 (U37012) cleavage
                  and polyadenylation specificity factor [Homo sapiens]
                  228045
Seq. No.
Seq. ID
                  LIB3189-050-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q4490321
BLAST score
                  272
E value
                  6.0e-24
Match length
                  145
% identity
                  41
NCBI Description (AJ011604) nitrate transporter [Arabidopsis thaliana]
Seq. No.
                  228046
Seq. ID
                  LIB3189-050-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g3885343
BLAST score
                 ., 239
E value
                  4.0e-20
Match length
                  88
                  47
% identity
NCBI Description (AC005623) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  228047
Seq. ID
                  LIB3189-050-P1-K1-G5
```

BLASTX

356

g3063396

Method NCBI GI

BLAST score

% identity

63



```
4.0e-34
E value
                  72
Match length
% identity
                  90
                  (AB012947) vcCyP [Vicia faba]
NCBI Description
                  228048
Seq. No.
                  LIB3189-050-P1-K1-G6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3097321
                  208
BLAST score
E value
                  2.0e-16
Match length
                  111
                  39
% identity
                  (AB013289) Bd 30K [Glycine max]
NCBI Description
                  228049
Seq. No.
                  LIB3189-050-P1-K1-G7
Seq. ID
                  BLASTX
Method
                  g2829869
NCBI GI
BLAST score
                  644
                  1.0e-67
E value
Match length
                  126
                   94
% identity
                  (AC002396) pyruvate dehydrogenase E1 alpha subunit
NCBI Description
                   [Arabidopsis thaliana]
                  228050
Seq. No.
                  LIB3189-050-P1-K1-G8
Seq. ID
                  BLASTX
Method
                  g1871185
NCBI GI
                  258
BLAST score
E value
                  6.0e-23
Match length
                  57
                   81
% identity
NCBI Description (U90439) seven in absentia isolog [Arabidopsis thaliana]
Seq. No.
                   228051
                   LIB3189-050-P1-K1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2829204
BLAST score
                   186
E value
                   4.0e-14
Match length
                   35
                   97
% identity
                  (AF044204) lipid transfer protein precursor [Gossypium
NCBI Description
                   hirsutum]
Seq. No.
                   228052
Seq. ID
                   LIB3189-050-P1-K1-H10
                  BLASTX
Method
NCBI GI
                   q4567281
BLAST score
                   174
                   2.0e-12
E value
                   57
Match length
```

NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]



```
228053
Seq. No.
                    LIB3189-050-P1-K1-H12
Seq. ID
Method
                    BLASTX
NCBI GI
                    q3334115
BLAST score
                    649
E value
                    4.0e-68
                    146
Match length
                    82
% identity
                    ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                     (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664
                     (AF006489) adenine nucleotide translocator 1 [Gossypium
                    hirsutum]
                    228054
Seq. No.
                    LIB3189-050-P1-K1-H3
Seq. ID
Method
                    BLASTX
NCBI GI
                    q3334113
BLAST score
                    459
E value
                    7.0e-46
                    89
Match length
                    98
% identity
NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >gi 1006831 (U35015)
                    acyl-CoA-binding protein [Gossypium hirsutum]
Seq. No.
                    228055
                    LIB3189-050-P1-K1-H4
Seq. ID
Method
                    BLASTX
NCBI GI
                    a113621
                     522
BLAST score
                     3.0e-53
E value
Match length
                    122
% identity
                    FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
NCBI Description
                     >gi 68196 pir ADZM fructose-bisphosphate aldolase (EC
                    4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850 emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A
                     cytoplasmic aldolase [Zea mays]
Seq. No.
                     228056
Seq. ID
                     LIB3189-050-P1-K1-H9
Method
                     BLASTX
NCBI GI
                     g1172874
BLAST score
                     213
E value
                     4.0e-17
Match length
                     45
% identity
                     78
                    DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
NCBI Description
                     >gi 479589 pir S34823 dehydration-induced protein RD22 -
                     Arabidopsis thaliana >gi 391608 dbj BAA01546 (D10703) rd22
                     [Arabidopsis thaliana] \overline{gi}_4471\overline{3}4 prf 19134\overline{2}1A rd22 gene
                     [Arabidopsis thaliana]
```

Seq. No. 228057

Seq. ID LIB3189-051-P1-K1-A10

Method BLASTX NCBI GI g3033400



570 BLAST score 6.0e - 59E value 132 Match length 80 % identity

(AC004238) putative Ser/Thr protein kinase [Arabidopsis NCBI Description

thaliana]

228058 Seq. No.

LIB3189-051-P1-K1-A11 Seq. ID

BLASTX Method g4335745 NCBI GI 353 BLAST score 2.0e-33 E value Match length 142 49 % identity

(AC006284) putative hydrolase (contains an NCBI Description

esterase/lipase/thioesterase active site serine domain

(prosite: PS50187) [Arabidopsis thaliana]

228059 Seq. No.

LIB3189-051-P1-K1-A2 Seq. ID

BLASTX Method g1174592 NCBI GI 731 BLAST score 8.0e-78 E value Match length 137 % identity 100

TUBULIN ALPHA-1 CHAIN >gi\_2119270\_pir\_\_\_S60233 alpha-tubulin NCBI Description

- garden pea >gi 525332 (U12589) alpha-tubulin [Pisum

sativum]

Seq. No. 228060

LIB3189-051-P1-K1-A3 Seq. ID

Method BLASTX NCBI GI q417103 BLAST score 670 E value 1.0e-70 134 Match length 100 % identity

NCBI Description HISTONE H3.2, MINOR >gi\_282871\_pir\_\_S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563 (U09458) histone H3.2 [Medicago sativa] >gi 488567 (U09460) histone H3.2 [Medicago sativa]  $>gi_488569$  ( $\overline{U}09461$ ) histone H3.2 [Medicago sativa]  $>gi_488575$  (U09464) histone H3.2

[Medicago sativa] >gi\_488577 (U09465) histone H3.2 [Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone H3 [Lolium temulentum] >gi 1435157 emb CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >qi 2558944 (AF024716) histone 3 [Gossypium hirsutum]

>qi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AFO93633) histone H3 [Oryza sativa] >gi 4038469 gb AAC97380 (AF109910) histone H3 [Porteresia coarctata] >gi 4490754 emb CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb CAB38917.1



## (AL035708) Histon H3 [Arabidopsis thaliana]

228061 Seq. No. Seq. ID LIB3189-051-P1-K1-A6 BLASTX Method NCBI GI q3915635 BLAST score 289 4.0e-26 E value Match length 105 66 % identity CYCLIN DELTA-1 >gi 2995130 emb CAA58285 (X83369) cyclin NCBI Description delta-1 [Arabidopsis thaliana] 228062 Seq. No. LIB3189-051-P1-K1-A7 Seq. ID BLASTX Method NCBI GI q2765837 BLAST score 243 E value 1.0e-20 Match length 83 % identity 64 NCBI Description (Z96936) NAP16kDa protein [Arabidopsis thaliana] 228063 Seq. No. Seq. ID LIB3189-051-P1-K1-A8 BLASTX Method NCBI GI q3264759 BLAST score 600 2.0e-62 E value Match length 151 % identity 79 (AF071889) 40S ribosomal protein S8 [Prunus armeniaca] NCBI Description 228064 Seq. No. LIB3189-051-P1-K1-A9 Seq. ID Method BLASTX NCBI GI q3874447 BLAST score 181 E value 2.0e-13 Match length 122 % identity 32 NCBI Description (Z81039) predicted using Genefinder; cDNA EST EMBL:T01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com Seq. No. 228065 Seq. ID LIB3189-051-P1-K1-B1 Method BLASTX NCBI GI g2760322 BLAST score 240 E value 4.0e-20 92 Match length

% identity 52
NCBI Description (AC002130) F1N21.7 [Arabidopsis thaliana]

Seq. No. 228066

32599

Seq. ID

Method NCBI GI



```
Seq. ID
                  LIB3189-051-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g1617270
BLAST score
                  433
                  6.0e-43
E value
Match length
                  103
                  73
% identity
                  (X94624) acyl-CoA synthetase [Brassica napus]
NCBI Description
Seq. No.
                  228067
Seq. ID
                  LIB3189-051-P1-K1-B3
Method
                  BLASTX
                  g4263771
NCBI GI
                   352
BLAST score
E value
                  3.0e-33
Match length
                  120
                  59
% identity
                  (AC006218) putative nonspecific lipid-transfer protein
NCBI Description
                  precursor [Arabidopsis thaliana]
                  228068
Seq. No.
                  LIB3189-051-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2995953
                  287
BLAST score
                  9.0e-26
E value
                  103
Match length
% identity
                   56
                  (AF053565) glutaredoxin I [Mesembryanthemum crystallinum]
NCBI Description
Seq. No.
                  228069
Seq. ID
                  LIB3189-051-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q3334115
BLAST score
                  526
E value
                   1.0e-53
Match length
                  124
% identity
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >qi 2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                  hirsutum]
                   228070
Seq. No.
                  LIB3189-051-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3790359
BLAST score
                  196
E value
                   5.0e-15
Match length
                  67
                   55
% identity
NCBI Description (AB013359) DPM2 [Rattus norvegicus]
Seq. No.
                   228071
```

32600

LIB3189-051-P1-K1-B9

BLASTX

g3252813



```
BLAST score
                    440
                    1.0e-43
E value
                    98
Match length
                    86
% identity
                    (AC004705) vacuolar sorting receptor-like protein
NCBI Description
                    [Arabidopsis thaliana] >gi 3810586 (AC005398) vacuolar
                    sorting receptor-like protein [Arabidopsis thaliana]
                    228072
Seq. No.
                    LIB3189-051-P1-K1-C1
Seq. ID
Method
                    BLASTX
                    q4337175
NCBI GI
                    414
BLAST score
                    1.0e-40
E value
Match length
                    118
% identity
                    66
NCBI Description
                    (AC006416) ESTs qb T20589, qb T04648, qb AA597906,
                    gb_T04111, gb_R841\overline{80}, gb_R654\overline{28}, gb_T444\overline{39}, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
                    gb AA720210 come from this gene. [Arabidopsis thaliana]
                    228073
Seq. No.
Seq. ID
                    LIB3189-051-P1-K1-C10
Method
                    BLASTX
                    a267082
NCBI GI
BLAST score
                    811
                    4.0e-87
E value
                    154
Match length
                    99
% identity
                    TUBULIN BETA-8 CHAIN >gi 320189 pir JQ1592 tubulin beta-8
NCBI Description
                    chain - Arabidopsis thalīana >gi 166908 (M84705) beta-8
                    tubulin [Arabidopsis thaliana]
                    228074
Seq. No.
Seq. ID
                    LIB3189-051-P1-K1-C12
Method
                    BLASTX
NCBI GI
                    g167367
BLAST score
                    642
E value
                    3.0e-67
Match length
                    154
% identity
                    81
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                    228075
Seq. No.
Seq. ID
                    LIB3189-051-P1-K1-C2
Method
                    BLASTX
NCBI GI
                    q4557062
                    175
BLAST score
                    6.0e-13
E value
Match length
                    61
% identity
                    64
```

NCBI Description (AC007045) hypothetical protein [Arabidopsis thaliana]

Seq. No. 228076

Seq. ID LIB3189-051-P1-K1-C4

Method BLASTX NCBI GI g2119045

32601

Seq. No.

Seq. ID

228081

LIB3189-051-P1-K1-D11



```
BLAST score
                  424
                  7.0e-42
E value
Match length
                  111
                  43
% identity
                  small nuclear ribonucleoprotein U1A - potato
NCBI Description
                  >gi 1050840 emb CAA90282 (Z49990) UlsnRNP-specific
                  protein, U1A [Solanum tuberosum]
                  228077
Seq. No.
                  LIB3189-051-P1-K1-C7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q548847
                  210
BLAST score
                  7.0e-17
E value
Match length
                  47
% identity
                  87
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S12
NCBI Description
                  >gi_1086182_pir__S39501 ribosomal protein S12 -
                  curled-leaved tobacco >gi 225248 prf 1211235CG ribosomal
                  protein S12 [Nicotiana tabacum]
                  228078
Seq. No.
                  LIB3189-051-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4567283
BLAST score
                   365
                  8.0e-35
E value
Match length
                  154
% identity
                  52
                  (AC006841) unknown protein [Arabidopsis thaliana]
NCBI Description
                  228079
Seq. No.
                  LIB3189-051-P1-K1-D1
Seq. ID
                  BLASTX
Method
                   g1351408
NCBI GI
                   457
BLAST score
E value
                   1.0e-45
Match length
                   136
                   68
% identity
                  VACUOLAR PROCESSING ENZYME PRECURSOR (VPE)
NCBI Description
                   >gi_1076563_pir__S51117 cystein proteinase - sweet orange
                   >gi 633185 emb CAA87720 (Z47793) cystein proteinase (by
                   similarity) [Citrus sinensis] >gi_1588548_prf__2208463A
                   vascular processing protease [Citrus sinensis]
                   228080
Seq. No.
Seq. ID
                   LIB3189-051-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   q2879811
                   534
BLAST score
                   1.0e-54
E value
Match length
                   111
% identity
NCBI Description (AJ223316) ribosomal protein L30 [Lupinus luteus]
```

32602



```
Method
                  BLASTX
NCBI GI
                  g2827559
BLAST score
                  160
                  8.0e-11
E value
Match length
                  42
% identity
                  71
NCBI Description
                  (AL021635) predicted protein [Arabidopsis thaliana]
                  >gi 3292808 emb CAA19798 (AL031018) putative protein
                  [Arabidopsis thaliana]
                  228082
Seq. No.
Seq. ID
                  LIB3189-051-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g3451075
BLAST score
                  542
E value
                  1.0e-55
Match length
                  151
% identity
                  66
NCBI Description (AL031326) putative protein [Arabidopsis thaliana]
Seq. No.
                  228083
Seq. ID
                  LIB3189-051-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q2244994
BLAST score
                  520
E value
                  2.0e-59
Match length
                  144
                  75
% identity
NCBI Description (Z97341) similarity to isp4 protein - fission yeast
                  [Arabidopsis thaliana]
Seq. No.
                  228084
Seq. ID
                  LIB3189-051-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q4539399
BLAST score
                  453
E value
                  3.0e-45
Match length
                  108
% identity
                  88
NCBI Description (AL035526) ras-like GTP-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  228085
Seq. ID
                  LIB3189-051-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g4204313
BLAST score
                  559
                  1.0e-57
E value
Match length
                  125
% identity
                  85
                 (AC003027) lcl prt seq No definition line found
NCBI Description
                  [Arabidopsis thaliana]
```

Seq. No. 228086

Seq. ID LIB3189-051-P1-K1-D8

Method BLASTX NCBI GI g2493895



BLAST score 553 E value 6.0e-57 Match length 132 % identity 81

NCBI Description CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE)

(O-ACETYLSERINE (THIOL)-LYASE) (CSASE)

>gi\_1071911\_pir\_\_S46438 cysteine synthase (EC 4.2.99.8) watermelon >gi\_540497\_dbj\_BAA05965\_ (D28777) cysteine

synthase [Citrullus lanatus]

Seq. No. 228087

Seq. ID LIB3189-051-P1-K1-D9

Method BLASTX
NCBI GI g1488043
BLAST score 274
E value 3.0e-24
Match length 84
% identity 68

NCBI Description (U63784) PAPS-reductase-like protein [Catharanthus roseus]

Seq. No. 228088

Seq. ID LIB3189-051-P1-K1-E1

Method BLASTX
NCBI GI g1928981
BLAST score 565
E value 3.0e-58
Match length 121
% identity 62

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

Seq. No. 228089

Seq. ID LIB3189-051-P1-K1-E10

Method BLASTX
NCBI GI 94512653
BLAST score 230
E value 4.0e-19
Match length 51
% identity 86

NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]

Seq. No. 228090

Seq. ID LIB3189-051-P1-K1-E2

Method BLASTX
NCBI GI 94559356
BLAST score 151
E value 1.0e-09
Match length 150
% identity 9

NCBI Description (AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No. 228091

Seq. ID LIB3189-051-P1-K1-E3

Method BLASTX
NCBI GI g2440015
BLAST score 446
E value 7.0e-46

BLAST score

E value

335

3.0e - 31



```
Match length
% identity
NCBI Description
                   (AF014960) multidrug resistance-associated protein 2;
                  AtMRP2 [Arabidopsis thaliana]
                   228092
Seq. No.
                  LIB3189-051-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2129499
BLAST score
                   784
E value
                   6.0e-84
Match length
                   158
                   92
% identity
                  fiber protein E6 (clone CKE6-4A) - upland cotton
NCBI Description
                  >gi 1000086 (U30506) E6 [Gossypium hirsutum]
                   228093
Seq. No.
                  LIB3189-051-P1-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g232024
BLAST score
                   791
                   9.0e-85
E value
Match length
                  149
% identity
                   99
                  PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland
NCBI Description
                   cotton >gi_2129498_pir__S65061 fiber protein E6 (clone
                   CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site
                   is putative; putative [Gossypium hirsutum] >gi_1000084
                   (U30505) E6 [Gossypium hirsutum]
Seq. No.
                   228094
Seq. ID
                   LIB3189-051-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   g3318611
BLAST score
                   216
E value
                   2.0e-17
Match length
                   41
% identity
                   100
NCBI Description
                  (AB016063) mitochondrial phosphate transporter [Glycine
                   228095
Seq. No.
Seq. ID
                   LIB3189-051-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   g3702333
BLAST score
                   245
E value
                   1.0e-20
Match length
                  131
% identity
                   42
NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   228096
Seq. ID
                  LIB3189-051-P1-K1-F6
Method
                  BLASTX
NCBI GI
                   g2129630
```



```
Match length
                  136
% identity
                  48
NCBI Description
                  lamin - Arabidopsis thaliana >gi 1262754 emb CAA65750
                   (X97023) lamin [Arabidopsis thaliana] >gi 3395760 (U77721)
                  unknown [Arabidopsis thaliana]
Seq. No.
                  228097
Seq. ID
                  LIB3189-051-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q3298548
BLAST score
                  360
E value
                  3.0e-34
Match length
                  115
% identity
                  61
NCBI Description
                  (AC004681) putative spliceosomal protein [Arabidopsis
                  thalianal
                  228098
Seq. No.
Seq. ID
                  LIB3189-051-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  q464849
BLAST score
                  826
E value
                  7.0e-89
Match length
                  156
                  99
% identity
NCBI Description
                  TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha
                  chain - almond >gi_20413_emb_CAA47635_ (X67162)
                  alpha-tubulin [Prunus dulcis]
                  228099
Seq. No.
Seq. ID
                  LIB3189-051-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g3449282
BLAST score
                  316
E value
                  3.0e-29
Match length
                  70
% identity
NCBI Description
                  (AB006139) phosphoribosylformimino-5-aminoimidazole
                  carboxamide ribotide isomerase [Arabidopsis thaliana]
                  >gi_3449284_dbj_BAA32457_ (AB008929)
                  N'-5'-phosphoribosyl-formimino-5-aminoimidazole-
                  4-carboxamide ribonucleotide isomerase [Arabidopsis
                  thaliana] >gi_4510353_gb_AAD21442.1_ (AC006921)
                  phosphoribosylformimino-5-aminoimidazole carboxamide
                  ribotide isomerase [Arabidopsis thaliana]
Seq. No.
                  228100
```

Seq. ID LIB3189-051-P1-K1-G3 Method BLASTX NCBI GI g2244833 BLAST score 181 E value 3.0e-13

Match length 138 % identity

NCBI Description (Z97337) centromere protein homolog [Arabidopsis thaliana]

Seq. No. 228101



```
LIB3189-051-P1-K1-G4
Seq. ID
                    BLASTX
Method
NCBI GI
                    q4106061
BLAST score
                    199
                    7.0e-16
E value
                    75
Match length
% identity
                   (AF053318) CCR4-associated factor 1 [Homo sapiens]
NCBI Description
Seq. No.
                    228102
                    LIB3189-051-P1-K1-H10
Seq. ID
Method
                    BLASTX
NCBI GI
                    q1710838
BLAST score
                    559
E value
                    1.0e-57
                    127
Match length
                    84
% identity
                    ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                    HYDROLASE) (ADOHCYASE) >gi 535584 (L36119)
                    adenosylhomocysteinase [Medicago sativa]
                    228103
Seq. No.
                    LIB3189-051-P1-K1-H11
Seq. ID
Method
                    BLASTX
                    q1706318
NCBI GI
BLAST score
                    193
                    2.0e-31
E value
Match length
                    92
                    69
% identity
                    GLUTAMATE DECARBOXYLASE (GAD) (ERT D1)
NCBI Description
                    >gi_1362098_pir__S56177 probable glutamate decarboxylase -tomato >gi_995555_emb_CAA56812_ (X80840) homology to pyroxidal-5'-phosphate-dependant glutamate decarboxylases;
                    putative start codon [Lycopersicon esculentum]
Seq. No.
                    228104
Seq. ID
                    LIB3189-051-P1-K1-H2
Method
                    BLASTX
NCBI GI
                    g3024013
BLAST score
                    358
E value
                     4.0e-34
Match length
                    114
% identity
                     61
                   EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT
NCBI Description
                     (EIF-2-ALPHA) >gi 2706460 emb CAA15918.1_ (AL021046)
                    translational initiation factor 2 alpha
                     [Schizosaccharomyces pombe]
                    228105
Seq. No.
                    LIB3189-051-P1-K1-H3
Seq. ID
                    BLASTX
Method
NCBI GI
                    g2129499
BLAST score
                    429
                     6.0e-80
E value
Match length
                    160
```

NCBI Description fiber protein E6 (clone CKE6-4A) - upland cotton

93

% identity



## >qi 1000086 (U30506) E6 [Gossypium hirsutum]

```
Seq. No.
                  228106
Seq. ID
                  LIB3189-051-P1-K1-H4
Method
                  BLASTX
                  g1718097
NCBI GI
BLAST score
                  474
                  1.0e-47
E value
Match length
                  130
% identity
                  64
                  VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
NCBI Description
                  (41 KD ACCESSORY PROTEIN) (DVA41) >gi 626048 pir A55016
                  lysosomal membrane protein DVA41 - slime mold
                  (Dictyostelium discoideum) >gi 532733 (U13150) vacuolar
                  ATPase subunit DVA41 [Dictyostelium discoideúm]
                  228107
Seq. No.
                  LIB3189-051-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2832625
BLAST score
                  465
E value
                  9.0e-47
Match length
                  113
                  76
% identity
                 (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  228108
                  LIB3189-051-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82263
BLAST score
                  755
                  1.0e-80
E value
                  148
Match length
                  97
% identity
                  ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
NCBI Description
                  c1 precursor (clone pC(1)3II) - potato
                  228109
Seq. No.
                  LIB3189-051-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1297190
BLAST score
                   428
E value
                   3.0e-42
Match length
                   112
                   72
% identity
NCBI Description
                   (U53501) Theoretical protein with similarity to GenBank
                  Accession Number L22302 serine/threonine protein kinase
                   [Arabidopsis thaliana]
                   228110
Seq. No.
                  LIB3189-052-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351279
BLAST score
                   416
                   7.0e-41
E value
Match length
                  122
```

32608

67

% identity



TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) NCBI Description >gi\_602590\_emb\_CAA58230\_ (X83227) triosephosphate isomerase [Petunia x hybrida] 228111 Seq. No. LIB3189-052-P1-K1-A4 Seq. ID BLASTX Method g2648032 NCBI GI 637 BLAST score 3.0e-78 E value 162 Match length 80 % identity (AJ001374) alpha-glucosidase [Solanum tuberosum] NCBI Description 228112 Seq. No. LIB3189-052-P1-K1-B12 Seq. ID BLASTX Method g1170567 NCBI GI 655 BLAST score 7.0e-69 E value 146 Match length 89 % identity MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) NCBI Description >gi\_1085960\_pir\_\_S52648 INO1 protein - Citrus paradisi >gi\_602565\_emb\_CAA83565\_ (Z32632) INO1 [Citrus x paradisi] 228113 Seq. No. LIB3189-052-P1-K1-B5 Seq. ID BLASTX Method g2811278 NCBI GI 711 BLAST score 2.0e-75 E value 149 Match length 87 % identity NCBI Description (AF043284) expansin [Gossypium hirsutum] 228114 Seq. No. LIB3189-052-P1-K1-B6 Seq. ID Method BLASTX NCBI GI g1170567 295 BLAST score E value 5.0e-27 69 Match length 84 % identity MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) NCBI Description >gi 1085960 pir\_\_S52648 INO1 protein - Citrus paradisi >gi 602565 emb CAA83565 (Z32632) INO1 [Citrus x paradisi] Seq. No. 228115 LIB3189-052-P1-K1-B7 Seq. ID Method BLASTX

Method BLASTX
NCBI GI 94204300
BLAST score 430
E value 2.0e-42
Match length 138
% identity 64

NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.

Seq. ID

228121

LIB3189-052-P1-K1-C8



```
Seq. No.
                  228116
                  LIB3189-052-P1-K1-B9
Seq. ID
Method
                  BLASTX
                  q1703375
NCBI GI
BLAST score
                  460
                  1.0e-45
E value
                  97
Match length
                  100
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420)
                  DcARF1 [Daucus carota]
                  228117
Seq. No.
                  LIB3189-052-P1-K1-C10
Seq. ID
Method
                  BLASTX
                  g1617274
NCBI GI
BLAST score
                  410
                  4.0e-40
E value
Match length
                  132
                  62
% identity
                 (Z72152) AMP-binding protein [Brassica napus]
NCBI Description
                  228118
Seq. No.
                  LIB3189-052-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3193303
                  304
BLAST score
                  9.0e-28
E value
                  92
Match length
                   61
% identity
NCBI Description
                  (AF069298) similar to several proteins containing a tandem
                  repeat region such as Plasmodium falciparum GGM tandem
                  repeat protein (GB:U27807); partial CDS [Arabidopsis
                  thaliana]
Seq. No.
                  228119
Seq. ID
                  LIB3189-052-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q3851670
BLAST score
                  144
E value
                   2.0e-13
Match length
                  62
% identity
                   65
NCBI Description (AF099906) J8 [Arabidopsis thaliana]
Seq. No.
                   228120
Seq. ID
                  LIB3189-052-P1-K1-C6
                  BLASTX
Method
NCBI GI
                  q3928150
BLAST score
                   462
E value
                   4.0e-46
                  117
Match length
                   79
% identity
NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]
```

32610



```
Method
                  BLASTX
                   g3377764
NCBI GI
BLAST score
                  233
                   5.0e-26 ...
E value
                   67
Match length
                  88
% identity
                  (AF079851) nodule-enhanced sucrose synthase [Pisum sativum]
NCBI Description
                  228122
Seq. No.
                  LIB3189-052-P1-K1-C9
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2736147
BLAST score
                   312
                   7.0e-29
E value
                  70
Match length
                   79
% identity
                  (AF021804) fatty acid hydroxylase Fahlp [Arabidopsis
NCBI Description
                   thaliana] >gi 3132481 (AC003096) fatty acid hydroxylase,
                   FAH1 [Arabidopsis thaliana]
                   228123
Seq. No.
                  LIB3189-052-P1-K1-D12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1332579
BLAST score
                   695
E value
                   2.0e-73
Match length
                  142
% identity
                   10
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
                   228124
Seq. No.
                  LIB3189-052-P1-K1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1091678
                   152
BLAST score
E value
                   8.0e-10
Match length
                   98
                   35
% identity
NCBI Description activator-like transposable element [Pennisetum glaucum]
                   228125
Seq. No.
Seq. ID
                   LIB3189-052-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   q1170747
BLAST score
                   338
                   1.0e-31
E value
Match length
                   79
% identity
                   84
NCBI Description
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >qi 167345
                   (M88324) late embryogenesis-abundant protein [Gossypium
                   hirsutum] >gi_167347 (M37697) Lea5-A late
                   embryogenesis-abundant protein [Gossypium hirsutum]
```

Seq. No. 228126

Seq. ID LIB3189-052-P1-K1-D5

Method BLASTX NCBI GI g2286153



```
527
BLAST score
E value
                   7.0e-54
                  109
Match length
                  96
% identity
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
                  228127
Seq. No.
                  LIB3189-052-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2829204
BLAST score
                  217
E value
                  8.0e-24
                  80
Match length
                  81
% identity
                  (AF044204) lipid transfer protein precursor [Gossypium
NCBI Description
                  hirsutum]
Seq. No.
                  228128
                  LIB3189-052-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4574320
BLAST score
                   225
E value
                   2.0e-18
Match length
                  78
% identity
                   64
                  (AF117224) wound-induced protein WI12 [Mesembryanthemum
NCBI Description
                  crystallinum]
                   228129
Seq. No.
                   LIB3189-052-P1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1916807
BLAST score
                   247
E value
                   3.0e-21
Match length
                   73
% identity
                   73
NCBI Description (U81162) auxin-binding protein [Prunus persica]
Seq. No.
                   228130
                   LIB3189-052-P1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3876865
BLAST score
                   164
                   3.0e-11
E value
                   113
Match length
% identity
                   35
                  (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177
NCBI Description
                   comes from this gene; cDNA EST EMBL: C09822 comes from this
                   gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST
                   yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co
Seq. No.
                   228131
```

Seq. ID LIB3189-052-P1-K1-E2

Method BLASTX
NCBI GI g626009
BLAST score 378
E value 7.0e-38



```
Match length
% identity
                   capsanthin-capsorubin synthase (EC 1.-.-.) - pepper
NCBI Description
                   >qi 468748 emb CAA54495 (X77289) capsanthin/capsorubin
                   synthase [Capsicum annuum] >gi_522120_emb_CAA53759_
                   (X76165) capsanthin/capsorubin sythase [Capsicum annuum]
                   228132
Seq. No.
                   LIB3189-052-P1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1174592
BLAST score
                   620
                   6.0e-65
E value
Match length
                   116
                   98
% identity
                   TUBULIN ALPHA-1 CHAIN >gi 2119270_pir__S60233 alpha-tubulin
NCBI Description
                   - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
                   sativum]
                   228133
Seq. No.
                   LIB3189-052-P1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4102861
BLAST score
                   394
                   2.0e-38
E value
Match length
                   79
 % identity
                   91
                   (AF016893) copper/zinc-superoxide dismutase [Populus
NCBI Description
                   tremuloides]
 Seq. No.
                   228134
                   LIB3189-052-P1-K1-F10
 Seq. ID
Method
                   BLASTX
 NCBI GI
                   g2129473
 BLAST score
                   288
 E value
                   9.0e-26
 Match length
                   135
                   44
 % identity
                   arabinogalactan-like protein - loblolly pine >gi_607774
 NCBI Description
                   (U09556) arabinogalactan-like protein [Pinus taeda]
                   228135
 Seq. No.
                   LIB3189-052-P1-K1-F11
 Seq. ID
                   BLASTX
 Method
                   g1928981
 NCBI GI
 BLAST score
                   446
 E value
                   1.0e-44
 Match length
                   101
 % identity
                   89
                   (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
 NCBI Description
                   oleracea var. botrytis]
                   228136
 Seq. No.
 Seq. ID
                   LIB3189-052-P1-K1-F12
```

32613

BLASTX

187

g2462748

Method NCBI GI

BLAST score



2.0e-14 E value Match length 45 89 % identity (AC002292) putative Clathrin Coat Assembly protein NCBI Description [Arabidopsis thaliana] 228137 Seq. No. LIB3189-052-P1-K1-F4 Seq. ID BLASTX Method g3123745 NCBI GI BLAST score 143 9.0e-09 E value 84 Match length 36 % identity (AB013447) aluminum-induced [Brassica napus] NCBI Description 228138 Seq. No. LIB3189-052-P1-K1-G10 Seq. ID BLASTX Method g1545805 NCBI GI 214 BLAST score 9.0e-18 E value 51 Match length 80 % identity (D64052) cytochrome P450 like TBP [Nicotiana tabacum] NCBI Description 228139 Seq. No. LIB3189-052-P1-K1-G11 Seq. ID BLASTX Method g99801 NCBI GI 346 BLAST score 1.0e-32 E value 110 Match length 70 % identity NCBI Description chaperonine 60K alpha chain - rape plastid (fragment) Seq. No. 228140 LIB3189-052-P1-K1-G12 Seq. ID BLASTX Method NCBI GI q4512664 BLAST score 530 4.0e-54 E value Match length 136 % identity 79 NCBI Description (AC006931) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana] >gi\_4544471\_gb\_AAD22378.1\_AC006580\_10 (AC006580) putative ribose phosphate pyrophosphokinase [Arabidopsis thaliana] 228141 Seq. No. LIB3189-052-P1-K1-G2 Seq. ID BLASTX Method

Method BLASTX
NCBI GI g544424
BLAST score 323
E value 3.0e-30
Match length 72
% identity 81



```
GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi 419755 pir S30147
  NCBI Description
                       glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                      >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
[Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding
                       protein [Arabidopsis thaliana]
                       >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119)
                       glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
                       228142
  Seq. No.
                       LIB3189-052-P1-K1-G3
  Seq. ID
  Method
                       BLASTX
  NCBI GI
                       g115492
  BLAST score
                       676
                       3.0e-71
  E value
  Match length
                       136
  % identity
                       57
  NCBI Description CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)
                       calmodulin-related protein [Petunia hybrida]
                       228143
  Seq. No.
                       LIB3189-052-P1-K1-G8
  Seq. ID
                       BLASTX
  Method
  NCBI GI
                       g2191168
  BLAST score
                       357
  E value
                       7.0e-34
  Match length
                       120
  % identity
                       57
                      (AF007270) contains similarity to myosin heavy chain
  NCBI Description
                       [Arabidopsis thaliana]
  Seq. No.
                       228144
                       LIB3189-052-P1-K1-G9
  Seq. ID
  Method
                       BLASTX
  NCBI GI
                       q132675
  BLAST score
                       280
  E value
                       5.0e-25
- Match length
                       80
  % identity
  NCBI Description CHLOROPLAST 50S RIBOSOMAL PROTEIN L14 >gi 71222 pir R5NT14
                       ribosomal protein L14 - common tobacco chloroplast >gi_11864_emb_CAA77379_ (Z00044) ribosomal protein L14 [Nicotiana tabacum] >gi_225233_prf__1211235BQ ribosomal
                       protein L14 [Nicotiana tabacum]
  Seq. No.
                       228145
  Seq. ID
                       LIB3189-052-P1-K1-H1
  Method
                       BLASTX
  NCBI GI
                       g544075
  BLAST score
                       494
  E value
                       6.0e - 50
  Match length
                       122
  % identity
                       29
  NCBI Description COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)
                       (P102) >gi_486768_pir__S35312 coatomer complex chain beta'
```

[Bos taurus]

- bovine >gi\_312732\_emb\_CAA51285\_ (X72756) beta prime cop



Seq. No. 228146

Seq. ID LIB3189-052-P1-K1-H11

Method BLASTX
NCBI GI g2129955
BLAST score 404
E value 2.0e-39
Match length 110
% identity 67

NCBI Description photoassimilate-responsive protein PAR-1b precursor -

common tobacco >gi\_871487\_emb\_CAA58731\_ (X83851) mRNA inducible by sucrose and salicylic acid expressed in sugar-accumulating tobacco plants [Nicotiana tabacum]

Seq. No. 228147

Seq. ID LIB3189-052-P1-K1-H2

Method BLASTX
NCBI GI g3413170
BLAST score 363
E value 1.0e-34
Match length 107
% identity 70

NCBI Description (AJ010227) 40S ribosomal protein S6 [Cicer arietinum]

Seq. No. 228148

Seq. ID LIB3189-053-P1-K1-A11

Method BLASTX
NCBI GI g2369714
BLAST score 381
E value 3.0e-61
Match length 132
% identity 88

NCBI Description (297178) elongation factor 2 [Beta vulgaris]

Seq. No. 228149

Seq. ID LIB3189-053-P1-K1-A3

Method BLASTX
NCBI GI g3914431
BLAST score 555
E value 3.0e-57
Match length 123
% identity 84

NCBI Description PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8)

(MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8)

>gi\_2285802\_dbj\_BAA21651\_ (D78173) 26S proteasome alpha

subunit [Spinacia oleracea]

Seq. No. 228150

Seq. ID LIB3189-053-P1-K1-A7

Method BLASTX
NCBI GI 93334138
BLAST score 352
E value 2.0e-33
Match length 82
% identity 79

NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi 669003 (U20502) calnexin

[Glycine max]

Seq. No.

228156



228151

Seq. No.

```
Seq. ID
                  LIB3189-053-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g115492
BLAST score
                  494
                  4.0e-50
E value
Match length
                  96
                  53
% identity
NCBI Description CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)
                  calmodulin-related protein [Petunia hybrida]
                  228152
Seq. No.
                  LIB3189-053-P1-K1-A9
Seq. ID
                  BLASTX
Method
NCBI GI
                  a3694872
BLAST score
                  507
                  2.0e-51
E value
Match length
                  120
                  80
% identity
                 (AF092547) profilin [Ricinus communis]
NCBI Description
                  228153
Seq. No.
Seq. ID
                  LIB3189-053-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  q3024126
BLAST score
                  539
                  2.0e-55
E value
Match length
                  124
                  85
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine
                  synthetase 1 [Catharanthus roseus]
Seq. No.
                  228154
Seq. ID
                  LIB3189-053-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g1710585
BLAST score
                  352
E value
                  2.0e-33
Match length
                  81
% identity
                  85
NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN PO >gi 1143507 emb CAA63786
                   (X93587) PO ribosomal protein [Lupinus luteus]
Seq. No.
                  228155
                  LIB3189-053-P1-K1-B12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q441457
BLAST score
                  530
E value
                  3.0e-54
                  99
Match length
% identity
                  98
                  (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                  esculentum]
```



Seq. ID LIB3189-053-P1-K1-B2 Method BLASTX NCBI GI q1752734 BLAST score 475 7.0e-48E value Match length 104 75 % identity NCBI Description (D78510) beta-glucan-elicitor receptor [Glycine max] Seq. No. 228157 Seq. ID LIB3189-053-P1-K1-B3 BLASTX Method NCBI GI q2493133 BLAST score 250 E value 2.0e-21 Match length 101 % identity 49 VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT) NCBI Description >gi 2183244 (AF002134) Vma8p [Candida albicans] Seq. No. 228158 LIB3189-053-P1-K1-B4 Seq. ID Method BLASTX NCBI GI g1084321 BLAST score 475 E value 7.0e-48118 Match length % identity 78 protochlorophyllide reductase (EC 1.3.1.33) - cucumber NCBI Description >gi\_2244614\_dbj\_BAA21089\_ (D50085) NADPH-protochlorophyllide oxidoreductase [Cucumis sativus] Seq. No. 228159 Seq. ID LIB3189-053-P1-K1-B5 Method BLASTX NCBI GI g3643611 BLAST score 353 E value 1.0e-33 96 Match length % identity NCBI Description (AC005395) putative casein kinase [Arabidopsis thaliana] Seq. No. 228160 Seq. ID LIB3189-053-P1-K1-B8 Method BLASTX NCBI GI g232024 BLAST score 773 1.0e-82 E value Match length 148 97 % identity PROTEIN E6 >gi 421806 pir A46130 fiber protein - upland NCBI Description

cotton >gi\_2129498\_pir\_\_S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi\_167323 (M92051) 5' start site

is putative; putative [Gossypium hirsutum] >gi\_1000084

(U30505) E6 [Gossypium hirsutum]

Seq. No. 228161



```
LIB3189-053-P1-K1-B9
Seq. ID
                  BLASTX
Method
                  g2088651
NCBI GI
                  206
BLAST score
                  2.0e-16
E value
                  112
Match length
                  38
% identity
                   (AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  228162
                  LIB3189-053-P1-K1-C1
Seq. ID
                  BLASTX
Method
                  g1076809
NCBI GI
                   554
BLAST score
                   5.0e-57
E value
                   150
Match length
                   76
% identity
                  H+-transporting ATPase (EC 3.6.1.35) - maize
NCBI Description
                   >qi 758355 emb CAA59800 (X85805) H(+)-transporting ATPase
                   [Zea mays]
                   228163
Seq. No.
                   LIB3189-053-P1-K1-C11
Seq. ID
                   BLASTX
Method
                   g2982303
NCBI GI
BLAST score
                   346
                   1.0e-32
E value
                   85
Match length
                   79
% identity
                  (AF051236) hypothetical protein [Picea mariana]
NCBI Description
                   228164
Seq. No.
                   LIB3189-053-P1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2459445
BLAST score
                   195
                   7.0e-15
E value
                   52
Match length
                   36
% identity
                  (AC002332) putative ribonucleoprotein [Arabidopsis
NCBI Description
                   thaliana]
                   228165
Seq. No.
                   LIB3189-053-P1-K1-C6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q70644
BLAST score
                   589
E value
                   4.0e-61
Match length
                   119
                   19
% identity
NCBI Description ubiquitin precursor - common sunflower (fragment)
Seq. No.
                   228166
                   LIB3189-053-P1-K1-C7
Seq. ID
```

32619

BLASTX

g586797

Method NCBI GI



```
229
BLAST score
                  6.0e-19
E value
                  101
Match length
                  43
% identity
NCBI Description HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III
                  228167
Seq. No.
                  LIB3189-053-P1-K1-D1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2792297
BLAST score
                  261
                  1.0e-22
E value
                  77
Match length
                  58
% identity
                  (AF039183) GAST-like gene product [Fragaria x ananassa]
NCBI Description
                  228168
Seq. No.
                  LIB3189-053-P1-K1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1170711
BLAST score
                  111
                  8.0e-09
E value
                  89
Match length
                  45
% identity
NCBI Description
                  SHAGGY RELATED PROTEIN KINASE ASK-ALPHA
                  >gi_541901_pir__S41596 protein kinase ASK-alpha (EC
                  2.7.1.-) - Arabidopsis thaliana >gi 460832 emb CAA53181_
                   (X75432) shaggy related kinase [Arabidopsis thaliana]
                  >gi 1769889 emb CAA48538 (X68525) serine /threonine
                  protein kinase [Arabidopsis thaliana]
Seq. No.
                  228169
                  LIB3189-053-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3334115
BLAST score
                  446
E value
                  2.0e-44
                  108
Match length
                  84
% identity
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                  hirsutum]
                   228170
Seq. No.
                  LIB3189-053-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2648032
BLAST score
                  164
E value
                   2.0e-11
```

Match length 36 % identity

NCBI Description (AJ001374) alpha-glucosidase [Solanum tuberosum]

Seq. No. 228171

LIB3189-053-P1-K1-D6 Seq. ID

Method BLASTX

32620

BLAST score

Match length

E value

676 2.0e-71

126



```
q3913633
NCBI GI
                  306
BLAST score
                  4.0e-28
E value
Match length
                  96
% identity
                  66
NCBI Description HYPOTHETICAL PROTEIN F8A5.25 >gi 2462742 (AC002292) Unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  228172
                  LIB3189-053-P1-K1-D9
Seq. ID
Method
                  BLASTX
                  g3885343
NCBI GI
                  176
BLAST score
E value
                  8.0e-13
Match length
                  64
% identity
                  45
NCBI Description (AC005623) hypothetical protein [Arabidopsis thaliana]
                  228173
Seq. No.
Seq. ID
                  LIB3189-053-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g967125
BLAST score
                - 689 -
E value
                  7.0e-73
Match length
                  136
                  93
% identity
NCBI Description (U08140) calcium dependent protein kinase [Vigna radiata]
                  228174
Seq. No.
                  LIB3189-053-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1498330
BLAST score
                  678
                  1.0e-71
E value
Match length
                  143
% identity
                  94
NCBI Description (U60498) actin [Glycine max]
Seq. No.
                  228175
                  LIB3189-053-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g464981
BLAST score
                  553
E value
                   6.0e-57
Match length
                  111
% identity
                  92
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762)
                  ubiquitin carrier protein [Lycopersicon esculentum]
                   228176
Seq. No.
                  LIB3189-053-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267082
```

32621

% identity



```
% identity
                  TUBULIN BETA-8 CHAIN >gi_320189_pir JQ1592 tubulin beta-8
NCBI Description
                  chain - Arabidopsis thaliana >gi 166908 (M84705) beta-8
                  tubulin [Arabidopsis thaliana]
                  228177
Seq. No.
Seq. ID
                  LIB3189-053-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g3204106
BLAST score
                  503
E value
                  5.0e-51
Match length
                  155
% identity
                  64
NCBI Description (AJ006763) putative beta-amilase [Cicer arietinum]
Seq. No.
                  228178
                  LIB3189-053-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2708747
BLAST score
                  268
E value
                  1.0e-23
Match length
                  114
% identity
                  47
                 (AC003952) putative glycine-rich, zinc-finger DNA-binding
NCBI Description
                  protein [Arabidopsis thaliana]
Seq. No.
                  228179
                  LIB3189-053-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829204
BLAST score
                  189
E value
                  1.0e-14
Match length
                  35
% identity
                  100
                  (AF044204) lipid transfer protein precursor [Gossypium
NCBI Description
                  hirsutum]
                  228180 '
Seq. No.
Seq. ID
                  LIB3189-053-P1-K1-E9
                  BLASTX
Method
NCBI GI
                  g4455209
BLAST score
                  335
E value
                  2.0e-31
Match length
                  91
                  74
% identity
NCBI Description (AL035440) putative Proline synthetase associated protein
                  [Arabidopsis thaliana]
Seq. No.
                  228181
                  LIB3189-053-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1076510
BLAST score
                  654
E value
                  1.0e-68
Match length
                  140
```

32622

NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean



>gi\_829119\_emb\_CAA52414\_ (X74403) cyclophilin [Phaseolus vulgaris]

Seq. No. 228182

Seq. ID LIB3189-053-P1-K1-F3

Method BLASTX
NCBI GI g3776084
BLAST score 190
E value 2.0e-14
Match length 60
% identity 58

NCBI Description (Y18251) NtN2 [Medicago truncatula]

Seq. No. 228183

Seq. ID LIB3189-053-P1-K1-F5

Method BLASTX
NCBI GI g4432866
BLAST score 258
E value 2.0e-22
Match length 101
% identity 45

NCBI Description (AC006300) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No. 228184

Seq. ID LIB3189-053-P1-K1-F7

Method BLASTX
NCBI GI g267069
BLAST score 301
E value 9.0e-28
Match length 54
% identity 98

NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594

tubulin alpha chain - Arabidopsis thaliana >gi\_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 228185

Seq. ID LIB3189-053-P1-K1-G1

Method BLASTX
NCBI GI g2829204
BLAST score 520
E value 5.0e-53
Match length 120
% identity 88

NCBI Description (AF044204) lipid transfer protein precursor [Gossypium

hirsutum]

Seq. No. 228186

Seq. ID LIB3189-053-P1-K1-G2

Method BLASTX
NCBI GI g3152576
BLAST score 291
E value 2.0e-26
Match length 83
% identity 71

NCBI Description (AC002986) Similar to liver-specific transport protein





## gb L27651 from Rattus norviegicus. [Arabidopsis thaliana] Seq. No. 228187 LIB3189-053-P1-K1-G3 Seq. ID Method BLASTX NCBI GI g2829927 BLAST score 262 E value 8.0e-23 Match length 134 45 % identity NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana] Seq. No. 228188 Seq. ID LIB3189-053-P1-K1-G5 Method BLASTX NCBI GI q3687243 BLAST score 245 E value 6.0e-21 Match length 61 % identity 79 NCBI Description (AC005169) putative ribosomal protein [Arabidopsis thaliana] Seq. No. 228189 LIB3189-053-P1-K1-H5 Seq. ID Method BLASTX NCBI GI q2924777 BLAST score 237 E value 3.0e-20Match length 86 % identity NCBI Description (AC002334) putative receptor protein kinase [Arabidopsis thaliana] Seq. No. 228190 Seq. ID LIB3189-053-P1-K1-H6. Method BLASTX NCBI GI q1703478 409 BLAST score E value 3.0e-4099 Match length 78 % identity NCBI Description (U40566) ubiquitin activating enzyme 2 [Arabidopsis thaliana] Seq. No. 228191

 Seq. ID
 LIB3189-053-P1-K1-H7

 Method
 BLASTX

 NCBI GI
 g1841462

 BLAST score
 312

 E value
 4.0e-29

Match length 77 % identity 79

NCBI Description (Y10991) Elongation factor 2 [Nicotiana tabacum]

Seq. No. 228192

Seq. ID LIB3189-053-P1-K1-H9



```
Method
                  BLASTX
NCBI GI
                  q3915847
BLAST score
                  192
E value
                  8.0e-15
Match length
                  52
                  75
% identity
                  40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
NCBI Description
                  40S ribosomal protein S2 [Arabidopsis thaliana]
                  228193
Seq. No.
Seq. ID
                  LIB3196-001-P1-M1-A1
                  BLASTX
Method
                  q1848277
NCBI GI
                  479
BLAST score
E value
                  2.0e-48
                  99
Match length
                   97
% identity
NCBI Description (U86136) telomerase-associated protein TP-1 [Homo sapiens]
                  228194
Seq. No.
                  LIB3196-001-P1-M1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q632962
BLAST score
                   312
                   1.0e-28
E value
Match length
                  101
                   60
% identity
NCBI Description (L29222) clk1-136; putative [Homo sapiens]
                   228195
Seq. No.
                   LIB3196-001-P1-M1-B11
Seq. ID .
Method
                   BLASTX
NCBI GI
                   g2493416
BLAST score
                   170
E value
                   5.0e-12
                  88
Match length
                   38
% identity
NCBI Description 'S100 CALCIUM-BINDING PROTEIN A13 >gi_2134853_pir__JC5064
                   calcium-binding protein S100 A13 - human
                   >qi 1694828 emb CAA68188 (X99920) S100 calcium-binding
                   protein A13 (S100A13) [Homo sapiens]
                   228196
Seq. No.
                   LIB3196-001-P1-M1-B12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g685073
BLAST score
                   461
E value
                   4.0e-46
                   108
Match length
                   78
% identity
NCBI Description SPRC=small proline-rich protein [human, odontogenic
                   keratocysts, Peptide Partial, 161 aa]
                   228197
Seq. No.
```

Seq: ID LIB3196-001-P1-M1-B2

Method BLASTX NCBI GI g1351173



```
664
BLAST score
E value
                    6.0e-70
                    134
Match length
                    98
% identity
                    SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)
NCBI Description
                    >gi_1050527_emb_CAA62635_ (X91257) seryl-tRNA synthetase
                    [Homo sapiens]
                    228198
Seq. No.
                    LIB3196-001-P1-M1-B3
Seq. ID
Method
                    BLASTX
                    g3283994
NCBI GI
BLAST score
                    143
                    5.0e-09
E value
                    48
Match length
                    60
% identity
                   (AF073293) M962 protein spliced isoform 2 [Homo sapiens]
NCBI Description
                    228199
Seq. No.
                    LIB3196-001-P1-M1-B4
Seq. ID
                    BLASTX
Method
                    g113944
NCBI GI
                    572
BLAST score
                    4.0e-59
E value
Match length
                    120
                    60
% identity
NCBI Description ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9)
                    (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN)
                    >gi_71756_pir__LUHU annexin I - human
>gi_34388_emb_CAA29338_ (X05908) lipocortin (AA 1-346)
                    [Homo sapiens] >gi 224956 prf 1204261A lipocortin [Homo
                    sapiens] >gi_45021\overline{0}1_ref \overline{N}P 0\overline{0}\overline{0}691.1 pANX1 annexin I
                    (lipocortin \overline{I})
                    228200
Seq. No.
Seq. ID
                    LIB3196-001-P1-M1-B6
Method
                    BLASTX
NCBI GI
                    q602467
BLAST score
                    554
                    3.0e-57
E value
Match length
                    103
% identity
                    60
NCBI Description (M27445) nidogen [Homo sapiens]
                    228201
Seq. No.
```

LIB3196-001-P1-M1-B7 Seq. ID

Method BLASTX NCBI GI g417570 BLAST score 565 E value 2.0e-58 Match length 133 % identity

DIHYDROOROTATE DEHYDROGENASE PRECURSOR (DIHYDROOROTATE NCBI Description

OXIDASE) (DHODEHASE) >gi\_478676\_pir S23762 dihydroorotate

oxidase (EC 1.3.3.1) - Arabidopsis Thaliana >gi 16449 emb CAA44695 (X62909) dihydroorotate

dehydrogenase [Arabidopsis thaliana]

NCBI GI

E value

BLAST score

g121116

3.0e-35

367



```
228202
Seq. No.
                  LIB3196-001-P1-M1-B8
Seq. ID
Method
                  BLASTX
                  q88044
NCBI GI
BLAST score
                   661
                   1.0e-69
E value
                  138
Match length
                   96
% identity
                   keratin 4, type II, cytoskeletal - human (fragment)
NCBI Description
                   >gi 34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA)
                   [Homo sapiens]
                   228203
Seq. No.
Seq. ID
                  LIB3196-001-P1-M1-B9
Method
                   BLASTX
NCBI GI
                   q50823
BLAST score
                   637
                   8.0e-67
E value
                   125
Match length
                   100
% identity
                  (X12507) initiation factor 4AII (AA 1 - 407) [Mus musculus]
NCBI Description
                   228204
Seq. No.
                   LIB3196-001-P1-M1-C1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2501432
                   544
BLAST score
                   6.0e-56
E value
Match length
                   107
                   96
% identity
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_2146981_pir__JC4894
                   ubiquitin-conjugating enzyme (EC 6.3.2.-) E2 - human
                   >gi_1181558_dbj_BAA11675_ (D83004) ubiquitin-conjugating
                   enzyme E2 UbcH-ben [Homo sapiens]
                   >qi 4507793 ref NP 003339.1 pUBE2N ubiquitin-conjugating
                   enzyme E2N (homologous to yeast UBC13)
                   228205
Seq. No.
                   LIB3196-001-P1-M1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g266690
BLAST score
                   306
E value
                   4.0e-28
Match length
                   95
 % identity
                   67
                   OLEOSIN 18.2 KD >gi_167363 (L00935) 18.2 kDa oleosin
NCBI Description
                   [Gossypium hirsutum] >gi 167365 (L00936) 18.2 kDa oleosin
                   [Gossypium hirsutum]
                   228206
 Seq. No.
                   LIB3196-001-P1-M1-C12
 Seq. ID
                   BLASTX
Method
```

32627



Match length 126 % identity 51

NCBI Description GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR)

(ADF) (BREVIN) (AGEL) >gi 71649\_pir\_\_FAHUP gelsolin

precursor, plasma - human >gi\_736249 emb\_CAA28000\_ (X04412) plasma gelsolin [Homo sapiens] >gi\_225304\_prf\_\_1211330A gelsolin [Homo sapiens] >gi\_4504165\_ref\_NP\_000168.1\_pGSN\_

gelsolin (amyloidosis, Finnish type)

Seq. No.

228207

Seq. ID LIB3196-001-P1-M1-C2

Method BLASTX
NCBI GI g121009
BLAST score 658
E value 3.0e-69
Match length 126
% identity 38

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA

SUBUNIT 2 (TRANSDUCIN BETA CHAIN 2) >gi\_71872\_pir\_\_RGBOB2 GTP-binding regulatory protein beta-2 chain - bovine (fragment) >gi\_163113 (M16480) guanine nucleotide-binding regulatory protein-beta-2 subunit [Bos taurus] >gi\_163785

(M36431) transducin beta-2 subunit [Bos taurus]

Seq. No. 228208

Seq. ID LIB3196-001-P1-M1-C6

Method BLASTX
NCBI GI g120649
BLAST score 450
E value 5.0e-45
Match length 102
% identity 89

NCBI Description

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER

>gi\_625203\_pir\_\_DEHUG3 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - human >gi\_182861 (M17851)

glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]

>gi\_182863 (J02642) glyceraldehyde 3-phosphate

dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi\_182977 (M33197) glyceraldehyde-3-phosphate dehydrogenase (EC

1.2.1.12) [Homo sapiens] >gi\_182981 (J04038)

glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]

>gi\_224880\_prf\_\_1203217A

dehydrogenase, glyceraldehydephosphate [Homo sapiens]

Seq. No. 228209

Seq. ID LIB3196-001-P1-M1-D12

Method BLASTX
NCBI GI 94204275
BLAST score 329
E value 1.0e-30
Match length 132
% identity 50

NCBI Description (AC004146) Unknown protein [Arabidopsis thaliana]

Seq. No. 228210

Seq. ID LIB3196-001-P1-M1-D2

Method BLASTX



```
NCBI GI
                   q2738949
BLAST score
                   440
                   9.0e-44
E value
Match length
                   94
                   87
% identity
                   (AF022213) cytosolic ascorbate peroxidase [Fragaria x
NCBI Description
                  ananassa]
Seq. No.
                   228211
                  LIB3196-001-P1-M1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3879734
BLAST score
                   175
                   3.0e-13
E value
Match length
                   46
                   70
% identity
                  (Z93388) predicted using Genefinder; cDNA EST EMBL:D70912
NCBI Description
                   comes from this gene; cDNA EST EMBL: D73452 comes from this
                   gene; cDNA EST EMBL:D71574 comes from this gene; cDNA EST
                   EMBL:D74229 comes from this gene; cDNA EST EMBL:D727
                   228212
Seq. No.
Seq. ID
                   LIB3196-001-P1-M1-D7
Method
                   BLASTX
                   q4539660
NCBI GI
BLAST score
                   461
                   3.0e-46
E value
Match length
                   132
% identity
NCBI Description
                  (AF061282) polyprotein [Sorghum bicolor]
                   228213
Seq. No.
                   LIB3196-001-P1-M1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q539636
BLAST score
                   420
                   2.0e-41
E value
                   108
Match length
                   76
% identity
                   membrane glycoprotein CLA-1 protein long form precursor -
NCBI Description
                   human >gi_397607_emb_CAA80277_ (Z22555) CLA-1 [Homo
                   sapiens]
                   228214
Seq. No.
                   LIB3196-001-P1-M1-E11
Seq. ID
                   {\tt BLASTX}
Method
                   g1706566
NCBI GI
BLAST score
                   694
E value
                   2.0e-73
                   140
Match length
                   98
% identity
```

% identity 98

NCBI Description MITOCHONDRIAL TRIFUNCTONAL ENZYME BETA SUBUNIT PRECURSOR (TP-BETA) [CONTAINS: 3-KETOACYL-COA THIOLASE (ACETYL-COA

ACYLTRANSFERASE) (BETA-KETOTHIOLASE)]

>gi\_543065\_pir\_\_JC2109 long-chain-fatty-acid beta-oxidation
multienzyme complex beta chain precursor, mitochondrial human >gi\_862458\_dbj\_BAA03942\_ (D16481) 3-ketoacyl-CoA



228215

228216

thiolase beta-subunit of trifunctional protein [Homo sapiens] >gi\_4504327\_ref\_NP\_000174.1\_pHADHB hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit

Seq. No. LIB3196-001-P1-M1-E7 Seq. ID BLASTX Method g3462807 NCBI GI 472 BLAST score 2.0e-47 E value 113 Match length 81 % identity

(AF082516) I-1 receptor candidate protein [Homo sapiens] NCBI Description

Seq. No. LIB3196-001-P1-M1-E8 Seq. ID BLASTX Method g2605714 NCBI GI 231 BLAST score 3.0e-19E value 60 Match length 80 % identity

(AF026275) beta-tonoplast intrinsic protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 228217 LIB3196-001-P1-M1-F1 Seq. ID BLASTX

Method g135422 NCBI GI 615 BLAST score 3.0e-64 E value 120 Match length 95 % identity

TUBULIN ALPHA-4 CHAIN >gi\_88945\_pir\_\_A25873 tubulin alpha NCBI Description

chain (version 2) - human >gi\_2119265\_pir\_\_I77427 alpha-tubulin isotype M-alpha-6 - mouse >gi\_202215 (M13444)

alpha-tubulin isotype M-alpha-6 [Mus musculus]

228218 Seq. No.

LIB3196-001-P1-M1-F10 Seq. ID

BLASTX Method g133867 NCBI GI 481 BLAST score 2.0e-48 E value Match length 112 % identity

NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi\_82722 pir\_S16577 ribosomal

protein S11 - maize >gi 22470 emb CAA39438 (X55967)

ribosomal protein S11 [Zea mays]

Seq. No. 228219

LIB3196-001-P1-M1-F7 Seq. ID

Method BLASTX NCBI GI g1929449 BLAST score 163



E value 9.0e-12 Match length 44 70 % identity NCBI Description (L63543) endodermin [Xenopus laevis] Seq. No. 228220 LIB3196-001-P1-M1-F9 Seq. ID Method BLASTX NCBI GI q547753 BLAST score 184 E value 4.0e-15 Match length 78 63 % identity NCBI Description KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4) Seq. No. 228221 LIB3196-001-P1-M1-G1 Seq. ID Method BLASTX NCBI GI q3024812 BLAST score 238 2.0e-20 E value Match length 60 % identity 78 NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >qi 2599050 (AF027705) vacuolar ATPase 16kDa subunit c [Ovis aries] 228222 Seq. No. Seq. ID LIB3196-001-P1-M1-G12 Method BLASTX NCBI GI g435480 BLAST score 249 E value 1.0e-21 71 Match length % identity 70 NCBI Description (X76679) MAL-b [Homo sapiens] Seq. No. 228223 Seq. ID LIB3196-001-P1-M1-G8 Method BLASTX NCBI GI g3152603 BLAST score 364 E value 8.0e-35 Match length 104 59 % identity NCBI Description (AC004482) unknown protein [Arabidopsis thaliana] Seq. No. 228224 Seq. ID LIB3196-001-P1-M1-H1

Method BLASTX
NCBI GI g1346348
BLAST score 153
E value 4.0e-10
Match length 101
% identity 38

NCBI Description KERATIN, TYPE II CYTOSKELETAL 6E (CYTOKERATIN 6E) (CK 6E) (K6E KERATIN) >gi\_2119223\_pir\_\_161770 keratin type II - human >gi 908803 (L42611) keratin type II [Homo sapiens]



```
Seq. No.
                  228225
Seq. ID
                  LIB3196-001-P1-M1-H10
Method
                  BLASTX
NCBI GI
                  g120649
BLAST score
                  597
                  4.0e-62
E value
Match length
                  118
                  97
% identity
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
                  >gi_625203_pir__DEHUG3 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - human >gi_182861 (M17851)
                  glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]
                  >gi_182863 (J02642) glyceraldehyde 3-phosphate
                  dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi_182977
                  (M33197) glyceraldehyde-3-phosphate dehydrogenase (EC
                  1.2.1.12) [Homo sapiens] >gi_182981 (J04038)
                  glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]
                  >gi 224880 prf 1203217A
                  dehydrogenase, glyceraldehydephosphate [Homo sapiens]
Seq. No.
                  228226
                  LIB3196-001-P1-M1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3122072
BLAST score
                  645
E value
                  1.0e-67
                  125
Match length
                  99
% identity
NCBI Description
                  ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION
                  FACTOR TU) (EF-TU) >gi_2119922_pir__I50226 elongation
                  factor 1 alpha - chicken >gi 488468 (L00677) elongation
                  factor 1 alpha [Gallus gallus]
Seq. No.
                  228227
Seq. ID
                  LIB3196-001-P1-M1-H8
Method
                  BLASTX
NCBI GI
                  q3811347
BLAST score
                  168
E value
                  8.0e-12
Match length
                  78
% identity
NCBI Description
                  (AF065215) cytosolic phospholipase A2 beta [Homo sapiens]
Seq. No.
                  228228
Seq. ID
                  LIB3196-001-P1-M1-H9
Method
                  BLASTX
NCBI GI
                  g4559312
BLAST score
                  360
```

E value 9.0e-35 Match length 80 % identity 89

NCBI Description (AF134149) 2-pore K+ channel subunit TOSS [Homo sapiens]

>gi 4574322 gb AAD24000.1 AF117708 1 (AF117708) tandem pore

domain potassium channel TWIK-2 [Homo sapiens]

Seq. No. 228229



Seq. ID LIB3196-002-P1-M1-A12 BLASTX Method NCBI GI g121116 BLAST score 277 E value 5.0e-25 Match length 77 74 % identity NCBI Description GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL) >gi\_71649\_pir\_\_FAHUP gelsolin precursor, plasma - human >gi\_736249 emb\_CAA28000 (X04412) plasma gelsolin [Homo sapiens] >gi\_225304 prf\_1211330A

Seq. No. 228230

Seq. ID LIB3196-002-P1-M1-A4

Method BLASTX
NCBI GI g114312
BLAST score 422
E value 1.0e-41
Match length 83
% identity 95

NCBI Description CALCIUM-TRANSPORTING ATPASE SARCOPLASMIC RETICULUM TYPE,

gelsolin (amyloidosis, Finnish type)

CLASS 2 ISOFORM (ENDOPLASMIC RETICULUM CLASS 2 CA(2+)

ATPASE) (CALCIUM PUMP) (SERCA2) (HK1) >gi\_86991\_pir\_\_A31981 Ca2+-transporting ATPase (EC 3.6.1.38) 1, renal - human

gelsolin [Homo sapiens] >gi 4504165 ref NP 000168.1 pGSN\_

>gi 306850 (M23114) HK1 [Homo sapiens]

Seq. No. 228231

Seq. ID LIB3196-002-P1-M1-A7

Method BLASTX
NCBI GI g3914685
BLAST score 526
E value 8.0e-54
Match length 117
% identity 86

NCBI Description 60S RIBOSOMAL PROTEIN L17 >gi 2668748 (AF034948) ribosomal

protein L17 [Zea mays]

Seq. No. 228232

Seq. ID LIB3196-002-P1-M1-B2

Method BLASTX
NCBI GI g3482913
BLAST score 235
E value 9.0e-23
Match length 87
% identity 67

NCBI Description (AC003970) Similar to MtN21, gi 2598575, Megicago

truncatula nodulation induced gene [Arabidopsis thaliana]

Seq. No. 228233

Seq. ID LIB3196-002-P1-M1-B4

Method BLASTX
NCBI GI g1854386
BLAST score 521
E value 3.0e-53
Match length 132

32633



```
% identity
NCBI Description
                  (AB001375) similar to soluble NSF attachment protein [Vitis
                  vinifera]
                  228234
Seq. No.
                  LIB3196-002-P1-M1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3335226
BLAST score
                  405
E value
                  1.0e-39
Match length
                  87
% identity
                  25
                  (AF077374) small proline-rich protein [Homo sapiens]
NCBI Description
Seq. No.
                  228235
                  LIB3196-002-P1-M1-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3293537
BLAST score
                  471
E value
                  2.0e-47
Match length
                  93
% identity
                  97
NCBI Description
                 (AF071059) zinc finger RNA binding protein [Mus musculus]
Seq. No.
                  228236
Seq. ID
                  LIB3196-002-P1-M1-B9
Method
                  BLASTX
NCBI GI
                  q4240147
BLAST score
                  293
                  2.0e-26
E value
Match length
                  66
                  94
% identity
NCBI Description (AB020636) KIAA0829 protein [Homo sapiens]
Seq. No.
                  228237
Seq. ID
                  LIB3196-002-P1-M1-C12
Method
                  BLASTX
NCBI GI
                  q113289
BLAST score
                  233
E value
                  3.0e-19
Match length
                  117
                  53
% identity
                  ACTIN >gi 100988 pir S24408 actin - Achlya bisexualis
NCBI Description
                  >gi 2290 emb CAA42559 (X59936) actin [Achlya bisexualis]
Seq. No.
                  228238
Seq. ID
                  LIB3196-002-P1-M1-C4
                  BLASTX
Method
NCBI GI
                  q432359
BLAST score
                  560
E value
                  2.0e-60
Match length
                  124
                  95
% identity
NCBI Description
                  (D23660) ribosomal protein [Homo sapiens]
```

Seq. No. 228239

Seq. ID LIB3196-002-P1-M1-C9

NCBI Description

elegans]



```
Method
                    BLASTX
NCBI GI
                    q405194
BLAST score
                    442
E value
                    6.0e-44
Match length
                    117
                    78
% identity
NCBI Description
                   (L10911) splicing factor [Homo sapiens]
Seq. No.
                    228240
Seq. ID
                    LIB3196-002-P1-M1-D12
Method
                    BLASTX
NCBI GI
                    q113944
BLAST score
                    663
                    8.0e-70
E value
Match length
                    137
% identity
                    56
                    ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9)
NCBI Description
                    (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN)
                    >gi_71756_pir__LUHU annexin I - human
                    >gi_34388_emb_CAA29338_ (X05908) lipocortin (AA 1-346)
[Homo sapiens] >gi_224956_prf__1204261A lipocortin [Homo
                    sapiens] >gi 45021\overline{0}1 ref \overline{NP} 0\overline{00}691.1 pANX1 annexin I
                    (lipocortin I)
Seq. No.
                    228241
Seq. ID
                    LIB3196-002-P1-M1-D6
Method
                    BLASTX
                    g4539330
NCBI GI
BLAST score
                    418
E value
                    3.0e-41
Match length
                    115
% identity
                    70
                    (AL035679) putative receptor-like protein kinase (fragment)
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                    228242
Seq. ID
                    LIB3196-002-P1-M1-D7
Method
                    BLASTX
NCBI GI
                    g671865
BLAST score
                    252
E value
                    8.0e-22
Match length
                    109
% identity
                    40
NCBI Description (X78801) ovomacroglobulin, ovostatin [Gallus gallus]
Seq. No.
                    228243
Seq. ID
                    LIB3196-002-P1-M1-D8
Method
                    BLASTX
NCBI GI
                    q2496887
BLAST score
                    264
E value
                    4.0e-23
Match length
                    114
% identity
                    52
```

HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III

>gi 732538 (U22832) C09F5.2 gene product [Caenorhabditis

NCBI GI

· E value

BLAST score

g2118384

1.0e-63

610



```
Seq. No.
                  228244
                  LIB3196-002-P1-M1-D9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2522261
BLAST score
                  248
                  2.0e-21
E value
                  52
Match length
                  92
% identity
NCBI Description (D88492) CPE-receptor [Chlorocebus aethiops]
                  228245
Seq. No.
                  LIB3196-002-P1-M1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2224565
BLAST score
                  529
                  3.0e-54
E value
                  120
Match length
% identity
                  85
NCBI Description (AB002310) KIAA0312 [Homo sapiens]
                  228246
Seq. No.
                  LIB3196-002-P1-M1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1001708
BLAST score
                  214
E value
                  3.0e-17
Match length
                  80
                  57
% identity
NCBI Description (D64004) NifS [Synechocystis sp.]
Seq. No.
                  228247
                  LIB3196-002-P1-M1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1293563
BLAST score
                  347
E value
                  3.0e-33
Match length
                  82
                  83
% identity
NCBI Description (U49188) Diff33 gene product [Homo sapiens]
Seq. No.
                  228248
                  LIB3196-002-P1-M1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351222
BLAST score
                  596
E value
                  5.0e-62
Match length
                  125
% identity
                  93
NCBI Description TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi 945087
                  (U31097) transcription factor TFIIB [Glycine max]
Seq. No.
                  228249
                  LIB3196-002-P1-M1-F10
Seq. ID
                  BLASTX
Method
```

32636

% identity



```
133
Match length
                  90
% identity
                  squamous cell carcinoma antigen 2 - human
NCBI Description
                  228250
Seq. No.
                  LIB3196-002-P1-M1-F12
Seq. ID
                  BLASTX
Method
                  g294668
NCBI GI
BLAST score
                  321
E value
                  9.0e-30
                  120
Match length
% identity
                   63
                  (L13242) beta-ketoacyl-ACP synthase [Ricinus communis]
NCBI Description
                  228251
Seq. No.
                  LIB3196-002-P1-M1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1363944
BLAST score
                  320
                  1.0e-29
E value
Match length
                   70
                   93
% identity
                  type I keratin 16 - human >gi_1195531_bbs_172338 (S79867)
NCBI Description
                   type I keratin 16, K16 [human, epidermal keratinocytes,
                   Peptide, 473 aa] [Homo sapiens]
Seq. No.
                   228252
                  LIB3196-002-P1-M1-F5
Seq. ID
Method
                  BLASTX
                   g3914935
NCBI GI
BLAST score
                   203
                   3.0e-16
E value
Match length
                   63
                   67
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN SA (P40) >gi 3204099 emb CAA07226
                   (AJ006759) ribosome-associated protein p40 [Cicer
                   arietinum]
                   228253
Seq. No.
                   LIB3196-002-P1-M1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3108187
                   277
BLAST score
E value
                   4.0e-25
                   55
Match length
                   96
% identity
NCBI Description (AC004663) Notch 3 [Homo sapiens]
                   228254
Seq. No.
                   LIB3196-002-P1-M1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4185792
                   392
BLAST score
E value
                   4.0e-38
Match length
                   77
```

32637

NCBI Description (AF095890) transcription factor E1AF [Homo sapiens]



```
228255
Seq. No.
                   LIB3196-002-P1-M1-F9
Seq. ID
Method
                   BLASTX
                   q113950
NCBI GI
                   494
BLAST score
                   5.0e-50
E value
Match length
                   116
                   52
% identity
                   ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN)
NCBI Description
                   (CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL ANTICOAGULANT PROTEIN IV) (PAP-IV) >gi_71761_pir__LUHU36 annexin II -
                   human >gi_219910_dbj_BAA00013_ (D00017) lipocortin II [Homo
                   sapiens]
                   228256
Seq. No.
                   LIB3196-002-P1-M1-G1
Seq. ID
Method
                   BLASTX
                   q280816
NCBI GI
BLAST score
                   152
                   2.0e-10
E value
                   60
Match length
                   60
% identity
NCBI Description
                   keratin 13, type I, cytoskeletal, short form - human
                   >gi_30377_emb_CAA36673_ (X52426) cytokeratin 13 [Homo
                   sapiens] >gi_3603253 (AF049259) keratin 13 [Homo sapiens]
                   >gi_4504911_ref_NP_002265.1_pKRT13_ keratin
Seq. No.
                   228257
                   LIB3196-002-P1-M1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2137308
BLAST score
                   276
                   1.0e-24
E value
Match length
                   73
% identity
                   77
NCBI Description G protein beta subuit like - mouse >gi 475012 dbj BAA06185
                   (D29802) G protein beta subuit like [Mus musculus]
Seq. No.
                   228258
Seq. ID
                   LIB3196-002-P1-M1-G4
Method
                   BLASTX
NCBI GI
                   g548710
BLAST score
                   351
                   2.0e-33
E value
Match length
                   114
% identity
                   40
                   RETICULOCALBIN 1 PRECURSOR >gi 346940 pir_A45337
NCBI Description
                   reticulocalbin - mouse >gi_220582_dbj_BAA02366_ (D13003)
```

reticulocalbin [Mus musculus] >gi\_968894 dbj\_BAA07896

(D43956) reticulocalbin [Mus musculus]

>gi 1581021 prf 2116329A reticulocalbin [Mus musculus]

228259 Seq. No.

Seq. ID LIB3196-002-P1-M1-G7

Method BLASTX NCBI GI g2500527



```
BLAST score
                    1.0e-63
E value
Match length
                   116
% identity
                    99
                   PROBABLE RNA-DEPENDENT HELICASE P68 (DEAD-BOX PROTEIN P68)
NCBI Description
                    (DEAD BOX PROTEIN 5) >gi_2137742_pir__I48385 RNA helicase
                    TNZ2 - mouse >gi 51263 emb_CAA46581_ (X65627) p68 RNA
                   helicase [Mus musculus]
                    228260
Seq. No.
                   LIB3196-002-P1-M1-G8
Seq. ID
Method
                   BLASTX
                    q3777596
NCBI GI
                    223
BLAST score
E value
                    6.0e-26
                    112
Match length
                    51
% identity
NCBI Description (AF095791) TACC2 protein [Homo sapiens]
                    228261
Seq. No.
                    LIB3196-002-P1-M1-H10
Seq. ID
                    BLASTX
Method
NCBI GI
                    g1170636
BLAST score
                    136
E value
                    5.0e-19
                    77
Match length
                    70
% identity
NCBI Description DIACYLGLYCEROL KINASE, ALPHA (DIGLYCERIDE KINASE)
                    (DGK-ALPHA) (DAG KINASE ALPHA) (80 KD DIACYLGLYCEROL KINASE) >gi_105839_pir__S12969 diacylglycerol kinase (EC 2.7.1.107) alpha - human >gi_30823_emb_CAA44396_ (X62535)
                    diacylglycerol kinase [Homo sapiens]
                    >qi 227338 prf 1702222A diacylglycerol kinase [Homo
                    sapiens]
Seq. No.
                    228262
                    LIB3196-002-P1-M1-H11
Seq. ID
                    BLASTX
Method
NCBI GI
                    g132573
BLAST score
                    363
E value
                    1.0e-34
Match length
                    80
% identity
                    14
NCBI Description PLACENTAL RIBONUCLEASE INHIBITOR (RIBONUCLEASE/ANGIOGENIN
                    INHIBITOR) (RAI) (RI) >gi_88562_pir__A31858
                    ribonuclease-angiogenin inhibitor - human >gi 307040
                    (M22414) ribonuclease inhibitor precursor [Homo sapiens]
                    >gi 226786 prf 1605207A RNase inhibitor [Homo sapiens]
                    228263
Seq. No.
                    LIB3196-002-P1-M1-H12
Seq. ID
Method
                    BLASTX
                    g1082318
NCBI GI
BLAST score
                    516
```

1.0e-52

102 91

E value Match length

% identity

NCBI GI

E value

BLAST score

Match length

g477138

6.0e-54

526

108





```
NCBI Description cystathionine beta-synthase (EC 4.2.1.22) - human
                  228264
Seq. No.
                  LIB3196-002-P1-M1-H3
Seq. ID
                  BLASTX
Method
                  q1754538
NCBI GI
                  470
BLAST score
                  3.0e-47
E value
                  96
Match length
                  94
% identity
                  (U66894) ESX [Homo sapiens] >gi 1841523 (U73843) ESE-1b
NCBI Description
                  [Homo sapiens] >gi_2338756 (AF017307) Ets-related
                  transcription factor [Homo sapiens] >gi_2384740 (AF016295)
                  Ets transcription factor [Homo sapiens] >gi_2459797
                   (U97156) epthelial-specific ets protein [Homo sapiens]
                  228265
Seq. No.
                  LIB3196-002-P1-M1-H5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g337999
BLAST score
                  596
                  1.0e-66
E value
                  134
Match length
                  93
% identity
                  (M63573) secreted cyclophilin-like protein [Homo sapiens]
NCBI Description
Seq. No.
                  228266
                  LIB3196-002-P1-M1-H7
Seq. ID
                  BLASTX
Method
                  q1617312
NCBI GI
BLAST score
                   365
                   7.0e-35
E value
Match length
                  126
                   57
% identity
                  (X92689) UDP-GalNAc:polypeptide
NCBI Description
                  N-acetylgalactosaminyltransferas [Homo sapiens]
                   228267
Seq. No.
                  LIB3196-002-P1-M1-H8
Seq. ID
                  BLASTX
Method
NCBI GI
                   q399012
BLAST score
                   299
E value
                   3.0e-27
Match length
                   100
                   65
% identity
                  ADP, ATP CARRIER PROTEIN, ISOFORM T2 (ADP/ATP TRANSLOCASE 3)
NCBI Description
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
                   >gi 280900 pir B43646 ADP, ATP carrier protein T2 - bovine
                   >gi 529417 (M24103) translocase [Bos taurus]
Seq. No.
                   228268
Seq. ID
                   LIB3196-002-P1-M1-H9
Method
                   BLASTX
```

32640



% identity carcinoma-associated antigen GA733-1 precursor - human NCBI Description >gi 31591 emb CAA31781 (X13425) GA733-1 protein (AA 1-323) [Homo sapiens] 228269 Seq. No. LIB3196-003-P1-M1-A1 Seq. ID Method BLASTX NCBI GI q130224 BLAST score 441 E value 6.0e-44115 Match length 74 % identity 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE NCBI Description GAMMA 1 (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148) >gi\_89333\_pir\_\_S00666 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) isozyme II - bovine >gi\_639\_emb\_CAA68406\_ (Y00301) phosphatidylinositol-specific phospholipase C. [Bos taurus] >gi 225974 prf 1404383A phospholipase C [Bos taurus] Seq. No. 228270 Seq. ID LIB3196-003-P1-M1-A2 Method BLASTX NCBI GI g2244974 BLAST score 147 2.0e-09 E value 90 Match length % identity 44 NCBI Description (Z97340) similarity to pore protein Pisum sativum [Arabidopsis thaliana] 228271 Seq. No. Seq. ID LIB3196-003-P1-M1-A4 Method BLASTX NCBI GI g226728 BLAST score 298 E value 4.0e-27 Match length 102 % identity 67 NCBI Description transcription factor ATF3 [Homo sapiens] Seq. No. 228272 LIB3196-003-P1-M1-A6 Seq. ID Method BLASTX NCBI GI q539663 BLAST score 450 E value 6.0e-45

Match length 98 % identity 88

NCBI Description PR264/SC35 protein - human >gi 35597 emb CAA44307 (X62447) PR 264 [Homo sapiens]  $>gi_4554\overline{1}9$  emb\_CAA $\overline{5}3383$  (X $\overline{7}5755$ )

PR264/SC35 [Homo sapiens] >gi 3335676 (AF077858) splicing

factor SC35 [Mus musculus] >gi 228504 prf 1805195B

RNA-binding protein PR264 [Homo sapiens]



```
Seq. No.
Seq. ID
                   LIB3196-003-P1-M1-A7
Method
                   BLASTX
NCBI GI
                   q3329390
BLAST score
                   605
                   4.0e-63
E value
                   117
Match length
                   98
% identity
NCBI Description (AF038960) SKD1 homolog [Homo sapiens]
Seq. No.
                   228274
                   LIB3196-003-P1-M1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q119540
BLAST score
                   662
                   9.0e-70
E value
Match length
                   128
                   100
% identity
NCBI Description DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA
                   PIGMENTOSUM GROUP D COMPLEMENTING PROTEIN) (DNA EXCISION
                   REPAIR PROTEIN ERCC-2) >gi_105956_pir__S10888 ERCC2 protein
                   - human
                   228275
Seq. No.
                   LIB3196-003-P1-M1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2605714
BLAST score
                   351
                   2.0e-33
E value
                   89
Match length
% identity
                   79
                   (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
NCBI Description
                   thaliana]
                   228276
Seq. No.
Seq. ID
                   LIB3196-003-P1-M1-B2
Method
                   BLASTX
NCBI GI
                   q125077
BLAST score
                   639
E value
                    4.0e-67
Match length
                   129
% identity
                    98
NCBI Description KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal,
                    long form - human >gi_34033_emb_CAA32786 (X14640) keratin
                   13 [Homo sapiens]
Seq. No.
                    228277
                   LIB3196-003-P1-M1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1730836
```

Method BLASTX
NCBI GI g1730836
BLAST score 208
E value 1.0e-16
Match length 120
% identity 43

NCBI Description HYPOTHETICAL 54.2 KD PROTEIN IN ZWF1-BLH1/LAP3 INTERGENIC REGION >gi 2131939 pir S63206 hypothetical protein YNL240c



- yeast (Saccharomyces cerevisiae)
>gi\_1183974\_emb\_CAA93358\_ (Z69381) N1114 [Saccharomyces
cerevisiae] >gi\_1302274\_emb\_CAA96145\_ (Z71516) ORF YNL240c
[Saccharomyces cerevisiae]

Seq. No. 228278

Seq. ID LIB3196-003-P1-M1-B8

Method BLASTX
NCBI GI g127148
BLAST score 561
E value 6.0e-58
Match length 108
% identity 99

NCBI Description MYOSIN LIGHT CHAIN ALKALI, SMOOTH-MUSCLE ISOFORM (MLC3SM)

(LC17B) (LC17-GI) >gi\_108819\_pir\_\_ S13671 myosin catalytic light chain A - bovine >gi\_1360691\_pir\_\_MOHU6N myosin

alkali light chain 6, nonmuscle form - human

>gi\_578\_emb\_CAA38721\_ (X54977) 17,000 dalton myosin light
chain [Bos taurus] >gi\_189018 (M22919) non-muscle myosin

light chain [Homo sapiens]

Seq. No. 228279

Seq. ID LIB3196-003-P1-M1-B9

Method BLASTX
NCBI GI g3024101
BLAST score 353
E value 1.0e-33
Match length 87
% identity 76

NCBI Description CHLORIDE CONDUCTANCE INDUCER PROTEIN MAT-8 PRECURSOR

>gi\_1082298\_pir\_\_A55571 chloride conductance inducer Mat-8
- human >gi\_1085026\_emb\_CAA63604\_ (X93036) MAT8 protein

[Homo sapiens]

Seq. No. 228280

Seq. ID LIB3196-003-P1-M1-C1

Method BLASTX
NCBI GI g1905874
BLAST score 546
E value 4.0e-56
Match length 111
% identity 95

NCBI Description (U90878) carboxyl terminal LIM domain protein [Homo

sapiens]

Seq. No. 228281

Seq. ID LIB3196-003-P1-M1-C2

Method BLASTX
NCBI GI g207905
BLAST score 541
E value 1.0e-55
Match length 122
% identity 89

NCBI Description (M18027) alpha globulin B [Artificial gene]

Seq. No. 228282

Seq. ID LIB3196-003-P1-M1-C4



```
BLASTX
Method
                   q3319958
NCBI GI
                   663
BLAST score
                   7.0e-70
E value
                   126
Match length
% identity
                   (AJ228139) VAKTI precursor [Homo sapiens]
NCBI Description
                   228283
Seq. No.
                   LIB3196-003-P1-M1-C5
Seq. ID
                   BLASTX
Method
                   g137578
NCBI GI
                   474
BLAST score
                   9.0e-48
E value
Match length
                   122
                   78
% identity
                   VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                   >gi_81545_pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi 207906 (M18027) alpha globulin A
                    [Artificial gene] >gi_226119_prf__1410330A vicilin gene A
                   [Saguinus oedipus]
                   228284
Seq. No.
                   LIB3196-003-P1-M1-C7
Seq. ID
                   BLASTX
Method
                   g1785488
NCBI GI
BLAST score
                   158
                   1.0e-10
E value
                   80
Match length
                   40
% identity
                  (D14590) flavonoid 3',5'-hydroxylase [Campanula medium]
NCBI Description
                   228285
Seq. No.
                   LIB3196-003-P1-M1-C8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q116075
BLAST score
                   188
                    3.0e-14
E value
                   80
Match length
                    55
% identity
NCBI Description CCAAT/ENHANCER BINDING PROTEIN BETA (C/EBP BETA) (NUCLEAR
                    FACTOR NF-IL6) (TRANSCRIPTION FACTOR 5) >gi_107921_pir__S12788 transcription factor NF-IL6 - human
                    >gi_35036_emb_CAA36794_ (X52560) nuclear factor NF-IL6 (AA
                    1-3\overline{4}5) [Homo sapiens]
Seq. No.
                    228286
                    LIB3196-003-P1-M1-C9
Seq. ID
Method
                    BLASTX
                    q207905
NCBI GI
                    509
BLAST score
E value
                    7.0e-52
                    120
Match length
 % identity
```

NCBI Description (M18027) alpha globulin B [Artificial gene]



Seq. No. 228287 Seq. ID Method

LIB3196-003-P1-M1-D1 BLASTX

NCBI GI q547712 BLAST score 592 E value 1.0e-61 Match length 121 96 % identity

NCBI Description EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)

>gi\_542153\_pir\_\_S38358 translation initiation factor eIF-4A

- rice >gi\_303844\_dbj\_BAA02152\_ (D12627) eukaryotic

initiation factor 4A [Oryza sativa]

Seq. No. 228288

Seq. ID LIB3196-003-P1-M1-D11

Method BLASTX NCBI GI q1928981 BLAST score 500 E value 8.0e-51 Match length 105 % identity 94

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

Seq. No. 228289

Seq. ID LIB3196-003-P1-M1-D12

Method BLASTX NCBI GI g416877 BLAST score 356 9.0e-61 E value Match length 126 % identity 91

NCBI Description TRANS-1, 2-DIHYDROBENZENE-1, 2-DIOL DEHYDROGENASE

(HIGH-AFFINITY HEPATIC BILE ACID-BINDING PROTEIN) (HBAB) >gi\_1071804\_pir\_\_A53436 3-alpha-hydroxysteroid/dihydrodiol
dehydrogenase (EC 1.1.1.-) - human >gi\_181549 (M86609)

dihydrodiol dehydrogenase [Homo sapiens]

>gi\_452484\_gb\_AAA16227.1\_ (U05684) dihydrodiol

dehydrogenase [Homo sapiens] >gi\_487135 (U05861) hepatic

dihydrodiol dehydrogenase [Homo sapiens]

Seq. No. 228290

Seq. ID LIB3196-003-P1-M1-D2

Method BLASTX NCBI GI g542184 BLAST score 206 E value 2.0e-16 Match length 108 % identity 40

NCBI Description globulin-1S, GLB1S - maize

Seq. No. 228291

Seq. ID LIB3196-003-P1-M1-D4

Method BLASTX NCBI GI g4406775 220 BLAST score E value 5.0e-18



```
Match length
                   77
% identity
                   58
                  (AC006836) unknown protein [Arabidopsis thaliana]
NCBI Description
                   228292
Seq. No.
Seq. ID
                  LIB3196-003-P1-M1-D9
Method
                   BLASTX
NCBI GI
                   g1504040
BLAST score
                   143
                   6.0e-09
E value
Match length
                   118
% identity
                   16
                  (D86983) similar to D.melanogaster peroxidasin(U11052)
NCBI Description
                   [Homo sapiens]
                   228293
Seq. No.
                  LIB3196-003-P1-M1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3915737
BLAST score
                   471
                   2.0e-47
E value
Match length
                   120
% identity
                   43
                  IMPORTIN ALPHA SUBUNIT (KARYOPHERIN ALPHA SUBUNIT) (KAP
NCBI Description
                   ALPHA) >gi 3228370 (AF017252) importin alpha [Lycopersicon
                   esculentum]
Seq. No.
                   228294
                   LIB3196-003-P1-M1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4417309
BLAST score
                   166
E value
                   1.0e-11
Match length
                   106
% identity
                   37
NCBI Description
                  (AC006446) putative pol polyprotein with a reverse
                   transcriptase domain [Arabidopsis thaliana]
                   228295
Seq. No.
Seq. ID
                   LIB3196-003-P1-M1-E11
Method
                   BLASTX
NCBI GI
                   q3746127
BLAST score
                   307
E value
                   4.0e-28
Match length
                   81
% identity
NCBI Description (U76253) E25B protein [Mus musculus]
Seq. No.
                   228296
                   LIB3196-003-P1-M1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3024665
BLAST score
                   202
E value
                   7.0e-16
Match length
                   114
% identity
                   41
```

NCBI Description STRICTOSIDINE SYNTHASE 3 PRECURSOR >gi 1754987 (U43946)

NCBI GI

BLAST score



## strictosidine synthase [Arabidopsis thaliana]

```
228297
Seq. No.
                  LIB3196-003-P1-M1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115502
BLAST score
                  585
E value
                  9.0e-61
                  120
Match length
                  49
% identity
                  CALMODULIN-RELATED PROTEIN NB-1 (CALMODULIN-LIKE PROTEIN)
NCBI Description
                  (CLP) >gi_71690_pir__MCHUNB calmodulin-related protein NB-1
                  - human >gi 29650_emb_CAA31809_ (X13461) hGH6
                  calmodulin-like protein [Homo sapiens] >gi_189081 (M58026)
                  NB-1 [Homo sapiens]
                  228298
Seq. No.
                  LIB3196-003-P1-M1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2146982
BLAST score
                  449
                  8.0e-45
E value
                  93
Match length
                  100
% identity
                  UDP-galactose translocator protein - human
NCBI Description
                  >gi_1526438_dbj_BAA12673_ (D84454) UDP-galactose
                  translocator [Homo sapiens]
                  228299
Seq. No.
                  LIB3196-003-P1-M1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2494144
                  209
BLAST score
                  9.0e-17
E value
                  118
Match length
% identity
                  (AC002329) predicted leucine-rich protein [Arabidopsis
NCBI Description
                  thaliana]
                  228300
Seq. No.
Seq. ID
                  LIB3196-003-P1-M1-F10
Method
                  BLASTX
NCBI GI
                  g3915742
BLAST score
                  580
E value
                   3.0e-60
Match length
                  121
% identity
NCBI Description LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi 167319
                   (M69188) legumin A [Gossypium hirsutum]
                  >qi 444320 prf 1906369A legumin A:ISOTYPE=D alloallele
                   [Gossypium hirsutum]
                   228301
Seq. No.
                  LIB3196-003-P1-M1-F11
Seq. ID
                  BLASTX
Method
```

32647

g4336349

526



E value 8.0e-54
Match length 110
% identity 91
NCBI Description (AF0828

NCBI Description (AF082871) arsenate resistance protein ARS2 [Homo sapiens]

Seq. No. 228302

Seq. ID LIB3196-003-P1-M1-F12

Method BLASTX
NCBI GI g586120
BLAST score 231
E value 3.0e-19
Match length 102
% identity 49

NCBI Description TRICHOHYALIN >gi\_539701\_pir\_\_A45973 trichohyalin - human

>gi\_292836 (L09190) trichohyalin [Homo sapiens]

Seq. No. 228303

Seq. ID LIB3196-003-P1-M1-F4

Method BLASTX
NCBI GI g729391
BLAST score 634
E value 2.0e-66
Match length 128
% identity 98

NCBI Description MITOCHONDRIAL TRIFUNCTONAL ENZYME ALPHA SUBUNIT PRECURSOR

(TP-ALPHA) [CONTAINS: LONG-CHAIN ENOYL-COA HYDRATASE ; LONG

CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE ]

>gi\_543064\_pir\_\_JC2108 long-chain-fatty-acid beta-oxidation
multienzyme complex alpha chain precursor, mitochondrial -

human >gi 862457\_dbj\_BAA03941\_ (D16480) enoyl-CoA

hydratase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit of

trifunctional protein [Homo sapiens]

>gi\_4504325\_ref\_NP\_000173.1\_pHADHA hydroxyacyl-Coenzyme A
dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme

A hydratase (trifunctional protein), alpha su

Seq. No. 228304

Seq. ID LIB3196-003-P1-M1-F7

Method BLASTX
NCBI GI g3646373
BLAST score 534
E value 8.0e-55
Match length 105
% identity 92

NCBI Description (AJ011078) RGP1 protein [Oryza sativa]

Seq. No. 228305

Seq. ID LIB3196-003-P1-M1-F8

Method BLASTX
NCBI GI g3337351
BLAST score 161
E value 4.0e-11
Match length 50
% identity 58

NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No. 228306



LIB3196-003-P1-M1-G12 Seq. ID Method BLASTX q4467804 NCBI GI BLAST score 625 2.0e-65 E value 117 Match length 95 % identity (AL031678) TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 NCBI Description PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3).) [Homo sapiens] 228307 Seq. No. LIB3196-003-P1-M1-G3 Seq. ID Method BLASTX NCBI GI g547753 348 BLAST score 6.0e-33 E value Match length 115 70 % identity NCBI Description KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4) Seq. No. 228308 LIB3196-003-P1-M1-G4 Seq. ID Method BLASTX NCBI GI g549063 316 BLAST score E value 3.0e-29Match length 81 74 % identity TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) NCBI Description >gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi 303835 dbj BAA02151 (D12626) 21kd polypeptide [Oryza sativa] Seq. No. 228309 Seq. ID LIB3196-003-P1-M1-G5 Method BLASTX NCBI GI g872116 BLAST score 305 6.0e-28E value Match length 122 % identity 44 NCBI Description (X79770) sti (stress inducible protein) [Glycine max] 228310 Seq. No. Seq. ID LIB3196-003-P1-M1-G6 Method BLASTX NCBI GI g4337025 BLAST score 351 E value 2.0e-33 Match length 123 % identity 59 NCBI Description (AF123253) AIM1 protein [Arabidopsis thaliana]

Seq. No. 228311

Seq. ID LIB3196-003-P1-M1-G7

Method BLASTX



```
NCBI GI
                   g120669
BLAST score
                   561
                   5.0e-58
E value
Match length
                   110
                   95
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi 19566 emb CAA42905 (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
                   228312
Seq. No.
                  LIB3196-003-P1-M1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g125105
BLAST score
                   623
                   3.0e-65
E value
Match length
                   126
                   99
% identity
                  KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5)
NCBI Description
                   (58 KD CYTOKERATIN) >gi 88051 pir A29904 keratin K5, 58K
                   type II, epidermal (version 1) - human >gi_307082 (M21389)
                   keratin type II [Homo sapiens]
                   >gi_4557890_ref_NP_000415.1_pKRT5 keratin
Seq. No.
                   228313
Seq. ID
                  LIB3196-003-P1-M1-H1
Method
                  BLASTX
                   g399888
NCBI GI
BLAST score
                   619
                   1.0e-64
E value
Match length
                   126
                   97
% identity
NCBI Description HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN
                   (HLA-DR ANTIGENS ASSOCIATED INVARIANT CHAIN) (P33) (CD74
                   ANTIGEN)
                   228314
Seq. No.
Seq. ID
                   LIB3196-003-P1-M1-H10
Method
                   BLASTX
NCBI GI
                   g3237306
BLAST score
                   625
                   2.0e-65
E value
Match length
                   126
% identity
                  (U92715) breast cancer antiestrogen resistance 3 protein
NCBI Description
                   [Homo sapiens] >gi_4502371_ref_NP_003558.1_pBCAR3_ breast
                   cancer antiestrogen resistance
                   228315
Seq. No.
Seq. ID
                   LIB3196-003-P1-M1-H12
```

Method BLASTX
NCBI GI g228298
BLAST score 215
E value 2.0e-17
Match length 64
% identity 69



60

80

% identity

```
NCBI Description transcription factor IIE:SUBUNIT=small 34kD [Homo sapiens]
Seq. No.
                    228316
Seq. ID
                    LIB3196-003-P1-M1-H2
Method
                    BLASTX
NCBI GI
                    g2347187
BLAST score
                    295
E value
                    9.0e-27
Match length
                    74
% identity
                   (AC002338) putative malonyl-CoA:Acyl carrier protein
NCBI Description
                    transacylase, 3' partial [Arabidopsis thaliana]
Seq. No.
                    228317
Seq. ID
                    LIB3196-003-P1-M1-H4
Method
                    BLASTX
NCBI GI
                    g386850
BLAST score
                    650
E value
                    2.0e-68
Match length
                    129
% identity
                    100
NCBI Description (M19723) keratin K5 [Homo sapiens]
Seq. No.
                    228318
Seq. ID
                    LIB3196-003-P1-M1-H5
Method
                    BLASTX
NCBI GI
                    g117528
BLAST score
                    309
E value
                    2.0e-28
Match length
                    90
% identity
                    81
NCBI Description
                   LAMBDA-CRYSTALLIN >gi_90077_pir__A31992 lambda-crystallin -
                    rabbit >gi_164905 (M22743) lambda-crystallin precursor
                    [Oryctolagus cuniculus]
Seq. No.
                    228319
Seq. ID
                    LIB3196-003-P1-M1-H7
Method
                    BLASTX
NCBI GI
                    q125080
BLAST score
                    616
E value
                    2.0e-64
Match length
                    125
% identity
                    100
NCBI Description
                   KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK
                    14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14
                    (epidermolysis bullosa simplex, Dowling-Meara, Koebner)
Seq. No.
                    228320
Seq. ID
                   LIB3196-003-P1-M1-H8
Method
                   BLASTX
NCBI GI
                    g4091080
BLAST score
                    262
E value
                    6.0e-23
Match length
```

32651

Seq. No.

Seq. ID

228325

LIB3196-004-P1-M1-C12



```
NCBI Description (AF045571) nucleic acid binding protein [Oryza sativa]
  Seq. No.
                     228321
  Seq. ID
                     LIB3196-004-P1-M1-A9
  Method
                     BLASTX
  NCBI GI
                     g113944
  BLAST score
                     605
  E value
                     4.0e-63
  Match length
                     124
  % identity
                     55
  NCBI Description ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9)
                     (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN)
                     >gi_71756_pir__LUHU annexin I - human
                     >gi_34388_emb_CAA29338_ (X05908) lipocortin (AA 1-346)
                     [Homo sapiens] >gi_224956_prf 1204261A lipocortin [Homo
                     sapiens] >gi_45021\overline{0}1_ref\overline{	ext{NP}}_0\overline{000}691.1_pANX1_ annexin I
                     (lipocortin I)
  Seq. No.
                     228322
  Seq. ID
                    LIB3196-004-P1-M1-B1
  Method
                    BLASTX
  NCBI GI
                    g4455217
  BLAST score
                    220
  E value
                     5.0e-18
  Match length
                    119
  % identity
                    44
 NCBI Description (AL035440) Avr9 elicitor response like protein [Arabidopsis
                    thaliana]
  Seq. No.
                    228323
  Seq. ID
                    LIB3196-004-P1-M1-B11
 Method
                    BLASTX
 NCBI GI
                    g2494305
  BLAST score
                    281
  E value
                    1.0e-52
 Match length
                    116
  % identity
                    97
 NCBI Description TRANSLATION INITIATION FACTOR EIF-2B BETA SUBUNIT (EIF-2B
                    GDP-GTP EXCHANGE FACTOR) >gi_1363072_pir__S56172
                    translation initiation factor eIF-2B beta chain - rabbit
                    >gi_1061200_emb_CAA88255_ (Z48222) protein synthesis
                    initiation factor eIF-2B beta subunit [Oryctolagus
                    cuniculus]
 Seq. No.
                    228324
 Seq. ID
                    LIB3196-004-P1-M1-B3
 Method
                    BLASTX
 NCBI GI
                    g4127947
 BLAST score
                    650
 E value
                    2.0e-68
 Match length
                    126
 % identity
                    97
 NCBI Description
                   (AJ010046) guanine nucleotide-exchange factor [Homo
                    sapiens]
```

32652



```
Method
                   BLASTX
NCBI GI
                   q1877202
BLAST score
                   543
E value
                   7.0e~56
Match length
                   120
% identity
                   90
                   (Y08915) alpha 4 protein [Homo sapiens]
NCBI Description
                   >gi_4557663 ref NP_001542.1_pIGBP1_ immunoglobulin-binding
                   protein
Seq. No.
                   228326
Seq. ID
                   LIB3196-004-P1-M1-C2
Method
                   BLASTX
NCBI GI
                   q125080
BLAST score
                   616
E value
                   2.0e-64
Match length
                   125
% identity
NCBI Description
                  KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK
                   14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal
                   - human >gi_386848 (J00124) keratin [Homo sapiens]
                   >gi_4504913_ref_NP_000517.1_pKRT14 keratin 14
                   (epidermolysis bullosa simplex, Dowling-Meara, Koebner)
Seq. No.
                   228327
Seq. ID
                   LIB3196-004-P1-M1-C3
Method
                  BLASTX
NCBI GI
                   q547753
BLAST score
                   322
E value
                   3.0e-55
Match length
                  124
% identity
                   96
NCBI Description KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)
Seq. No.
                  228328
Seq. ID
                  LIB3196-004-P1-M1-C6
Method
                  BLASTX
NCBI GI
                  q631131
BLAST score
                  534
E value
                  1.0e-54
Match length
                  109
% identity
                  98
NCBI Description
                  epithelial cell marker protein 1 - human >gi 187302
                  (M93010) epithelial cell marker protein 1 [Homo sapiens]
Seq. No.
                  228329
Seq. ID
                  LIB3196-004-P1-M1-C8
Method
                  BLASTX
NCBI GI
                  g2961346
BLAST score
                  143
E value
                  4.0e-14
Match length
                  54
% identity
NCBI Description
                  (AL022140) pectinesterase like protein [Arabidopsis
```

Seq. No. 228330

thaliana]

NCBI Description

Seq. No.



```
Seq. ID
                   LIB3196-004-P1-M1-C9
Method
                   BLASTX
NCBI GI
                   g1346344
BLAST score
                   620
E value
                   7.0e-65
Match length
                   123
% identity
                   100
NCBI Description
                  KERATIN, TYPE II CYTOSKELETAL 6A (CYTOKERATIN 6A) (CK 6A)
                   (K6A KERATIN) >gi_2119221_pir__A57398 keratin type II -
                   human >gi_908779 (L42583) keratin type II [Homo sapiens]
Seq. No.
                   228331
Seq. ID
                   LIB3196-004-P1-M1-D10
Method
                   BLASTX
NCBI GI
                   q70753
BLAST score
                   262
E value
                   5.0e-23
Match length
                   78
% identity
                   68
NCBI Description histone H3 - garden pea >gi_82610_pir__S00373 histone H3 -
Seq. No.
                   228332
Seq. ID
                  LIB3196-004-P1-M1-D3
Method
                  BLASTX
NCBI GI
                   q1710015
BLAST score
                   643
E value
                   1.0e-67
Match length
                   125
% identity
                   98
NCBI Description RAS-RELATED PROTEIN RAB-12 >gi 631513_pir _S40207 rab12
                  protein - dog >gi_437985_emb_CAA80471_ (Z22818) Rab12
                  protein [Canis familiaris]
Seq. No.
                  228333
Seq. ID
                  LIB3196-004-P1-M1-D7
Method
                  BLASTX
NCBI GI
                  g1346344
BLAST score
                  393
E value
                  2.0e-38
Match length
                  109
% identity
                  76
NCBI Description
                  KERATIN, TYPE II CYTOSKELETAL 6A (CYTOKERATIN 6A) (CK 6A)
                   (K6A KERATIN) >gi_2119221_pir__A57398 keratin type II -
                  human >gi_908779 (L42583) keratin type II [Homo sapiens]
Seq. No.
                  228334
Seq. ID
                  LIB3196-004-P1-M1-E1
Method
                  BLASTX
NCBI GI
                  q4099482
BLAST score
                  550
E value
                  1.0e-56
Match length
                  125
% identity
                  86
```

32654

(U87791) eRFS [Homo sapiens]

228335



Seq. ID LIB3196-004-P1-M1-E2

Method BLASTX
NCBI GI g1170499
BLAST score 586
E value 8.0e-61
Match length 125
% identity 89

NCBI Description TRANSLATION INITIATION FACTOR IF-2, MITOCHONDRIAL PRECURSOR

(IF-2MT) >gi\_1082869\_pir\_\_A55628 translation initiation factor IF-2 precursor, mitochondrial - human >gi 609492

(L34600) initiation factor 2 [Homo sapiens] >gi\_4505277\_ref\_NP\_002444.1\_pMTIF2 mitochondrial

translational initiation factor

Seq. No. 228336

Seq. ID LIB3196-004-P1-M1-F1

Method BLASTX
NCBI GI g125080
BLAST score 612
E value 5.0e-64
Match length 124
% identity 100

NCBI Description KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK

14) >gi\_2144816\_pir\_\_KRHUE keratin, 50K type I cytoskeletal

- human >gi\_386848 (J00124) keratin [Homo sapiens] >gi\_4504913 ref NP 000517.1 pKRT14 keratin 14

(epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No. 228337

Seq. ID LIB3196-004-P1-M1-F2

Method BLASTX
NCBI GI g1922935
BLAST score 558
E value 1.0e-57
Match length 120
% identity 98

NCBI Description (U47924) B-cell receptor associated protein [Homo sapiens]

>gi\_2289906 (AC002397) BAP [Mus musculus]

Seq. No. 228338

Seq. ID LIB3196-004-P1-M1-F5

Method BLASTX
NCBI GI g3176690
BLAST score 279
E value 7.0e-25
Match length 119
% identity 55

NCBI Description (AC003671) Similar to ubiquitin ligase gb D63905 from S.

cerevisiae. EST gb R65295 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 228339

Seq. ID LIB3196-004-P1-M1-F6

Method BLASTX
NCBI GI g3882081
BLAST score 594
E value 8.0e-62

```
Match length
                    119
 % identity
                    33
 NCBI Description (AJ012552) polyubiquitin [Vicia faba]
 Seq. No.
                   228340
 Seq. ID
                   LIB3196-004-P1-M1-G3
 Method
                   BLASTX
 NCBI GI
                   q4262292
 BLAST score
                   312
 E value
                   1.0e-28
 Match length
                   123
 % identity
                   50
 NCBI Description (AF072506) envelope protein precursor [Homo sapiens]
 Seq. No.
                   228341
 Seq. ID
                   LIB3196-004-P1-M1-G5
 Method
                   BLASTX
 NCBI GI
                   g167311
 BLAST score
                   501
 E value
                   6.0e-51
Match length
                   108
 % identity
                   90
 NCBI Description (M83301) 2S albumin storage protein [Gossypium hirsutum]
 Seq. No.
                   228342
 Seq. ID
                   LIB3196-004-P1-M1-G7
Method
                   BLASTX
NCBI GI
                   g4218961
BLAST score
                   513
E value
                   3.0e-52
Match length
                   121
% identity
                   87
NCBI Description (AF093130) caspase 9 short isoform [Homo sapiens]
Seq. No.
                   228343
Seq. ID
                   LIB3196-004-P1-M1-H11
Method
                   BLASTX
NCBI GI
                   g3776021
BLAST score
                   579
E value
                   4.0e-60
Match length
                   114
% identity
                   97
NCBI Description (AJ010472) RNA helicase [Arabidopsis thaliana]
Seq. No.
                   228344
Seq. ID
                   LIB3196-004-P1-M1-H12
Method
                   BLASTX
NCBI GI
                   g88044
BLAST score
                   605
E value
                   4.0e-63
Match length
                   125
% identity
                   97
NCBI Description
                  keratin 4, type II, cytoskeletal - human (fragment)
                   >gi_34073_emb_CAA30534 (X07695) cytokeratin 4 (408 AA)
```

Seq. No. 228345

[Homo sapiens]



```
Seq. ID
                   LIB3196-004-P1-M1-H2
Method
                   BLASTX
NCBI GI
                   g137578
BLAST score
                   470
E value
                   3.0e-47
Match length
                   95
 % identity
                   94
NCBI Description
                   VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
                   >gi_81545_pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                    [Artificial gene] >gi_226119_prf_ 1410330A vicilin gene A
                   [Saguinus oedipus]
Seq. No.
                   228346
Seq. ID
                   LIB3196-004-P1-M1-H4
Method
                   BLASTX
NCBI GI
                   g1076668
BLAST score
                   606
E value
                   3.0e-63
Match length
                   119
% identity
                   95
NCBI Description
                   NADH dehydrogenase (EC 1.6.99.3) - potato
                   >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase
                   [Solanum tuberosum]
Seq. No.
                   228347
Seq. ID
                   LIB3196-005-P1-M1-A1
Method
                   BLASTX
NCBI GI
                   g1596167
BLAST score
                   334
E value
                   3.0e-31
Match length
                   117
% identity
                   56
NCBI Description
                  (D87953) RTP [Homo sapiens] >gi_3046386 (AF004162)
                   {\tt nickel-specific} induction {\tt protein} [Homo sapiens]
Seq. No.
                   228348
Seq. ID
                   LIB3196-005-P1-M1-A10
Method
                   BLASTX
NCBI GI
                   g346219
BLAST score
                   298
E value
                   4.0e-27
Match length
                  124
% identity
                   59
NCBI Description keratin K4a - human (fragment)
Seq. No.
                  228349
Seq. ID
                  LIB3196-005-P1-M1-A12
Method
                  BLASTX
NCBI GI
                  q1173209
BLAST score
                  532
E value
                  1.0e-54
Match length
                  106
% identity
                  99
NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal
```

protein S16 protein - upland cotton

>gi\_439654\_emb\_CAA53567\_ (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]

Seq. No. 228350

Seq. ID LIB3196-005-P1-M1-A4

Method BLASTX
NCBI GI g3869127
BLAST score 230
E value 4.0e-19
Match length 66
% identity 64

NCBI Description (AB019527) LDOC1 protein [Homo sapiens]

Seq. No. 228351

Seq. ID LIB3196-005-P1-M1-A6

Method BLASTX
NCBI GI g579930
BLAST score 563
E value 4.0e-58
Match length 112
% identity 96

NCBI Description (X68314) glutathione peroxidase-GI [Homo sapiens]

>gi\_4504103\_ref\_NP\_002074.1\_pGPX2\_ glutathione peroxidase 2

(gastrointestinal)

Seq. No. 228352

Seq. ID LIB3196-005-P1-M1-A8

Method BLASTX
NCBI GI g137578
BLAST score 378
E value 2.0e-36
Match length 129
% identity 57

NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)

>gi\_81545\_pir\_\_S06398 alpha-globulin type A precursor upland cotton >gi\_167371 (M19378) vicilin precursor
[Gossypium hirsutum] >gi\_207906 (M18027) alpha globulin A
[Artificial gene] >gi\_226119\_prf\_\_1410330A vicilin gene A

[Saguinus oedipus]

Seq. No. 228353

Seq. ID LIB3196-005-P1-M1-A9

Method BLASTX
NCBI GI g421989
BLAST score 302
E value 1.0e-27
Match length 94
% identity 61

NCBI Description serpin - barley >gi\_19071\_emb\_CAA78822\_ (Z15116) protein zx

[Hordeum vulgare] >gi\_444778\_prf\_\_1908213A protein Zx

[Hordeum vulgare]

Seq. No. 228354

Seq. ID LIB3196-005-P1-M1-B1

Method BLASTX NCBI GI g2501446 BLAST score 512



E value 4.0e-52 Match length 98 % identity 100

NCBI Description UBIQUITIN-LIKE PROTEIN SMT3C (UBIQUITIN-HOMOLOGY DOMAIN

PROTEIN PIC1) (UBIQUITIN-LIKE PROTEIN UBL1)

(UBIQUITIN-RELATED PROTEIN SUMO-1) (GAP MODIFYING PROTEIN 1) (GMP1) (SENTRIN) >gi\_1518694 (U61397) ubiquitin-homology domain protein PIC1 [Homo sapiens] >gi\_1574948 (U38784) similar to ubiquitin and to yeast Smt3p (suppressor of MIF2); Method: conceptual translation supplied by author [Homo sapiens] >gi\_1703503 (U72722) gap modifying protein 1 [Homo sapiens] >gi\_1762973 (U67122) SUMO-1 [Homo sapiens]

>gi\_1769602 (U8311 $\overline{7}$ ) sentrin [Homo sapiens]

>gi\_1770521\_emb\_CAA67898\_ (X99586) SMT3C protein [Homo sapiens] >gi\_2645737 (AF033353) ubiquitin-homology domain protein [Mus musculus] >gi\_4507801\_ref\_NP\_003343.1\_pUBL1\_

ubiquitin-like 1 (sentrin)

Seq. No.

228355 Seq. ID LIB3196-005-P1-M1-B10

Method BLASTX NCBI GI g2501494 BLAST score 315 E value 4.0e-29 Match length 107 % identity 57

NCBI Description FLAVONOL 3-O-GLUCOSYLTRANSFERASE 5 (UDP-GLUCOSE FLAVONOID

3-O-GLUCOSYLTRANSFERASE 5) >gi\_542015\_pir\_\_\$41951

UTP-glucose glucosyltransferase - cassava >gi\_453249\_emb CAA54612 (X77462) UTP-glucose glucosyltransferase [Manihot esculenta]

Seq. No. 228356

Seq. ID LIB3196-005-P1-M1-B11

Method BLASTX NCBI GI g1703290 BLAST score 143 E value 2.0e-11 Match length 86 % identity 45

NCBI Description ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR

(ALPHA-2-MRAP) (LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN-ASSOCIATED PROTEIN 1) (RAP) (HEPARIN BINDING

PROTEIN-44) (HBP-44) >gi\_478425\_pir\_\_JX0281 heparin-binding protein-44 precursor - mouse >gi\_460892\_bbs\_142288 (S67967) heparin binding protein-44, HBP-44 [mice, Peptide, 360 aa]

[Mus sp.]

Seq. No. 228357

Seq. ID LIB3196-005-P1-M1-B12

Method BLASTX NCBI GI g1488647 BLAST score 480 E value 2.0e-48 Match length 116 % identity 82

NCBI Description (X99937) RNA helicase [Spinacia oleracea]



Seq. No. 228358

Seq. ID LIB3196-005-P1-M1-B3

Method BLASTX NCBI GI g3023847 BLAST score 654 E value 8.0e-69 Match length 130 % identity 27

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE

PROTEIN >gi\_2385376\_emb\_CAA69934 (Y08678) G protein beta

subunit-like [Medicago sativa]

Seq. No. 228359

Seq. ID LIB3196-005-P1-M1-B4

Method BLASTX NCBI GI g125080 BLAST score 668 E value 2.0e-70 Match length 135 % identity 99

NCBI Description KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK

14) >gi\_2144816\_pir\_\_KRHUE keratin, 50K type I cytoskeletal - human >gi\_386848 (J00124) keratin [Homo sapiens] >gi\_4504913\_ref\_NP\_000517.1\_pKRT14\_ keratin 14

(epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No. 228360

Seq. ID LIB3196-005-P1-M1-B5

Method BLASTX NCBI GI q3676473 BLAST score 270 E value 8.0e-24 Match length 119 % identity 48

NCBI Description (AF053886) (R)-(+)-mandelonitrile lyase isoform MDL5

precursor [Prunus serotina]

Seq. No. 228361

Seq. ID LIB3196-005-P1-M1-B6

Method BLASTX NCBI GI g137578 BLAST score 500 E value 7.0e-51Match length 118 % identity

NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)

>gi\_81545 pir S06398 alpha-globulin type A precursor upland cotton >gi 167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi 207906 (M18027) alpha globulin A [Artificial gene] >gi 226119 prf 1410330A vicilin gene A

[Saguinus oedipus]

Seq. No. 228362

Seq. ID LIB3196-005-P1-M1-B7

Method BLASTX NCBI GI g3122072

NCBI Description



```
BLAST score
                  603
                  8.0e-63
E value
                  121
Match length
                  98
% identity
                  ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION
NCBI Description
                  FACTOR TU) (EF-TU) >gi_2119922_pir__I50226 elongation
                  factor 1 alpha - chicken >gi_488468 (L00677) elongation
                  factor 1 alpha [Gallus gallus]
                  228363
Seq. No.
                  LIB3196-005-P1-M1-B8
Seq. ID
                  BLASTX
Method
                  g137578
NCBI GI
                   453
BLAST score
                  2.0e-45
E value
                  109
Match length
                  84
% identity
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                  >gi_81545_pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                   [Artificial gene] >gi_226119_prf__1410330A vicilin gene A
                   [Saguinus oedipus]
                   228364
Seq. No.
                   LIB3196-005-P1-M1-C10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q586120
                   148
BLAST score
                   1.0e-09
E value
                   46
Match length
                   57
% identity
                   TRICHOHYALIN >gi 539701_pir__A45973 trichohyalin - human
NCBI Description
                   >gi 292836 (L09190) trichohyalin [Homo sapiens]
                   228365
Seq. No.
                   LIB3196-005-P1-M1-C12
Seq. ID
                   BLASTX
Method
                   g2500376
NCBI GI
                   466
BLAST score
                   9.0e-47
E value
                   95
Match length
                   93
 % identity
NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi_4262177_gb_AAD14494_
                   (AC005508) 23552 [Arabidopsis thaliana]
                   228366
 Seq. No.
                   LIB3196-005-P1-M1-C3
 Seq. ID
 Method
                   BLASTX
                   g3834310
 NCBI GI
                   549
 BLAST score
                   2.0e-56
 E value
 Match length
                   105
 % identity
                   (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
```

32661

gb D83004 from Homo sapiens. ESTs gb\_T88233, gb Z24464, gb\_N37265, gb\_H36151, gb\_Z34711, gb\_AA040983, and gb\_T22122



come from this gene. [Arabidopsis thaliana]

```
228367
Seq. No.
                  LIB3196-005-P1-M1-C4
Seq. ID
                  BLASTX
Method
                  g3043548
NCBI GI
                  340
BLAST score
                  5.0e - 32
E value
                  131
Match length
                  50
% identity
                  (AB011084) KIAA0512 protein [Homo sapiens]
NCBI Description
                  228368
Seq. No.
                  LIB3196-005-P1-M1-C5
Seq. ID
                  BLASTX
Method
                  g1632831
NCBI GI
BLAST score
                  347
                  8.0e-33
E value
                  74
Match length
                  93
% identity
                  (Z49698) orf [Ricinus communis]
NCBI Description
                  228369
Seq. No.
                  LIB3196-005-P1-M1-C8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3395429
BLAST score
                  172
E value
                   3.0e-12
                  94
Match length
                   41
% identity
                 (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   228370
Seq. No.
                  LIB3196-005-P1-M1-D1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4008441
BLAST score
                   214
E value
                   3.0e-17
Match length
                   62
% identity
                   63
                  (AL034488) predicted using Genefinder; cDNA EST yk433c6.3
NCBI Description
                   comes from this gene; cDNA EST EMBL: D72601 comes from this
                   gene; cDNA EST EMBL: D75524 comes from this gene; cDNA EST
                   yk433c6.5 comes from this gene [Caenorhabditis elegans]
                   228371
Seq. No.
Seq. ID
                   LIB3196-005-P1-M1-D2
Method
                   BLASTX
NCBI GI
                   q631131
BLAST score
                   272
E value
                   3.0e-48
Match length
                   107
% identity
                   98
NCBI Description epithelial cell marker protein 1 - human >gi_187302
                   (M93010) epithelial cell marker protein 1 [Homo sapiens]
```

Seq. No. 228372



```
LIB3196-005-P1-M1-D4
 Seq. ID
                     BLASTX
 Method
NCBI GI
                     q2498629
                     598
 BLAST score
                     3.0e-62
 E value
                     135
 Match length
                     31
 % identity
                     TRANSCRIPTIONAL REPRESSOR NF-X1 >gi_2135825_pir__I38869
 NCBI Description
                     NFX1 - human >gi 563217 (U15306) NFX1 [Homo sapiens]
                     >qi 4505387 ref NP 002495.1_pNFX1_ nuclear transcription
                     factor, X-box binding
 Seq. No.
                     228373
                     LIB3196-005-P1-M1-E3
 Seq. ID
                     BLASTX
 Method
 NCBI GI
                     q114374
                     583
 BLAST score
                     1.0e-60
 E value
                      120
 Match length
                      99
 % identity
                     SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-1 CHAIN (SODIUM
 NCBI Description
                      PUMP) (NA+/K+ ATPASE) >gi_88220_pir_A24414
Na+/K+-exchanging ATPase (EC 3.6.1.37) alpha-1 chain -
                      human >gi 28927_emb_CAA27840_ (X04297) ATPase alpha subunit (aa 1-1023) [Homo sapiens] >gi_219942_dbj_BAA00061_
                      (D00099) Na, K-ATPase alpha-subunit [Homo sapiens]
                      >gi_356169_prf__1208322A ATPase alpha, Na/K [Homo sapiens]
  Seq. No.
                      228374
                      LIB3196-005-P1-M1-E5
  Seq. ID
                      BLASTX
 Method
                      g1346347
  NCBI GI
                      661
  BLAST score
                      1.0e-69
  E value
                      134
  Match length
                      99
  % identity
  NCBI Description KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D)
                      (K6D KERATIN) >gi_2119225_pir__I61769 keratin type II -
                      human (fragment) \overline{>}gi_9148\overline{3}3 (\overline{L4}2610) keratin type II [Homo
                      sapiens]
                      228375
  Seq. No.
                      LIB3196-005-P1-M1-E6
  Seq. ID
                      BLASTX
  Method
                      g3746127
  NCBI GI
                      348
  BLAST score
                      6.0e-33
  E value
  Match length
                      88
                      77
  % identity
  NCBI Description (U76253) E25B protein [Mus musculus]
                      228376
  Seq. No.
                      LIB3196-005-P1-M1-E7
  Seq. ID
  Method
                      BLASTX
                      g399365
  NCBI GI
```

502

5.0e-51

BLAST score

E value



```
Match length
                   117
                   85
% identity
                   ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (CLASS 3)
NCBI Description
                   >gi_178402 (M74542) aldehyde dehydrogenase type III [Homo
                   sapiens] >gi 4502035 ref NP 000682.1 pALDH3 aldehyde
                   dehydrogenase
                   228377
Seq. No.
                   LIB3196-005-P1-M1-E9
Seq. ID
Method
                   BLASTX
                   g683553
NCBI GI
BLAST score
                   151
                   6.0e-10
E value
                   93
Match length
% identity
                   41
                   (Z48450) oleosin-like protein [Citrus sinensis]
NCBI Description
                   >gi 1582679 prf 2119230A oleosin homolog [Citrus sinensis]
                   228378
Seq. No.
                   LIB3196-005-P1-M1-F10
Seq. ID
                   BLASTX
Method
                   g1173055
NCBI GI
BLAST score
                   611
                   9.0e-64
E value
                   122
Match length
% identity
                   99
                   60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__$42497
NCBI Description
                   ribosomal protein L11.e - alfalfa >gi_1076504_pir__S51819
                   RL5 ribosomal protein - alfalfa >gi_463252_emb_CAA55090_
                   (X78284) RL5 ribosomal protein [Medicago sativa]
                   228379
Seq. No.
                   LIB3196-005-P1-M1-F11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1174470
                   457
BLAST score
E value
                   1.0e-45
Match length
                   124
                   69
% identity
                   OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)
NCBI Description
                   (INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A
                   integral membrane protein [Mus musculus]
                   228380
Seq. No.
                   LIB3196-005-P1-M1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4049480
BLAST score
                   145
E value
                   4.0e-09
Match length
                   58
% identity
NCBI Description (Y18001) ATPase subunit 8 [Papio hamadryas]
```

Seq. No. 228381

Seq. ID LIB3196-005-P1-M1-F7

Method BLASTX



```
q3396098
NCBI GI
BLAST score
                  160
                  6.0e-11
E value
                  51
Match length
                  57
% identity
                  (AF080236) pyridoxamine 5'-phosphate oxidase [Schizophyllum
NCBI Description
                  commune]
                  228382
Seq. No.
                  LIB3196-005-P1-M1-F8
Seq. ID
Method
                  BLASTX
                  g4056459
NCBI GI
BLAST score
                  114
                  1.0e-09
E value
Match length
                  95
% identity
                   45
                  (AC005990) Contains similarity to qb L26505 Met30p from
NCBI Description
                  Saccharomyces cerevisiae. [Arabidopsis thaliana]
Seq. No.
                  228383
                  LIB3196-005-P1-M1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g113950
                  562
BLAST score
                   5.0e-58
E value
Match length
                  113
                   59
% identity
                  ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN)
NCBI Description
                   (CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL ANTICOAGULANT
                   PROTEIN IV) (PAP-IV) >gi_71761_pir__LUHU36 annexin II -
                  human >gi_219910_dbj_BAA00013_ (D00017) lipocortin II [Homo
                   sapiens]
                   228384
Seq. No.
                  LIB3196-005-P1-M1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4490330
BLAST score
                   623
E value
                   3.0e-65
Match length
                   129
% identity
                   96
NCBI Description
                  (AL035656) splicing factor-like protein [Arabidopsis
                   thaliana]
                   228385
Seq. No.
Seq. ID
                   LIB3196-005-P1-M1-G3
Method
                   BLASTX
NCBI GI
                   q3915742
BLAST score
                   498
E value
                   2.0e-50
Match length
                   98
```

% identity 94

LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi 167319 NCBI Description

(M69188) legumin A [Gossypium hirsutum]

>gi\_444320\_prf\_\_1906369A legumin A:ISOTYPE=D alloallele

[Gossypium hirsutum]



```
228386
Seq. No.
                     LIB3196-005-P1-M1-G5
Seq. ID
                     BLASTX
Method
                     q126156
NCBI GI
BLAST score
                     419
                     3.0e-41
E value
                     130
Match length
                     65
% identity
                     LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
NCBI Description
                     >gi 72288 pir__FWCNBB beta-globulin B precursor (clone 134)
                     - upland cotton >gi_167373 (M16936) vicilin precursor
                     [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                     protein C134 [Saguinus oedipus]
                     228387
Seq. No.
                     LIB3196-005-P1-M1-H10
Seq. ID
                     BLASTX
Method
                     g4469023
NCBI GI
                     437
BLAST score
E value
                     2.0e-43
                     98
Match length
                     86
% identity
                    (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
                     228388
Seq. No.
                     LIB3196-005-P1-M1-H12
Seq. ID
Method
                     BLASTX
NCBI GI
                     q1076398
BLAST score
                     148
E value
                     1.0e-09
                     39
Match length
                     69
% identity
                     ribosomal protein L2 - Arabidopsis thaliana
NCBI Description
                     >gi_572523_emb_CAA57902_ (X82556) ribosomal protein L2
                     [Arabidopsis thaliana]
                     228389
Seq. No.
                     LIB3196-005-P1-M1-H3
Seq. ID
Method
                     BLASTX
NCBI GI
                     g730165
BLAST score
                     305
E value
                     7.0e-28
                     95
Match length
                     67
% identity
                     EARLY NODULIN 93 (N-93) >gi_486679_pir__S34801 nodulin (clone GmN93) - soybean >gi_218262_dbj_BAA02724_ (D13506) early nodulin [Glycine max] >gi_3763851_dbj_BAA33816_
NCBI Description
                     (AB018378) early nodulin [Glycine max]
                     >gi 447138 prf 1913422D nodulin [Glycine max]
Seq. No.
                     228390
                     LIB3196-005-P1-M1-H4
Seq. ID
                     BLASTX
Method
```

32666

g3435086

3.0e-59

572

NCBI GI

E value

BLAST score



```
Match length
                  130
                  89
% identity
                  (AF004222) RTN2-A [Homo sapiens]
NCBI Description
                  228391
Seq. No.
                  LIB3196-005-P1-M1-H7
Seq. ID
                  BLASTX
Method
                  g88044
NCBI GI
BLAST score
                  625
                  2.0e-65
E value
                  132
Match length
% identity
                  97
                  keratin 4, type II, cytoskeletal - human (fragment)
NCBI Description
                  >gi 34073 emb CAA30534 (X07695) cytokeratin 4 (408 AA)
                   [Homo sapiens]
                  228392
Seq. No.
                  LIB3196-005-P1-M1-H8
Seq. ID
                  BLASTX
Method
                  q124224
NCBI GI
                   580
BLAST score
                   4.0e-60
E value
Match length
                  114
                   95
% identity
                  INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)
NCBI Description
                   >gi_100345_pir__S21060 translation initiation factor eIF-5A
                   - common tobacco >gi_19887_emb_CAA45105_ (X63543)
                   eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]
                   228393
Seq. No.
                  LIB3196-006-P1-M1-A1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4539405
                   489
BLAST score
                   1.0e-49
E value
                   116
Match length
                   81
% identity
                   (AL049524) putative ribosomal protein L9, cytosolic
NCBI Description
                   [Arabidopsis thaliana]
                   228394
Seq. No.
                   LIB3196-006-P1-M1-A11
Seq. ID
Method
                   BLASTX
                   q1872200
NCBI GI
                   180
BLAST score
                   2.0e-13
E value
Match length
                   82
% identity
                   (U22376) alternatively spliced product using exon 13A [Homo
NCBI Description
```

sapiens]

228395 Seq. No.

LIB3196-006-P1-M1-A7 Seq. ID

BLASTX Method NCBI GI g337358 BLAST score 404 E value 1.0e-39



```
Match length
                  82
                  99
% identity
                  (L03357) RET tyrosine kinase/cAMP protein kinase A subunit
NCBI Description
                  RI [Homo sapiens]
                  228396
Seq. No.
                  LIB3196-006-P1-M1-B1
Seq. ID
                  BLASTX
Method
                  g1346344
NCBI GI
BLAST score
                  156
                  1.0e-10
E value
                  31
Match length
                  97
% identity
                  KERATIN, TYPE II CYTOSKELETAL 6A (CYTOKERATIN 6A) (CK 6A)
NCBI Description
                   (K6A KERATIN) >gi_2119221_pir__A57398 keratin type II -
                  human >qi 908779 (L42583) keratin type II [Homo sapiens]
Seq. No.
                  228397
                  LIB3196-006-P1-M1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3445201
BLAST score
                  281
                   4.0e-25
E value
                  61
Match length
                  80
% identity
                 (AC004786) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  228398
                  LIB3196-006-P1-M1-B12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g137578
BLAST score
                  533
                  1.0e-54
E value
                  122
Match length
                   89
% identity
NCBI Description
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
                   >gi_81545_pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                   [Artificial gene] >gi_226119_prf__1410330A vicilin gene A
                   [Saguinus oedipus]
                   228399
Seq. No.
                  LIB3196-006-P1-M1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q125105
BLAST score
                   195
E value
                   3.0e-18
Match length
                   78
                   72
% identity
                  KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5)
NCBI Description
```

(58 KD CYTOKERATIN) >gi\_88051\_pir\_\_A29904 keratin K5, 58K

type II, epidermal (version 1) - human >gi 307082 (M21389)

keratin type II [Homo sapiens]

>gi\_4557890\_ref\_NP\_000415.1\_pKRT5\_ keratin

Seq. No. 228400



```
LIB3196-006-P1-M1-B3
Seq. ID
Method
                       BLASTX
                       q2924781
NCBI GI
                       537
BLAST score
                       4.0e-55
E value
Match length
                       125
                       81
% identity
                       (AC002334) putative cellulose synthase [Arabidopsis
NCBI Description
                       thaliana]
                       228401
Seq. No.
                       LIB3196-006-P1-M1-B4
Seq. ID
                       BLASTX
Method
NCBI GI
                       q116075
                       437
BLAST score
                       2.0e-43
E value
                       89
Match length
                       99
% identity
                       CCAAT/ENHANCER BINDING PROTEIN BETA (C/EBP BETA) (NUCLEAR
NCBI Description
                       FACTOR NF-IL6) (TRANSCRIPTION FACTOR 5)
                       >gi 107921 pir__S12788 transcription factor NF-IL6 - human
                       >gi_35036_{emb}CAA36794_{(X52560)} nuclear factor NF-IL6 (AA
                       1-3\overline{4}5) [Homo sapiens]
                       228402
Seq. No.
                       LIB3196-006-P1-M1-B6
Seq. ID
                       BLASTX
Method
                       g4176446
NCBI GI
                       241
BLAST score
                       2.0e-20
E value
                       120
Match length
                       36
% identity
                       (AL022238) dJ1042K10.2.1 (novel protein with probable
NCBI Description
                        rabGAP domains and Src homology domain 3) (isoform 1) [Homo
                       sapiens]
Seq. No.
                        228403
                       LIB3196-006-P1-M1-B8
Seq. ID
Method
                       BLASTX
NCBI GI
                        q133014
BLAST score
                        471
                        2.0e-47
E value
Match length
                        91
                        100
% identity
                        60S RIBOSOMAL PROTEIN L7A (PLA-X POLYPEPTIDE) (SURF-3)
NCBI Description
                       >gi_71116_pir__R5HU7A ribosomal protein L7a - human
>gi_71117_pir__R5RT7A ribosomal protein L7a - rat
>gi_34203_emb_CAA36383_(X52138) L7a protein [Homo sapiens]
>gi_35512_emb_CAA29889_(X06705) PLA-X polypeptide [Homo sapiens] >gi_36647_emb_CAA43925_(X61923) ribosomal protein
L7a [Homo sapiens] >gi_56956_emb_CAA33117_(X15013)
ribosomal protein L7a (AA 1-266) [Rattus rattus] >gi_337495
                        (M36072) ribosomal protein L7a large subunit [Homo sapiens]
                        >gi 1584354 prf 2122395A nuclear hormone
                        receptor-associated protein [Homo sapiens]
```

>gi 4506661 ref NP 000963.1 pRPL7A\_ ribosomal protein L7a



```
Seq. No.
                  228404
                  LIB3196-006-P1-M1-C1
Seq. ID
Method
                  BLASTX
                  g125077
NCBI GI
                  496
BLAST score
                  2.0e-50
E value
                  119
Match length
                  87
% identity
                  KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK
NCBI Description
                  13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal,
                  long form - human >gi_34033 emb_CAA32786_ (X14640) keratin
                  13 [Homo sapiens]
                  228405
Seq. No.
                  LIB3196-006-P1-M1-C10
Seq. ID
Method
                  BLASTX
                  g3746541
NCBI GI
                  201
BLAST score
                  1.0e-15
E value
                  46
Match length
                  87
% identity
                  (AF059273) glucocorticoid modulatory element binding
NCBI Description
                  protein 2 [Rattus norvegicus]
                   228406
Seq. No.
                  LIB3196-006-P1-M1-C11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1346342
                   347
BLAST score
                   8.0e-33
E value
                   118
Match length
                   65
% identity
                   KERATIN, TYPE I CYTOSKELETAL 17 (CYTOKERATIN 17) (K17) (CK
NCBI Description
                   17) (VERSION 2) >gi_186685 (M28439) keratin type 16 [Homo
                   sapiens]
                   228407
Seq. No.
                   LIB3196-006-P1-M1-C3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2662341
BLAST score
                   579
                   4.0e-60
E value
Match length
                   114
                   98
% identity
                   (D63580) EF-1 alpha [Oryza sativa]
NCBI Description
                   >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza
                   satīva] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha
                   [Oryza sativa]
                   228408
Seq. No.
                   LIB3196-006-P1-M1-C4
Seq. ID
                   BLASTX
Method
```

NCBI GI g1173256
BLAST score 525
E value 1.0e-53
Match length 100
% identity 100

E value

Match length

7.0e-23

108



```
40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal
NCBI Description
                  protein S4 - upland cotton >gi_488739_emb_CAA55882_
                  (X79300) ribosomal protein, small subunit 4e (RS4e)
                  [Gossypium hirsutum]
                  228409
Seq. No.
                  LIB3196-006-P1-M1-C5
Seq. ID
                  BLASTX
Method
                  g464621
NCBI GI
                  319
BLAST score
                  1.0e-29
E value
Match length
                  108
                  58
% identity
                  60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374_pir__S28586
NCBI Description
                  ribosomal protein ML16 - common ice plant
                  >qi 19539 emb CAA49175 (X69378) ribosomal protein YL16
                  [Mesembryanthemum crystallinum]
Seq. No.
                  228410
                  LIB3196-006-P1-M1-C9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2435521
BLAST score
                  411
                  2.0e-40
E value
                  120
Match length
                  14
% identity
NCBI Description
                  (AF024504) contains similarity to Nicotiana tabacum
                  membrane-associated salt-inducible protein (GB:U08285)
                  [Arabidopsis thaliana]
                  228411
Seq. No.
                  LIB3196-006-P1-M1-D1
Seq. ID
Method
                  BLASTX
                  g2662415
NCBI GI
                  216
BLAST score
                  1.0e-17
E value
Match length
                  51
% identity
                  71
NCBI Description (U97494) metallothionein-like protein [Prunus armeniaca]
                  228412
Seq. No.
                  LIB3196-006-P1-M1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q541675
                  535
BLAST score
                   6.0e-55
E value
Match length
                  119
% identity
                  89
NCBI Description (X76342) alternative ORF [Homo sapiens]
                   228413
Seq. No.
Seq. ID
                  LIB3196-006-P1-M1-D4
Method
                  BLASTX
NCBI GI
                   g1172995
BLAST score
                  262
```

32671



% identity

60S RIBOSOMAL PROTEIN L22 >gi\_1083790\_pir\_\_S52084 ribosomal NCBI Description

protein L22 - rat >gi\_710295\_emb\_CAA55204\_ (X78444)

ribosomal protein L22 [Rattus norvegicus]

>gi 1093952 prf 2105193A ribosomal protein L22 [Rattus

norvegicus]

Seq. No.

228414

Seq. ID

LIB3196-006-P1-M1-D5

Method NCBI GI BLASTX g416917

BLAST score

212

E value

6.0e-30

Match length % identity

86 77

NCBI Description

DESMOGLEIN 1 PRECURSOR (DESMOSOMAL GLYCOPROTEIN 1) (DG1)

>gi 319948 pir IJHUG1 desmoglein 1 precursor - human >gi 30506 emb CAA39976 (X56654) desmoglein type 1 [Homo

sapiens] >gi 3983129 (AF097935) desmoglein 1 [Homo sapiens]

>gi 4503401 ref NP 001933.1 pDSG1 desmoglein

Seq. No.

228415

Seq. ID

LIB3196-006-P1-M1-D6

Method NCBI GI BLASTX q3915742

BLAST score

346 1.0e-32

E value Match length

127 57

% identity NCBI Description

LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi 167319

(M69188) legumin A [Gossypium hirsutum]

>gi 444320 prf 1906369A legumin A:ISOTYPE=D alloallele

[Gossypium hirsutum]

Seq. No.

228416

Seq. ID

LIB3196-006-P1-M1-D8

Method NCBI GI BLASTX g120649 576

BLAST score E value

1.0e-59

Match length

% identity

112

NCBI Description

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER

>gi\_625203\_pir\_\_DEHUG3 glyceraldehyde-3-phosphate

dehydrogenase (EC 1.2.1.12) - human >gi 182861 (M17851) glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]

>gi\_182863 (J02642) glyceraldehyde 3-phosphate

dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi 182977 (M33197) glyceraldehyde-3-phosphate dehydrogenase (EC

1.2.1.12) [Homo sapiens] >gi 182981 (J04038)

glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]

>gi\_224880\_prf\_\_1203217A

dehydrogenase, glyceraldehydephosphate [Homo sapiens]

Seq. No.

228417

Seq. ID

LIB3196-006-P1-M1-E11

Method

BLASTX



99

% identity

NCBI Description

```
NCBI GI
                  q629693
                  180
BLAST score
E value
                  3.0e-13
Match length
                  74
                  50
% identity
                  probable integrase - common tobacco (fragment)
NCBI Description
                  >qi 530742 emb CAA56791 (X80830) integrase [Nicotiana
                  tabacum]
                  228418
Seq. No.
                  LIB3196-006-P1-M1-E12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3915742
BLAST score
                  580
                   3.0e-60
E value
                  121
Match length
% identity
                   91
                  LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi 167319
NCBI Description
                   (M69188) legumin A [Gossypium hirsutum]
                   >qi 444320 prf 1906369A legumin A:ISOTYPE=D alloallele
                   [Gossypium hirsutum]
                   228419
Seq. No.
                   LIB3196-006-P1-M1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q544129
BLAST score
                   433
                   5.0e-43
E value
Match length
                   114
% identity
                   74
                  VIGNAIN PRECURSOR (BEAN ENDOPEPTIDASE) (CYSTEINE PROTEINASE
NCBI Description
                   EP-C1) >gi 20994 emb CAA44816 (X63102) endopeptidase
                   [Phaseolus vulgaris]
                   228420
Seq. No.
                   LIB3196-006-P1-M1-E7
Seq. ID
                   BLASTX
Method
                   g1245046
NCBI GI
BLAST score
                   607
                   3.0e-63
E value
                   130
Match length
                   87
% identity
                   (U45285) specific 116-kDa vacuolar proton pump subunit
NCBI Description
                   [Homo sapiens]
                   228421
Seq. No.
                   LIB3196-006-P1-M1-E8
Seq. ID
                   BLASTX
Method
                   g479532
NCBI GI
BLAST score
                   457
                   1.0e-45
E value
Match length
                   94
```

binding protein [Homo sapiens]

GTP-binding regulatory protein Gs alpha chain - human

>gi\_1335091\_emb\_CAA39484\_ (X56009) alpha subunit of GsGTP



228422

Seq. No.

```
LIB3196-006-P1-M1-E9
  Seq. ID
Method
                    BLASTX
  NCBI GI
                    q207905
  BLAST score
                     609
                     1.0e-63
  E value
  Match length
                    127
  % identity
                     91
                    (M18027) alpha globulin B [Artificial gene]
  NCBI Description
                     228423
  Seq. No.
                    LIB3196-006-P1-M1-F10
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g2136189
  BLAST score
                     586
                     7.0e-61
  E value
  Match length
                     115
  % identity
                     97
  NCBI Description
                    specific granule protein, 28K, precusor - human
                     >gi_1213613_emb_CAA63984_ (X94323) SGP28 protein [Homo
                     sapiens] >gi 1587691 prf 2207217A SGP28 protein [Homo
                     sapiens]
  Seq. No.
                     228424
                     LIB3196-006-P1-M1-F11
  Seq. ID
                     BLASTX
  Method
  NCBI GI
                     g4457221
  BLAST score
                     184
  E value
                     1.0e-13
  Match length
                     56
                     62
  % identity
                    (AF127797) putative bZIP DNA-binding protein [Capsicum
  NCBI Description
                     chinense]
                     228425
  Seq. No.
                     LIB3196-006-P1-M1-F12
  Seq. ID
                     BLASTX
  Method
                     g4335763
  NCBI GI
  BLAST score
                     250
                     2.0e-21
  E value
                     88
  Match length
                     51
  % identity
                    (AC006284) unknown protein [Arabidopsis thaliana]
  NCBI Description
                     228426
  Seq. No.
                     LIB3196-006-P1-M1-F2
  Seq. ID
                     BLASTX
  Method
  NCBI GI
                     g3043584
  BLAST score
                     643
                     2.0e-67
  E value
  Match length
                     132
  % identity
                     96
  NCBI Description (AB011102) KIAA0530 protein [Homo sapiens]
                     228427
  Seq. No.
                     LIB3196-006-P1-M1-F5
  Seq. ID
  Method
                     BLASTX
```



NCBI GI g3885334 BLAST score 554 E value 4.0e-57 Match length 126 % identity 82

NCBI Description (AC005623) putative argonaute protein [Arabidopsis

thaliana]

Seq. No. 228428

Seq. ID LIB3196-006-P1-M1-F6

Method BLASTX
NCBI GI g113339
BLAST score 651
E value 2.0e-68
Match length 131
% identity 95

NCBI Description ADENOSINE DEAMINASE (ADENOSINE AMINOHYDROLASE)

>gi\_67782\_pir\_\_ DUHUA adenosine deaminase (EC 3.5.4.4) human >gi\_28380\_emb\_CAA26734\_ (X02994) adenosine deaminase
[Homo sapiens] >gi\_178077 (M13792) adenosine deaminase

[Homo sapiens]

Seq. No. 228429

Seq. ID LIB3196-006-P1-M1-G12

Method BLASTX
NCBI GI g547751
BLAST score 625
E value 2.0e-65
Match length 127
% identity 99

NCBI Description KERATIN, TYPE I CYTOSKELETAL 17 (CYTOKERATIN 17) (K17) (CK

17) (39.1) (VERSION 1) >gi\_422802\_pir\_\_S30433 keratin 17, cytoskeletal - human >gi\_30379\_emb\_CAA79626\_ (Z19574) cytokeratin 17 [Homo sapiens] >gi\_34075\_emb\_CAA44451\_

(X62571) keratin related product [Homo sapiens] >gi 4557701 ref\_NP\_000413.1\_pKRT17\_ keratin

Seq. No. 228430

Seq. ID LIB3196-006-P1-M1-G8

Method BLASTX
NCBI GI g137578
BLAST score 545
E value 4.0e-56
Match length 125
% identity 89

NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)

>gi\_81545\_pir\_\_S06398 alpha-globulin type A precursor upland cotton >gi\_167371 (M19378) vicilin precursor

[Gossypium hirsutum] >gi\_207906 (M18027) alpha globulin A [Artificial gene] >gi\_226119\_prf\_\_1410330A vicilin gene A

[Saguinus oedipus]

Seq. No. 228431

Seq. ID LIB3196-006-P1-M1-G9

Method BLASTX NCBI GI g547753 BLAST score 619



8.0e-65 E value Match length 130 98 % identity KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4) NCBI Description 228432 Seq. No. LIB3196-006-P1-M1-H1 Seq. ID Method BLASTX g125080 NCBI GI BLAST score 387 2.0e-37 E value 76 Match length % identity 100 KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK NCBI Description 14) >gi\_2144816\_pir\_\_KRHUE keratin, 50K type I cytoskeletal - human >gi\_386848 (J00124) keratin [Homo sapiens] >gi 4504913 ref NP 000517.1 pKRT14 keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner) 228433 Seq. No. LIB3196-006-P1-M1-H3 Seq. ID Method BLASTX NCBI GI g1346349 BLAST score 611 E value 8.0e-64 Match length 123 % identity 99 KERATIN, TYPE II CYTOSKELETAL 6F (CYTOKERATIN 6F) (CK 6F) NCBI Description (K6F KERATIN) >gi\_2119219\_pir\_\_I61771 keratin type II human >gi 908805 (L42612) keratin type II [Homo sapiens] 228434 Seq. No. LIB3196-006-P1-M1-H4 Seq. ID Method BLASTX NCBI GI q337760 BLAST score 520 E value 3.0e-53Match length 107 38 % identity (M60255) cerebroside sulfate activator protein [Homo NCBI Description sapiens] Seq. No. 228435 LIB3196-006-P1-M1-H8 Seq. ID Method BLASTX NCBI GI q1711507 BLAST score 378 E value 2.0e-36 Match length 91 76 % identity SIGNAL RECOGNITION PARTICLE 19 KD PROTEIN (SRP19) NCBI Description

>qi 624221 (U19030) signal recognition particle 19 kDa

protein subunit SRP19 [Oryza sativa]

Seq. No. 228436

LIB3196-006-P1-M1-H9 Seq. ID

Method BLASTX

32676



58

% identity

```
NCBI GI
                  g3894178
BLAST score
                  428
E value
                  2.0e-42
                  125
Match length
% identity
                  68
                  (AC005312) putative nucleic acid binding protein
NCBI Description
                  [Arabidopsis thaliana]
                  228437
Seq. No.
                  LIB3196-007-P1-M1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g129951
BLAST score
                  409
                  2.0e-42
E value
Match length
                  94
% identity
                  83
                  BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40)
NCBI Description
                  >gi_72060_pir__NBHUC8 decorin precursor - human >gi 181170
                   (M14219) proteoglycan core protein [Homo sapiens]
                  >gi 4503271 ref NP 001911.1 pDCN decorin
Seq. No.
                  228438
                  LIB3196-007-P1-M1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q125080
BLAST score
                  529
E value
                  2.0e-54
Match length
                  108
                  99
% identity
                  KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK
NCBI Description
                  14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal
                  - human >gi 386848 (J00124) keratin [Homo sapiens]
                  >gi 4504913 ref NP_000517.1_pKRT14_ keratin 14
                   (epidermolysis bullosa simplex, Dowling-Meara, Koebner)
                  228439
Seq. No.
                  LIB3196-007-P1-M1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3970680
BLAST score
                  222
                  4.0e-18
E value
Match length
                  68
                  59
% identity
NCBI Description (AL034388) 67A9.b [Drosophila melanogaster]
                  228440
Seq. No.
                  LIB3196-007-P1-M1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g730832
                  174
BLAST score
                  1.0e-12
E value
Match length
                  53
```

32677

(PROBABLE PROTEINASE INHIBITOR P322) >gi 99949 pir

probable proteinase inhibitor (Bowman-Birk) p322 - soybean >gi\_18748\_emb\_CAA78359\_ (Z13956) a protein similar to

NCBI Description 8.4 KD SULFUR-RICH PROTEIN PRECURSOR (SE60 PROTEIN)



potato tuber protein p322 homolgous to Bowman-Birk
Proteinase Inhibitor [Glycine max]

```
228441
Seq. No.
Seq. ID
                  LIB3196-007-P1-M1-B10
Method
                  BLASTX
                  q4263711
NCBI GI
BLAST score
                  277
                  2.0e-24
E value
                  63
Match length
                  76
% identity
                   (AC006223) putative CCR4-associated transcription factor
NCBI Description
                   [Arabidopsis thaliana]
                  228442
Seq. No.
                  LIB3196-007-P1-M1-B12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1653702
BLAST score
                  204
                   2.0e-16
E value
                   61
Match length
                   66
% identity
                   (D90915) dihydrolipoamide acetyltransferase component (E2)
NCBI Description
                  of pyruvate dehydrogenase complex [Synechocystis sp.]
                  228443
Seq. No.
                  LIB3196-007-P1-M1-B2
Seq. ID
                  BLASTX
Method
                   g2500378
NCBI GI
BLAST score
                   419
                   3.0e-41
E value
                   83
Match length
                   92
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L37
                   228444
Seq. No.
                   LIB3196-007-P1-M1-B3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4539292
BLAST score
                   244
                   9.0e-21
E value
Match length
                   47
                   91
% identity
                   (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   228445
                   LIB3196-007-P1-M1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g167367
BLAST score
                   489
                   2.0e-49
E value
Match length
                   128
% identity
                   76
                  (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
```

32678

228446

Seq. No.

% identity

NCBI Description

97



```
Seq. ID
                  LIB3196-007-P1-M1-C1
Method
                  BLASTX
                  q423072
NCBI GI
BLAST score
                  198
                  3.0e-15
E value
                  136
Match length
                  35
% identity
                  ribosomal protein L7 - human >gi 1335288 emb CAA41026_
NCBI Description
                  (X57958) ribosomal protein L7 [Homo sapiens]
                  228447
Seq. No.
Seq. ID
                  LIB3196-007-P1-M1-C11
                  BLASTX
Method
                  g87774
NCBI GI
                  628
BLAST score
                   9.0e-66
E value
                  128
Match length
% identity
                  hypothetical protein - human (clone 266) (fragment)
NCBI Description
                   >gi 34081 emb_CAA29248_ (X05803) gene product (clone 266)
                   (266 AA) [Homo sapiens]
                   228448
Seq. No.
Seq. ID
                   LIB3196-007-P1-M1-C12
                   BLASTX
Method
NCBI GI
                   q136479
                   502
BLAST score
                   5.0e-51
E value
                   99
Match length
                   99
% identity
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN (TCTP) (P23)
NCBI Description
                   >qi 88948 pir S06590 IgE-dependent histamine-releasing
                   factor - human >qi 37496 emb CAA34200 (X16064) tumor
                   protein (AA 1 - 172) [Homo sapiens]
                   >qi 4507669 ref NP 003286.1 pTPT1 tumor protein,
                   translationally-controlled
Seq. No.
                   228449
Seq. ID
                   LIB3196-007-P1-M1-C2
Method
                   BLASTX
                   q81546
NCBI GI
BLAST score
                   522
                   2.0e-53
E value
Match length
                   119
                   88
% identity
                   alpha-globulin type B precursor (tandem 1) - upland cotton
NCBI Description
                   (fragment)
                   228450
Seq. No.
                   LIB3196-007-P1-M1-C3
Seq. ID
                   BLASTX
Method
                   g163412
NCBI GI
                   550
BLAST score
                   1.0e-56
E value
                   105
Match length
```

(M63009) NADH dehydrogenase [Bos taurus]

```
228451
Seq. No.
                  LIB3196-007-P1-M1-C6
Seq. ID
                  BLASTX
Method
                  g1658197
NCBI GI
BLAST score
                  591
                  2.0e-61
E value
                  125
Match length
                  86
% identity
                  (U74630) calreticulin [Ricinus communis] >gi_1763297
NCBI Description
                  (U74631) calreticulin [Ricinus communis]
                  228452
Seq. No.
                  LIB3196-007-P1-M1-C8
Seq. ID
                  BLASTX
Method
                  g1362093
NCBI GI
BLAST score
                  452
                  4.0e-45
E value
                  108
Match length
% identity
                  hypothetical protein (clone TPP15) - tomato (fragment)
NCBI Description
                  >gi 924632 (U20595) unknown [Solanum lycopersicum]
Seq. No.
                  228453
                  LIB3196-007-P1-M1-C9
Seq. ID
                  BLASTX
Method
                   q3298540
NCBI GI
BLAST score
                   564
                   2.0e-58
E value
                   119
Match length
                   87
% identity
NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]
                   228454
Seq. No.
                   LIB3196-007-P1-M1-D2
Seq. ID
Method
                   BLASTX
                                                                              13
                   q3688598
NCBI GI
BLAST score
                   530
                   3.0e-54
E value
                   115
Match length
                   83
% identity
NCBI Description (AB009029) Cycloartenol Synthase [Panax ginseng]
                   228455
Seq. No.
                   LIB3196-007-P1-M1-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g133041
                   520
BLAST score
E value
                   4.0e-53
                   100
Match length
                   100
% identity
                  60S ACIDIC RIBOSOMAL PROTEIN PO (L10E)
NCBI Description
                   >gi 71137 pir__R5HUPO acidic ribosomal protein PO - human
                   >qi 190232 (M17885) acidic ribosomal phosphoprotein (P0)
                   [Homo sapiens] >gi_2935618_gb_AAC05176_ (AC004263) 60S
                   ACIDIC RIBOSOMAL PROTEIN; match to P05388 (PID:g133041)
                   [Homo sapiens] >gi_4506667_ref_NP_000993.1 pRPLP0
```



## ribosomal protein, large, PO

```
Seq. No.
                    228456
                   LIB3196-007-P1-M1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                    g133041
BLAST score
                    182
                    5.0e-14
E value
Match length
                    50
                    74
% identity
                    60S ACIDIC RIBOSOMAL PROTEIN PO (L10E)
NCBI Description
                    >gi_71137_pir__R5HUPO acidic ribosomal protein PO - human
>gi_190232 (M17885) acidic ribosomal phosphoprotein (PO)
                    [Homo sapiens] >gi 2935618 gb AAC05176_ (AC004263) 60S
                    ACIDIC RIBOSOMAL PROTEIN; match to P05388 (PID:g133041)
                    [Homo sapiens] >gi_4506667_ref_NP_000993.1_pRPLP0_ribosomal protein, large, P0
                    228457
Seq. No.
                    LIB3196-007-P1-M1-D9
Seq. ID
Method
                    BLASTX
NCBI GI
                    q1076316
BLAST score
                    162
E value
                    3.0e-11
                    74
Match length
% identity
                    45
                    drought-induced protein Di19 - Arabidopsis thaliana
NCBI Description
                    >qi 469110 emb CAA55321 (X78584) Di19 [Arabidopsis
                    thaliana]
                    228458
Seq. No.
                    LIB3196-007-P1-M1-E11
Seq. ID
                    BLASTX
Method
NCBI GI
                    g224877
                    502
BLAST score
                    5.0e-51
E value
                    99
Match length
                    96
% identity
NCBI Description deaminase a, adenosine [Homo sapiens]
                    228459
Seq. No.
Seq. ID
                    LIB3196-007-P1-M1-E2
                    BLASTX
Method
NCBI GI
                    g2352925
BLAST score
                    138
E value
                    4.0e-19
                    113
Match length
                    56
% identity
NCBI Description (AF012864) plastidic 3-deoxy-D-arabino-heptulosonate
                    7-phosphate synthase 2 [Petroselinum crispum]
                    228460
Seq. No.
                    LIB3196-007-P1-M1-E4
Seq. ID
                    BLASTX
Method
NCBI GI
                    q1723292
                    245
BLAST score
```

8.0e-21

E value



130 Match length 42 % identity HYPOTHETICAL 60.5 KD PROTEIN C13D6.04C IN CHROMOSOME I NCBI Description >gi 1204166 emb CAA93544 (Z69725) unknown [Schizosaccharomyces pombe] 228461 Seq. No. Seq. ID LIB3196-007-P1-M1-E9 Method BLASTX NCBI GI g4558591 BLAST score 430 1.0e-42 E value Match length 112 % identity 71 (ACO06555) putative beta-1,3-glucanase [Arabidopsis NCBI Description thaliana] 228462 Seq. No. Seq. ID LIB3196-007-P1-M1-F1 Method BLASTX NCBI GI g2736151 BLAST score 215 E value 3.0e-17 Match length 82 % identity 50 (AF021935) mytonic dystrophy kinase-related Cdc42-binding NCBI Description kinase [Rattus norvegicus] 228463 Seq. No. LIB3196-007-P1-M1-F10 Seq. ID BLASTX Method g115492 NCBI GI 475 BLAST score E value 8.0e-48 94 Match length 52 % identity NCBI Description CALMODULIN-RELATED PROTEIN >gi 169205 (M80831) calmodulin-related protein [Petunia hybrida] Seq. No. 228464 LIB3196-007-P1-M1-F3 Seq. ID BLASTXMethod g2129636 NCBI GI BLAST score 248 E value 3.0e-21 110 Match length 52 % identity NCBI Description lipase - Arabidopsis thaliana >gi\_1145627 (U38916) lipase [Arabidopsis thaliana] 228465 Seq. No. LIB3196-007-P1-M1-F4 Seq. ID BLASTX Method

Method BLASTX
NCBI GI g4415996
BLAST score 676
E value 2.0e-71
Match length 130



```
% identity
NCBI Description (AF059290) beta-tubulin 4 [Eleusine indica]
                  228466
Seq. No.
                  LIB3196-007-P1-M1-F5
Seq. ID
                  BLASTX
Method
                  q3212854
NCBI GI
                  164
BLAST score
E value
                  2.0e-11
                  128
Match length
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
                  228467
Seq. No.
                  LIB3196-007-P1-M1-F6
Seq. ID
                  BLASTX
Method
                  q1483218
NCBI GI
                   547
BLAST score
                   3.0e-56
E value
Match length
                  129
                   75
% identity
NCBI Description (X99793) induced upon wounding stress [Arabidopsis
                  thaliana]
                   228468
Seq. No.
                  LIB3196-007-P1-M1-G10
Seq. ID
                   BLASTX
Method
                   q1170097
NCBI GI
                   569
BLAST score
                   8.0e-59
E value
Match length
                   118
                   89
% identity
                  GLUTATHIONE S-TRANSFERASE MU 5 (GSTM5-5) (CLASS-MU)
NCBI Description
                   >gi 423000 pir A46048 glutathione transferase (EC
                   2.5.1.18) class mu, GSTM5 - human >gi_468260 (L02321)
                   glutathione S-transferase GSTM5-5 [Homo sapiens]
                   >qi 4504181 ref NP 000842.1 pGSTM5_ glutathione
                   S-transferase M5
                   228469
Seq. No.
                   LIB3196-007-P1-M1-G11
Seq. ID
                   BLASTX
Method
                   g125077
NCBI GI
                   158
BLAST score
                   1.0e-10
E value
Match length
                   31
% identity
                   100
                   KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK
NCBI Description
                   13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal,
                   long form - human >gi_34033_emb_CAA32786_ (X14640) keratin
                   13 [Homo sapiens]
                   228470
Seq. No.
Seq. ID
                   LIB3196-007-P1-M1-G2
```

 ${\tt BLASTX}$ 

615

g3023858

Method

NCBI GI BLAST score



E value 3.0e-64 Match length 128 % identity 55

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE

PROTEIN >gi 1256608 (U44850) G protein beta subunit

[Glycine max]

Seq. No. 228471

Seq. ID LIB3196-007-P1-M1-G3

Method BLASTX
NCBI GI g232031
BLAST score 220
E value 6.0e-18
Match length 67
% identity 60

NCBI Description ELONGATION FACTOR 1 BETA' >gi 322851 pir S29224

translation elongation factor eEF-1 beta' chain - rice >gi 218161 dbj BAA02253 (D12821) elongation factor 1 beta'

[Oryza sativa]

Seq. No. 228472

Seq. ID LIB3196-007-P1-M1-G6

Method BLASTX
NCBI GI g461776
BLAST score 304
E value 1.0e-27
Match length 53
% identity 96

NCBI Description CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL

PROLINE-RICH SQUAMOUS CELL MARKER) >gi\_251369\_bbs\_108679 (S40060) spr1=small proline rich squamous cell marker [Rhesus monkeys, tracheobronchial epithelium, Peptide, 89 aa] [Rhesus monkeys] >gi\_342297 (M83999) small proline-rich

protein [Macaca mulatta]

Seq. No. 228473

Seq. ID LIB3196-007-P1-M1-H1

Method BLASTX
NCBI GI g3861488
BLAST score 324
E value 4.0e-30
Match length 77
% identity 82

NCBI Description (AF060902) vesicle soluble NSF attachment protein receptor

VTI2 [Homo sapiens]

Seq. No. 228474

Seq. ID LIB3196-007-P1-M1-H11

Method BLASTX
NCBI GI g4406656
BLAST score 434
E value 5.0e-43
Match length 98
% identity 86

NCBI Description (AF131820) Unknown [Homo sapiens]

Seq. No. 228475

Seq. No.

228480



```
LIB3196-007-P1-M1-H3
Seq. ID
                  BLASTX
Method
                  q547008
NCBI GI
BLAST score
                  279
                  7.0e-25
E value
                  122
Match length
                   52
% identity
                   (S70314) alpha-adducin=calmodulin-binding protein
NCBI Description
                   {alternatively spliced, clone IT10C1} [human, frontal
                  cortex, Peptide Partial, 207 aa] [Homo sapiens]
                   228476
Seq. No.
                  LIB3196-007-P1-M1-H5
Seq. ID
                  BLASTX
Method
                   a2244898
NCBI GI
                   247
BLAST score
                   4.0e-21
E value
                   69
Match length
                   68
% identity
                  (Z97338) strong similarity to protein phosphatase 2A
NCBI Description
                   regulatory chain, 74K [Arabidopsis thaliana]
                   228477
Seq. No.
                   LIB3196-007-P1-M1-H6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2160694
                   205
BLAST score
                   3.0e-16
E value
                   72
Match length
                   58
% identity
                   (U73528) B' regulatory subunit of PP2A [Arabidopsis
NCBI Description
                   thaliana]
                   228478
Seq. No.
                   LIB3196-007-P1-M1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1717824
BLAST score
                   372
                   1.0e-35
E value
Match length
                   84
                   50
% identity
                   TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE
NCBI Description
                   TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN)
                   >gi 950004 (U25147) citrate transporter protein [Homo
                   sapiens]
Seq. No.
                   .228479
                   LIB3196-008-P1-M1-A11
Seq. ID
                   {\tt BLASTX}
Method
                   q3294467
NCBI GI
                   226
BLAST score
                   1.0e-22
E value
                   63
Match length
 % identity
                  (U89341) phosphoglucomutase 1 [Zea mays]
NCBI Description
```



```
LIB3196-008-P1-M1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1843399
BLAST score
                  258
                  2.0e-22
E value
                  61
Match length
% identity
                  (AB000467) unnamed protein product [Homo sapiens]
NCBI Description
                  228481
Seq. No.
                  LIB3196-008-P1-M1-A3
Seq. ID
                  BLASTX
Method
                  q3901014
NCBI GI
BLAST score
                  235
E value
                  9.0e-20
Match length
                  55
                  76
% identity
                  (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                  sylvatica]
                  228482
Seq. No.
                  LIB3196-008-P1-M1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g119530
BLAST score
                  651
                  2.0e-68
E value
Match length
                  128
                   98
% identity
                  PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR
NCBI Description
                   (ERP72) >gi_87320_pir__A23723 protein disulfide-isomerase
                   (EC 5.3.4.1) ERp72 precursor - human >gi_181508 (J05016)
                  protein disulfide isomerase-related protein [Homo sapiens]
                   228483
Seq. No.
                   LIB3196-008-P1-M1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g87653
BLAST score
                   273
                   3.0e-24
E value
Match length
                   78
% identity
                   76
NCBI Description heterogeneous ribonuclear particle protein C - human
                   >gi 306875 (M16342) C protein [Homo sapiens]
Seq. No.
                   228484
Seq. ID
                   LIB3196-008-P1-M1-B11
Method
                   BLASTX
                   q125077
NCBI GI
                   442
BLAST score
E value
                   2.0e-44
                   92
Match length
                   98
% identity
                  KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK
NCBI Description
                   13) >gi 71526_pir__KRHU3 keratin 13, type I, cytoskeletal,
```

13 [Homo sapiens]

long form - human >gi\_34033\_emb\_CAA32786\_ (X14640) keratin

% identity



```
228485
Seq. No.
                  LIB3196-008-P1-M1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1346347
BLAST score
                  427
                  2.0e-42
E value
Match length
                  107
                  85
% identity
                  KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D)
NCBI Description
                  (K6D KERATIN) >gi_2119225_pir___161769 keratin type II -
                  human (fragment) >gi 914833 (L42610) keratin type II [Homo
                  sapiens]
                  228486
Seq. No.
Seq. ID
                  LIB3196-008-P1-M1-B2
                  BLASTX
Method
                  q1885356
NCBI GI
                  205
BLAST score
                  9.0e-17
E value
Match length
                  45
                  82
% identity
NCBI Description (U59323) type 1 RNA helicase pNORF1 [Homo sapiens]
                  228487
Seq. No.
                  LIB3196-008-P1-M1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q346219
BLAST score
                  245
                   7.0e-21
E value
Match length
                  124
% identity
                   51
NCBI Description keratin K4a - human (fragment)
                   228488
Seq. No.
Seq. ID
                  LIB3196-008-P1-M1-B4
Method
                  BLASTX
NCBI GI
                   g137578
                   596
BLAST score
                   5.0e-62
E value
                  117
Match length
% identity
                   97
NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
                   >gi 81545 pir S06398 alpha-globulin type A precursor -
                   upland cotton >gi 167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi 207906 (M18027) alpha globulin A
                   [Artificial gene] >gi 226119 prf 1410330A vicilin gene A
                   [Saguinus oedipus]
                   228489
Seq. No.
                   LIB3196-008-P1-M1-B9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g284779
                   184
BLAST score
                   3.0e-26
E value
Match length
                   76
                   73
```

NCBI Description Ras guanine nucleotide exchange factor son-of-sevenless





```
(sos) 1 - mouse >gi_54135_emb_CAA77662_ (Z11574) mouse Son of sevenless 1 [Mus musculus]
```

```
228490
Seq. No.
                  LIB3196-008-P1-M1-C1
Seq. ID
                  BLASTX
Method
                  g3868758
NCBI GI
                  235
BLAST score
E value
                  5.0e-20
                  59
Match length
% identity
                  75
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
                  228491
Seq. No.
                  LIB3196-008-P1-M1-C11
Seq. ID
                  BLASTX
Method
                  g3334405
NCBI GI
                  432
BLAST score
                  5.0e-43
E value
Match length
                  91
                  99
% identity
                  VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
NCBI Description
                  >gi_2267583 (AF009338) vacuolar H+-ATPase subunit E
                  [Gossypium hirsutum]
                  228492
Seq. No.
                  LIB3196-008-P1-M1-C12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g484102
BLAST score
                  227
E value
                  8.0e-19
                  97
Match length
                   52
% identity
NCBI Description (U02082) guanine nucleotide regulatory protein [Homo
                   sapiens] >gi_3041860 (AC004534) guanine nucleotide
                   regulatory protein [Homo sapiens]
                   228493
Seq. No.
                  LIB3196-008-P1-M1-C2
Seq. ID
                  BLASTX
Method
                   g3334115
NCBI GI
                   335
BLAST score
                   2.0e-31
E value
                   84
Match length
                   80
 % identity
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                   hirsutum]
```

 Seq. No.
 228494

 Seq. ID
 LIB3196-008-P1-M1-C6

 Method
 BLASTX

 NCBI GI
 g2315449

 BLAST score
 190

E value 2.0e-14 Match length 84



```
% identity
                  (AF016448) similar to Saccharomyces cerevisiae nuclear
NCBI Description
                  protein SNF7 (SP:P39929)in one region and the chromosome
                  segregation protein SMC2 (SP:P38989) in another
                  [Caenorhabditis elegans]
                  228495
Seq. No.
                  LIB3196-008-P1-M1-D10
Seq. ID
                  BLASTX
Method
                  g1703121
NCBI GI
                  646
BLAST score
E value
                  7.0e-68
                  127
Match length
                  99
% identity
NCBI Description ACTIN, CYTOPLASMIC TYPE 5 >gi 63007_emb_CAA26486 (X02648)
                  put. type 5 nonmuscle actin [Gallus gallus]
                  228496
Seq. No.
                  LIB3196-008-P1-M1-D11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3935151
                  307
BLAST score
E value
                  2.0e-28
                  89
Match length
% identity
                  61
NCBI Description (AC005106) T25N20.15 [Arabidopsis thaliana]
                  228497
Seq. No.
                  LIB3196-008-P1-M1-D9
Seq. ID
                  BLASTX
Method
NCBI GI
                   q462013
                   565
BLAST score
                   2.0e-58
E value
                   125
Match length
% identity
                   90
                  ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
NCBI Description
                   >gi_542022_pir__S39558 HSP90 homolog - Madagascar
                  periwinkle >gi_348696 (L14594) heat shock protein 90
                   [Catharanthus roseus]
Seq. No.
                   228498
                   LIB3196-008-P1-M1-E12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4510347
                   155
BLAST score
E value
                   2.0e-10
Match length
                   60
% identity
NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]
                   228499
Seq. No.
                   LIB3196-008-P1-M1-E2
Seq. ID
                   BLASTX
Method
                   g2995405
NCBI GI
                   357
BLAST score
```

5.0e-34

118

E value Match length



```
% identity
                  (Y12432) polyprotein [Ananas comosus]
NCBI Description
                  228500
Seq. No.
                  LIB3196-008-P1-M1-E4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g119165
                  411
BLAST score
                  3.0e-41
E value
                  127
Match length
                  72
% identity
                  ELONGATION FACTOR 1-GAMMA (EF-1-GAMMA)
NCBI Description
                  >gi_105918_pir__S22655 translation elongation factor eEF-1
                  gamma chain - human >gi_31102_emb_CAA45089_ (X63526)
                  homologue to elongation factor 1-gamma from A.salina [Homo
                  sapiens] >gi_31104_emb_CAA77630_ (Z11531) elongation
                  factor-1-gamma [Homo sapiens]
                  >gi_4503481_ref_NP_001395.1_pEEF1G_ eukaryotic translation
                   elongation factor 1 gamma
                  228501
Seq. No.
                  LIB3196-008-P1-M1-E5
Seq. ID
                  BLASTX
Method
                  g2252630
NCBI GI
                   142
BLAST score
                   3.0e-09
E value
                   45
Match length
                   64
% identity
NCBI Description (U95973) hypothetical protein [Arabidopsis thaliana]
                   228502
Seq. No.
                   LIB3196-008-P1-M1-E6
Seq. ID
                   BLASTX
Method
                   g1663567
NCBI GI
                   364
BLAST score
E value
                   8.0e-35
                   72
Match length
                   92
% identity
NCBI Description (U60800) semaphorin [Homo sapiens]
                   228503
Seq. No.
                   LIB3196-008-P1-M1-E8
Seq. ID
                   BLASTX
Method
                   q167367
NCBI GI
                   425
BLAST score
                   3.0e-42
E value
Match length
                   101
                   82
 % identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                   228504
 Seq. No.
                   LIB3196-008-P1-M1-F1
 Seq. ID
                   \mathtt{BLASTX}
Method
                   g113950
 NCBI GI
 BLAST score
                   355
                   4.0e-34
 E value
```

70

Match length



```
% identity
                  ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN)
NCBI Description
                  (CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL ANTICOAGULANT
                  PROTEIN IV) (PAP-IV) >gi_71761_pir__LUHU36 annexin II -
                  human >gi_219910_dbj_BAA00013_ (D00017) lipocortin II [Homo
                  sapiens]
                  228505
Seq. No.
                  LIB3196-008-P1-M1-F11
Seq. ID
Method
                  BLASTX
                  g4325372
NCBI GI
BLAST score
                  227
                  7.0e-19
E value
                  99
Match length
                  42
% identity
                  (AF128396) contains similarity to protein disulfide
NCBI Description
                  isomerases [Arabidopsis thaliana]
                  228506
Seq. No.
                  LIB3196-008-P1-M1-F2
Seq. ID
                  BLASTX
Method
                  g423485
NCBI GI
                  151
BLAST score
                  4.0e-10
E value
Match length
                  55
                  64
% identity
                  interferon response element-binding factor IREBF-2 - mouse
NCBI Description
                   (fragment) >gi_293675 (L13610) IFN-response element binding
                  factor 2 [Mus musculus]
                   228507
Seq. No.
                   LIB3196-008-P1-M1-F7
Seq. ID
                   BLASTX
Method
                   g1362009
NCBI GI
                   429
BLAST score
E value
                   1.0e-42
Match length
                   106
% identity
                   50
NCBI Description ubiquitin-like protein 7 - Arabidopsis thaliana
                   228508
Seq. No.
                   LIB3196-008-P1-M1-F8
Seq. ID
                   BLASTX
Method
                   g137578
NCBI GI
                   456
BLAST score
                   7.0e-46
E value
                   90
Match length
                   98
 % identity
                   VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                   >gi 81545_pir_ S06398 alpha-globulin type A precursor -
                   upland cotton >gi 167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                   [Artificial gene] >gi_226119_prf__1410330A vicilin gene A
                   [Saguinus oedipus]
```

Seq. No. 228509

Seq. ID LIB3196-008-P1-M1-G1



```
BLASTX
Method
                  g1350984
NCBI GI
BLAST score
                  314
                  5.0e-29
E value
                  71
Match length
                  89
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S3A >gi 469248 (L31645) ribosomal
                  protein S3a [Helianthus annuus]
Seq. No.
                  228510
                  LIB3196-008-P1-M1-G10
Seq. ID
                  BLASTX
Method
                  q3776005
NCBI GI
BLAST score
                  165
                  1.0e-11
E value
                  40
Match length
                  82
% identity
NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]
                  228511
Seq. No.
                  LIB3196-008-P1-M1-G11
Seq. ID
Method
                  BLASTX
                  q2224549
NCBI GI
                  557
BLAST score
E value
                  1.0e-57
Match length
                  104
                  99
% identity
NCBI Description (AB002302) KIAA0304 [Homo sapiens]
                  228512
Seq. No.
                  LIB3196-008-P1-M1-G12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1709233
BLAST score
                  314
                  5.0e-29
E value
                  94
Match length
                  67
% identity
NCBI Description NADH-CYTOCHROME B5 REDUCTASE >gi_162941 (M83104) cytochrome
                  b-5 reductase [Bos taurus]
                  228513
Seq. No.
Seq. ID
                  LIB3196-008-P1-M1-G5
                  BLASTX
Method
NCBI GI
                  g129881
                  576
BLAST score
                  1.0e-59
E value
                  126
Match length
% identity
NCBI Description PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
                  ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                   (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                   (PPI-PFK) >gi 482294_pir A36094
                  pyrophosphate--fructose-6-phosphate 1-phosphotransferase
                   (EC 2.7.1.90) alpha chain - potato (cv. Kennebec)
```

>gi\_169538 (M55190) pyrophosphate-fructose 6-phosphate
1-phosphotransferase alpha-subunit [Solanum tuberosum]



```
228514
Seq. No.
                  LIB3196-008-P1-M1-H12
Seq. ID
                  BLASTX
Method
                  g137578
NCBI GI
BLAST score
                  518
                  5.0e-53
E value
                  99
Match length
% identity
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                  >gi_81545_pir__S06398 alpha-globulin type A precursor -
                  upland cotton >gi_167371 (M19378) vicilin precursor
                  [Gossypium hirsutum] >gi 207906 (M18027) alpha globulin A
                  [Artificial gene] >gi 226119 prf 1410330A vicilin gene A
                  [Saguinus oedipus]
                  228515
Seq. No.
                  LIB3196-008-P1-M1-H2
Seq. ID
Method
                  BLASTX
                  q1731146
NCBI GI
BLAST score
                  191
                  2.0e-14
E value
                  49
Match length
                  71
% identity
                  HYPOTHETICAL 42.1 KD PROTEIN ZK1307.9 IN CHROMOSOME III
NCBI Description
                  >gi_3881615_emb_CAA87435_ (Z47358) similar to YJU2 protein
                  [Caenorhabditis elegans]
Seq. No.
                  228516
                  LIB3196-008-P1-M1-H3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2072966
BLAST score
                  314
                  1.0e-47
E value
Match length
                  133
% identity
                  72
NCBI Description (U93570) p40 [Homo sapiens]
                  228517
Seq. No.
                  LIB3196-008-P1-M1-H6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g119165
BLAST score
                  326
                  3.0e-30
E value
                  59
Match length
                   98
% identity
NCBI Description ELONGATION FACTOR 1-GAMMA (EF-1-GAMMA)
                  >gi 105918 pir S22655 translation elongation factor eEF-1
                  gamma chain - human >gi_31102_emb_CAA45089_ (X63526)
                  homologue to elongation factor 1-gamma from A.salina [Homo
                   sapiens] >gi 31104 emb CAA77630_ (Z11531) elongation
                   factor-1-gamma [Homo sapiens]
                   >gi 4503481 ref NP 001395.1 pEEF1G eukaryotic translation
                  elongation factor 1 gamma
```

228518

BLASTX

LIB3196-008-P1-M1-H7

Seq. No. Seq. ID

Method

Method

NCBI GI

BLASTX

g2135748



```
q585241
NCBI GI
BLAST score
                  151
                  7.0e-10
E value
Match length
                  85
                  47
% identity
                  HISTONE H1 >gi 629668 pir S45662 histone H1 - tomato
NCBI Description
                  >gi 424100 (U0\overline{3}391) histone H1 [Lycopersicon esculentum]
Seq. No.
                  228519
                  LIB3196-008-P1-M1-H8
Seq. ID
Method
                  BLASTX
                  q2997745
NCBI GI
BLAST score
                  301
                  1.0e-27
E value
Match length
                  65
% identity
                  92
                  (AF054840) tetraspan TM4SF; Tspan-3 [Homo sapiens]
NCBI Description
                  228520
Seq. No.
Seq. ID
                  LIB3196-009-P1-M1-A11
Method
                  BLASTX
                   q137578
NCBI GI
BLAST score
                   562
E value
                   4.0e-58
                   113
Match length
% identity
                   97
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                   >gi_81545_pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi 167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi 207906 (M18027) alpha globulin A
                   [Artificial gene] >gi_226119_prf_1410330A vicilin gene A
                   [Saguinus oedipus]
                   228521
Seq. No.
Seq. ID
                   LIB3196-009-P1-M1-A12
Method
                   BLASTX
NCBI GI
                   g3123349
BLAST score
                   206
E value
                   2.0e-16
Match length
                   85
% identity
                   48
NCBI Description (AJ005788) hypothetical protein [Cicer arietinum]
                   228522
Seq. No.
                   LIB3196-009-P1-M1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g100488
BLAST score
                   266
                   2.0e-23
E value
                   88
Match length
                   57
% identity
NCBI Description TNP2 protein - garden snapdragon
Seq. No.
                   228523
Seq. ID
                   LIB3196-009-P1-M1-A5
```

Seq. No.

Seq. ID Method

228528

BLASTX

LIB3196-009-P1-M1-C1



```
300
BLAST score
                     1.0e-27
E value
                     84
Match length
                     35
% identity
                    MLN 62 protein - human >gi_2135749_pir__S60681 MLN 62 protein - human >gi_951277_emb_CAA56491_ (X80200) cystein
NCBI Description
                     rich domain associated to RING and TRAF protein [Homo
                     sapiens]
                     228524
Seq. No.
                     LIB3196-009-P1-M1-B1
Seq. ID
                     BLASTX
Method
                     g1037127
NCBI GI
                     666
BLAST score
                     3.0e-70
E value
                     133
Match length
                     95
% identity
                     Mig-6=mitogen-inducible gene mig-6 product [human, WI-38
NCBI Description
                     cells, Peptide, 462 aa]
                     228525
Seq. No.
                     LIB3196-009-P1-M1-B4
Seq. ID
                     BLASTX
Method
                     g804996
NCBI GI
                     252
BLAST score
                     1.0e-21
E value
                     64
Match length
                     77
% identity
                     (Z49216) mitoxantrone-resistance associated gene [Homo
NCBI Description
                     sapiens]
                     228526
Seq. No.
                     LIB3196-009-P1-M1-B7
Seq. ID
                     BLASTX
Method
                     g3043714
NCBI GI
                     509
BLAST score
                     6.0e-52
E value
Match length
                     117
                     85
% identity
                     (AB011167) KIAA0595 protein [Homo sapiens]
NCBI Description
                     228527
Seq. No.
                     LIB3196-009-P1-M1-B8
Seq. ID
                     BLASTX
Method
                     q547712
NCBI GI
                     550
BLAST score
E value
                      1.0e-56
Match length
                     110
% identity
                      97
                     EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)
NCBI Description
                     >gi_542153_pir__S38358 translation initiation factor eIF-4A - rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic initiation factor 4A [Oryza sativa]
```



```
NCBI GI
                     q181969
BLAST score
                     440
E value
                     8.0e-44
                     113
Match length
                     79
% identity
NCBI Description (M19997) elongation factor 2 [Homo sapiens]
                     228529
Seq. No.
                     LIB3196-009-P1-M1-C10
Seq. ID
Method
                     BLASTX
                     g2920535
NCBI GI
BLAST score
                     146
E value
                     2.0e-09
                     76
Match length
                     49
% identity
NCBI Description (AF018081) type XVIII collagen [Homo sapiens]
                     228530
Seq. No.
                     LIB3196-009-P1-M1-C11
Seq. ID
Method
                     BLASTX
NCBI GI
                     g113287
BLAST score
                     701
E value
                     2.0e-74
Match length
                     130
% identity
                     100
NCBI Description ACTIN, ALPHA SKELETAL MUSCLE (ALPHA-ACTIN 1)
                     >gi_71610_pir_ ATHU actin, skeletal muscle - human
>gi_71612_pir_ ATRT actin, skeletal muscle - rat
>gi_71613_pir_ ATCH actin alpha, skeletal muscle - chicken
>gi_90264_pir_ A24904_actin, skeletal muscle - mouse
                     >gi_55577_emb_CAA24529_ (V01218) actin [Rattus norvegicus] >gi_63029_emb_CAA24753_ (V01507) a-actin [Gallus gallus]
                     >gi 178029 (J00068) alpha-actin [Homo sapiens] >gi 309088
                     (M12866) actin [Mus musculus] >gi 337746 (M20543)
                     alpha-skeletal actin precursor [Homo sapiens] >gi 387081
                     (M12347) alpha-actin [Mus musculus] >gi 790202 (U16368)
                     skeletal alpha actin [Sus scrofa] >gi 223503 prf 0809315A
                     actin [Rattus norvegicus]
                     >gi 4501881 ref NP 001091.1 pACTA1 actin, alpha 1,
                     skeletal muscle
Seq. No.
                     228531
                     LIB3196-009-P1-M1-C12
Seq. ID
Method
                     BLASTX
NCBI GI
                     g4539005
BLAST score
                     194
E value
                     6.0e-15
Match length
                     122
% identity
                     36
NCBI Description (AL049481) putative oxidoreductase [Arabidopsis thaliana]
Seq. No.
                     228532
Seq. ID
                     LIB3196-009-P1-M1-C2
```

Method BLASTX
NCBI GI g1945609
BLAST score 599
E value 2.0e-62

BLAST score

E value

159 7.0e-11



```
Match length
                  100
% identity
NCBI Description (AB003102) 26S proteasome subunit p44.5 [Homo sapiens]
                  228533
Seq. No.
                  LIB3196-009-P1-M1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3845568
BLAST score
                  199
                  2.0e-15
E value
Match length
                  77
                  52
% identity
NCBI Description (AB012042) keratin 6 beta [Mus musculus]
Seq. No.
                  228534
                  LIB3196-009-P1-M1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1170097
                  257
BLAST score
E value
                  3.0e-22
                  59
Match length
% identity
                  GLUTATHIONE S-TRANSFERASE MU 5 (GSTM5-5) (CLASS-MU)
NCBI Description
                  >qi 423000 pir A46048 glutathione transferase (EC
                  2.5.1.18) class mu, GSTM5 - human >gi_468260 (L02321) -
                  glutathione S-transferase GSTM5-5 [Homo sapiens]
                  >gi 4504181 ref NP 000842.1_pGSTM5_ glutathione
                  S-transferase M5
                   228535
Seq. No.
                  LIB3196-009-P1-M1-C7
Seq. ID
                  BLASTX
Method
                  g3738257
NCBI GI
                   458
BLAST score
                   7.0e-46
E value
                   96
Match length
                   94
% identity
                  (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
NCBI Description
                   nigra]
                   228536
Seq. No.
                   LIB3196-009-P1-M1-C9
Seq. ID
                   BLASTX
Method
                   g2119228
NCBI GI
BLAST score
                   189
                   3.0e-14
E value
                   111
Match length
                   46
% identity
NCBI Description keratin K4a - human (fragment) >gi 313159 emb CAA47914
                   (X67683) keratin K4a [Homo sapiens]
                   228537
 Seq. No.
                   LIB3196-009-P1-M1-D1
 Seq. ID
                   BLASTX
Method
NCBI GI
                   q730832
```



Match length % identity NCBI Description

8.4 KD SULFUR-RICH PROTEIN PRECURSOR (SE60 PROTEIN)

(PROBABLE PROTEINASE INHIBITOR P322) >gi 99949 pir S24965 probable proteinase inhibitor (Bowman-Birk) p322 - soybean >qi 18748 emb CAA78359 (Z13956) a protein similar to

potato tuber protein p322 homolgous to Bowman-Birk

Proteinase Inhibitor [Glycine max]

Seq. No.

LIB3196-009-P1-M1-D10 Seq. ID

Method BLASTX NCBI GI g3776559 BLAST score 251 1.0e-21 E value Match length 56

% identity

(AC005388) Strong similarity to gene F14J9.26 gi\_3482933 NCBI Description

cdc2 protein kinase homolog from A. thaliana BAC

gb AC003970. ESTs gb Z35332 and gb\_F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No.

228539

228538

LIB3196-009-P1-M1-D2 Seq. ID

79

Method BLASTX NCBI GI q2072425 281 BLAST score 4.0e-25 E value 54 Match length 98 % identity

(U83115) non-lens beta gamma-crystallin like protein [Homo NCBI Description

sapiens]

228540 Seq. No.

LIB3196-009-P1-M1-D3 Seq. ID

Method BLASTX NCBI GI g2500354 BLAST score 499 E value 8.0e-51 Match length 101 95 % identity

60S RIBOSOMAL PROTEIN L10 (EQM) >gi\_1902894\_dbj\_BAA19462\_ NCBI Description

(AB001891) QM family protein [Solanum melongena]

228541 Seq. No.

Seq. ID LIB3196-009-P1-M1-D4

Method BLASTX NCBI GI q1916613 192 BLAST score 1.0e-14 E value 94 Match length 50 % identity

NCBI Description (U62029) acetyl-CoA carboxylase [Arabidopsis thaliana]

228542 Seq. No.

LIB3196-009-P1-M1-D5 Seq. ID

BLASTX Method



```
g1082337
NCBI GI
                  654
BLAST score
                  8.0e-69
E value
Match length
                  131
% identity
                  DNA helicase Q1 - human >gi_531243_dbj_BAA07200_ (D37984)
NCBI Description
                  DNA helicase Q1 [Homo sapiens]
                  228543
Seq. No.
                  LIB3196-009-P1-M1-D7
Seq. ID
Method
                  BLASTX
                  q3641280
NCBI GI
                  170
BLAST score
                   4.0e-12
E value
Match length
                  33
                   100
% identity
                   (AF074382) IkB kinase gamma subunit [Homo sapiens]
NCBI Description
                   >qi 4504631 ref NP 003630.1_pIKBKG_ inhibitor of kappa
                   light polypeptide gene enhancer in B-cells, kinase gamma
                   228544
Seq. No.
                  LIB3196-009-P1-M1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2501439
                   464
BLAST score
E value
                   1.0e-46
                   99
Match length
                   87
% identity
                   UBIQUITIN FUSION DEGRADATION PROTEIN 1 HOMOLOG (UB FUSION
NCBI Description
                   PROTEIN 1) >gi_1654348 (U64445) ubiquitin
                   fusion-degradation 1 like protein; UFD1p [Mus musculus]
                   228545
Seq. No.
                   LIB3196-009-P1-M1-D9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2137308
                   530
BLAST score
                   3.0e-54
E value
                   102
Match length
                   40
% identity
NCBI Description G protein beta subuit like - mouse >gi_475012_dbj_BAA06185_
                   (D29802) G protein beta subuit like [Mus musculus]
                   228546
Seq. No.
                   LIB3196-009-P1-M1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g120669
                   441
BLAST score
                   7.0e-44
E value
                   88
Match length
                   92
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi 66014 pir DEJMG glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi 19566 emb CAA42905 (X60347) glyceraldehyde
```

3-phosphate dehydrogenase [Magnolia liliiflora]



```
228547
Seq. No.
                  LIB3196-009-P1-M1-E4
Seq. ID
                  BLASTX
Method
                  g2196542
NCBI GI
                  179
BLAST score
                  3.0e-13
E value
                  45
Match length
                   76
% identity
NCBI Description (AF001894) glycine-rich protein [Oryza sativa]
                   228548
Seq. No.
                  LIB3196-009-P1-M1-F1
Seq. ID
                   BLASTX
Method
                   q3319958
NCBI GI
                   575
BLAST score
                   2.0e-59
E value
                   115
Match length
                   11
% identity
NCBI Description (AJ228139) VAKTI precursor [Homo sapiens]
                   228549
Seq. No.
                   LIB3196-009-P1-M1-F10
Seq. ID
                   BLASTX
Method
                   g1407625
NCBI GI
                   174
BLAST score
                   1.0e-12
E value
                   32
Match length
                   56
% identity
NCBI Description (U40317) PTPsigma [Homo sapiens]
                   228550
Seq. No.
                   LIB3196-009-P1-M1-F11
Seq. ID
                   BLASTX
Method
                   q167367
NCBI GI
                   374
BLAST score
                   4.0e-36
E value
Match length
                   102
 % identity
                   72
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
 Seq. No.
                   228551
                   LIB3196-009-P1-M1-F2
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g2642435
                   447
 BLAST score
 E value
                   1.0e-44
 Match length
                   104
                   79
 % identity
 NCBI Description (AC002391) MYB-related protein [Arabidopsis thaliana]
                   228552
 Seq. No.
                   LIB3196-009-P1-M1-F9
 Seq. ID
                   {\tt BLASTX}
 Method
                   g3915742
 NCBI GI
                    443
 BLAST score
```

3.0e-44

96

E value

Match length



```
% identity
                  LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi 167319
NCBI Description
                   (M69188) legumin A [Gossypium hirsutum]
                  >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele
                   [Gossypium hirsutum]
                  228553
Seq. No.
                  LIB3196-009-P1-M1-G1
Seq. ID
                  BLASTX
Method
                   g220141
NCBI GI
                   471
BLAST score
                   2.0e-47
E value
                   88
Match length
                   99
% identity
NCBI Description (D01038) VLA-3 alpha subunit [Homo sapiens]
                   228554
Seq. No.
                   LIB3196-009-P1-M1-G10
Seq. ID
                   BLASTX
Method
                   g4098244
NCBI GI
                   314
BLAST score
                   5.0e-29
E value
                   94
Match length
                   66
% identity
NCBI Description (U76409) homeobox 1 protein [Lycopersicon esculentum]
                   228555
Seq. No.
                   LIB3196-009-P1-M1-G11
 Seq. ID
                   BLASTX
Method
                   g2135121
NCBI GI
                   387
BLAST score
                   6.0e-38
E value
                   79
Match length
                   95
 % identity
                   flightless-I homolog - human (fragment) >gi_440177 (U01184)
 NCBI Description
                   flightless-I homolog [Homo sapiens]
                   228556
 Seq. No.
                   LIB3196-009-P1-M1-G3
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g2459420
 BLAST score
                   464
                   1.0e-46
 E value
                   112
 Match length
                   82
 % identity
                   (AC002332) putative ribosomal protein L17 [Arabidopsis
 NCBI Description
                   thaliana]
                    228557
 Seq. No.
                   LIB3196-009-P1-M1-G5
 Seq. ID
                   BLASTX
 Method
                    g4455246
 NCBI GI
                    202
 BLAST score
                    3.0e-16
 E value
                   55
 Match length
                    69
 % identity
 NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
```



```
228558
Seq. No.
                  LIB3196-009-P1-M1-G8
Seq. ID
                  BLASTX
Method
                  q3980397
NCBI GI
                  427
BLAST score
                  3.0e-42
E value
                  117
Match length
                  68
% identity
                  (AC004561) putative protein phosphatase 2C [Arabidopsis
NCBI Description
                  thaliana]
                  228559
Seq. No.
                  LIB3196-009-P1-M1-G9
Seq. ID
                  BLASTX
Method
                  g137578
NCBI GI
                  541
BLAST score
                  1.0e-55
E value
                  103
Match length
                  100
% identity
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                  >gi_81545_pir__S06398 alpha-globulin type A precursor -
                  upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                   [Artificial gene] >gi 22\overline{6}119_prf __1410330A vicilin gene A
                   [Saguinus oedipus]
                   228560
Seq. No.
                   LIB3196-009-P1-M1-H10
Seq. ID
                   BLASTX
Method
                   q1890152
NCBI GI
                   259
BLAST score
                   1.0e-22
E value
                   69
Match length
                   68
% identity
NCBI Description (X92510) allene oxide synthase [Arabidopsis thaliana]
                   228561
Seq. No.
                   LIB3196-009-P1-M1-H12
Seq. ID
                   BLASTX
Method
                   g683553
NCBI GI
BLAST score
                   265
                   3.0e-23
E value
                   87
Match length
 % identity
NCBI Description (Z48450) oleosin-like protein [Citrus sinensis]
                   >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]
                   228562
 Seq. No.
                   LIB3196-009-P1-M1-H2
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g3122072
                   585
 BLAST score
                    9.0e-61
 E value
                   112
 Match length
                    99
 % identity
 NCBI Description ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION
```



FACTOR TU) (EF-TU) >gi\_2119922\_pir\_\_\_I50226 elongation factor 1 alpha - chicken >gi\_488468 (L00677) elongation factor 1 alpha [Gallus gallus]

228563 Seq. No. LIB3196-009-P1-M1-H6 Seq. ID BLASTX Method NCBI GI q82228 BLAST score 295 1.0e-26 E value 72 Match length % identity hypothetical protein 77 - common tobacco chloroplast NCBI Description >gi 225199 prf 1211235AD ORF 77 [Nicotiana tabacum] 228564 Seq. No. LIB3196-009-P1-M1-H9 Seq. ID BLASTX Method g226120 NCBI GI 258 BLAST score 9.0e-23 E value 74 Match length 54 % identity NCBI Description vicilin gene B [Saguinus oedipus] 228565 Seq. No. LIB3196-010-P1-M1-A3

 Seq. No.
 228565

 Seq. ID
 LIB3196-010-P1-M1-A3

 Method
 BLASTX

 NCBI GI
 g3551523

 BLAST score
 201

 E value
 1.0e-15

E value 1.0e Match length 119 % identity 34

NCBI Description (AB017026) oxysterol-binding protein [Mus musculus]

Seq. No. 228566

Seq. ID LIB3196-010-P1-M1-A4

Method BLASTX
NCBI GI g2738949
BLAST score 500
E value 9.0e-51
Match length 108
% identity 88

NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x

ananassa]

Seq. No. 228567

Seq. ID LIB3196-010-P1-M1-B1

Method BLASTX
NCBI GI g1352450
BLAST score 480
E value 1.0e-48
Match length 97
% identity 99

NCBI Description INTERLEUKIN-1 ALPHA PRECURSOR (IL-1 ALPHA)

(HEMATOPOIETIN-1) >gi\_644806 (U19844) interleukin-1 alpha

[Macaca mulatta]



```
228568
Seq. No.
                  LIB3196-010-P1-M1-B10
Seq. ID
                  BLASTX
Method
                  g2119228
NCBI GI
                  196
BLAST score
                  3.0e-15
E value
                  67
Match length
                   61
% identity
                  keratin K4a - human (fragment) >gi_313159_emb_CAA47914_
NCBI Description
                   (X67683) keratin K4a [Homo sapiens]
                  228569
Seq. No.
                  LIB3196-010-P1-M1-B3
Seq. ID
                  BLASTX
Method
                   g2369766
NCBI GI
                   449
BLAST score
                   9.0e-45
E value
                   127
Match length
                   70
% identity
                  (AJ001304) hypothetical protein [Citrus x paradisi]
NCBI Description
                   228570
Seq. No.
                   LIB3196-010-P1-M1-B6
Seq. ID
                   BLASTX
Method
                   g3063647
NCBI GI
                   491
BLAST score
                   1.0e-49
E value
                   132
Match length
                   74
% identity
                  (AF057285) intersectin-EH binding protein Ibpl [Mus
NCBI Description
                   musculus]
                   228571
Seq. No.
                   LIB3196-010-P1-M1-B8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2736153
                   178
BLAST score
                   5.0e-13
E value
                   77
Match length
                   49
 % identity
                   (AF021936) myotonic dystrophy kinase-related Cdc42-binding
NCBI Description
                   kinase MRCK-beta [Rattus norvegicus]
 Seq. No.
                   228572
                   LIB3196-010-P1-M1-C1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g114127
 BLAST score
                   664
                   6.0e-70
 E value
                   130
 Match length
                   100
 % identity
                   ADP-RIBOSYLATION FACTOR 5 >gi_105230_pir__A23741
 NCBI Description
                   ADP-ribosylation factor 5 - human >gi 2137130 pir JC4949
                   ADP-ribosylation factor type 5 - mouse >gi_178987 (M57567)
                   ADP-ribosylation factor [Homo sapiens] >gi_438870 (L12384)
```

ADP-ribosylation factor 5 [Rattus norvegicus]



>gi\_1565215\_dbj\_BAA13494\_ (D87902) ARF5 [Mus musculus]
>gi\_2088529 (U73002) ADP-ribosylation factor 5 [Homo
sapiens] >gi\_4502209\_ref\_NP\_001653.1\_pARF5\_

ADP-ribosylation factor

Seq. No. 228573

Seq. ID LIB3196-010-P1-M1-C10

Method BLASTX
NCBI GI g3327136
BLAST score 604
E value 5.0e-63
Match length 115
% identity 99

NCBI Description (AB014561) KIAA0661 protein [Homo sapiens]

Seq. No. 228574

Seq. ID LIB3196-010-P1-M1-C2

Method BLASTX
NCBI GI g2497543
BLAST score 274
E value 3.0e-24
Match length 115
% identity 46

NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi\_542061\_pir\_S41379

pyruvate kinase - common tobacco >gi\_444023\_emb\_CAA82628\_

(Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No. 228575

Seq. ID LIB3196-010-P1-M1-C3

Method BLASTX
NCBI GI g137578
BLAST score 499
E value 1.0e-50
Match length 98
% identity 97

NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)

>gi\_81545\_pir\_\_S06398 alpha-globulin type A precursor upland cotton >gi\_167371 (M19378) vicilin precursor
[Gossypium hirsutum] >gi\_207906 (M18027) alpha globulin A
[Artificial gene] >gi\_226119\_prf\_\_1410330A vicilin gene A

[Saguinus oedipus]

Seq. No. 228576

Seq. ID LIB3196-010-P1-M1-C4

Method BLASTX
NCBI GI g3947733
BLAST score 204
E value 4.0e-16
Match length 111
% identity 42

NCBI Description (AJ009719) NL25 [Solanum tuberosum]

Seq. No. 228577

Seq. ID LIB3196-010-P1-M1-D4

Method BLASTX
NCBI GI g2078350
BLAST score 598



```
3.0e-62
E value
                   128
Match length
% identity
                   (U95923) transaldolase [Solanum tuberosum]
NCBI Description
                   228578
Seq. No.
                   LIB3196-010-P1-M1-D8
Seq. ID
                   BLASTX
Method
                   g126156
NCBI GI
                   290
BLAST score
                   4.0e-26
E value
                   96
Match length
                   61
% identity
                   LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
NCBI Description
                   >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134)
                   - upland cotton >gi_167373 (M16936) vicilin precursor
                   [Gossypium hirsutum] >gi_1171335 (U43727) legumin B
[Gossypium hirsutum] >gi_225582_prf__1306412C storage
                   protein C134 [Saguinus oedipus]
                   228579
Seq. No.
                   LIB3196-010-P1-M1-E1
Seq. ID
                   BLASTX
Method .
                   q126047
NCBI GI
                   715
BLAST score
                    6.0e-76
E value
                   134
Match length
                    100
% identity
                   L-LACTATE DEHYDROGENASE M CHAIN (LDH-A)
NCBI Description
                    >gi_65922_pir__DEHULM L-lactate dehydrogenase (EC 1.1.1.27)
                    chain M - human >gi_34313_emb_CAA26088_ (X02152) lactate
                    dehydrogenase-A [Homo sapiens] >gi_780261_emb_CAA26879_
                    (X03077) lactate dehydrogenase-A [Homo sapiens]
                    228580
Seq. No.
                    LIB3196-010-P1-M1-E10
Seq. ID
Method
                    BLASTX
                    g3876766
NCBI GI
                    224
BLAST score
                    2.0e-18
E value
                    93
Match length
 % identity
                    (Z69637) predicted using Genefinder; Similarity to E.coli
 NCBI Description
                    hypothetical protein YCAC (SW:YCAC_ECOLI) [Caenorhabditis
                    elegans]
 Seq. No.
                    228581
                    LIB3196-010-P1-M1-E11
 Seq. ID
 Method
                    BLASTX
                    q464444
 NCBI GI
                    171
 BLAST score
                    5.0e-23
 E value
                    90
 Match length
                    63
 % identity
                    PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
 NCBI Description
                    COMPLEX 30 KD SUBUNIT) >gi 541889 pir_ S39900 proteasome -
```

Arabidopsis thaliana >gi\_166830 (M98495) proteasome



## [Arabidopsis thaliana]

```
228582
Seq. No.
                   LIB3196-010-P1-M1-E2
Seq. ID
                   BLASTX
Method
                   g126047
NCBI GI
                   263
BLAST score
                   4.0e-23
E value
                   65
Match length
                   80
% identity
                   L-LACTATE DEHYDROGENASE M CHAIN (LDH-A)
NCBI Description
                   >gi_65922_pir__DEHULM L-lactate dehydrogenase (EC 1.1.1.27)
                   chain M - human >gi_34313_emb_CAA26088_ (X02152) lactate
                   dehydrogenase-A [Homo sapiens] >gi_780261_emb_CAA26879_
                   (X03077) lactate dehydrogenase-A [Homo sapiens]
                   228583
Seq. No.
                   LIB3196-010-P1-M1-E5
Seq. ID
                   BLASTX
Method
                   q464444
NCBI GI
BLAST score
                   546
                   4.0e-56
E value
                   118
Match length
                   90
% identity
                   PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                   COMPLEX 30 KD SUBUNIT) >gi 541889_pir__S39900 proteasome -
                   Arabidopsis thaliana ^{\circ} > gi_1\overline{6}6830 (\overline{M}984\overline{95}) proteasome
                   [Arabidopsis thaliana]
                   228584
Seq. No.
                   LIB3196-010-P1-M1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q115613
                   520
BLAST score
                   4.0e-53
E value
Match length
                   129
% identity
                   73
                   CALCIUM-DEPENDENT PROTEASE, SMALL (REGULATORY) SUBUNIT
NCBI Description
                    (CALPAIN) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP)
                   >gi 67666 pir_ CIPGL calpain (EC 3.4.22.17) light chain -
                   pig >gi 164403 (M11778) calpain I light subunit (EC
                   3.4.22.17) [Sus scrofa] >gi_164405 (M11779) pig calpain I
                   light subunit (EC 3.4.22.17) [Sus scrofa]
                    228585
 Seq. No.
                   LIB3196-010-P1-M1-E9
 Seq. ID
Method
                   BLASTX
                    q137578
 NCBI GI
                    525
 BLAST score
                    1.0e-53
 E value
                   119
Match length
                    52
 % identity
                   VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
 NCBI Description
                    >gi_81545_pir__S06398 alpha-globulin type A precursor -
                    upland cotton >gi_167371 (M19378) vicilin precursor
                    [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                    [Artificial gene] >gi_226119_prf__1410330A vicilin gene A
```



## [Saguinus oedipus]

```
228586
Seq. No.
                   LIB3196-010-P1-M1-F11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q88044
                   627
BLAST score
                   1.0e-65
E value
                   133
Match length
                    96
% identity
                   keratin 4, type II, cytoskeletal - human (fragment)
NCBI Description
                   >gi_34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA)
                    [Homo sapiens]
                    228587
Seq. No.
                    LIB3196-010-P1-M1-F3
Seq. ID
                    BLASTX
Method
NCBI GI
                    g542200
                    372
BLAST score
                    9.0e-36
E value
                    129
Match length
                    53
% identity
                    hypothetical protein - garden asparagus
NCBI Description
                    >gi_452714_emb_CAA54526 (X77320) unknown [Asparagus
                    officinalis]
                    228588
Seq. No.
                    LIB3196-010-P1-M1-F4
Seq. ID
                    BLASTX
Method
                    g3738257
NCBI GI
BLAST score
                    438
                    2.0e-43
E value
Match length
                    92
% identity
                   (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
NCBI Description
                    nigra]
                    228589
Seq. No.
                    LIB3196-010-P1-M1-G11
Seq. ID
                    BLASTX
Method
NCBI GI
                    q125077
BLAST score
                    190
                    8.0e-17
E value
Match length
                    58
                    73
 % identity
                    KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK
 NCBI Description
                    13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi_34033_emb_CAA32786_ (X14640) keratin
                    13 [Homo sapiens]
                    228590
 Seq. No.
                    LIB3196-010-P1-M1-G8
 Seq. ID
                    BLASTX
 Method
                    g2586071
 NCBI GI
                    317
 BLAST score
                     3.0e-29
 E value
```

126

Match length



% identity

```
NCBI Description (AF027728) kinesin-related protein [Xenopus laevis]
                  228591
Seq. No.
                  LIB3196-010-P1-M1-G9
Seq. ID
                  BLASTX
Method
                  g728836
NCBI GI
                  144
BLAST score
                  4.0e-09
E value
                  129
Match length
                  29
% identity
NCBI Description ALU SUBFAMILY SP WARNING ENTRY !!!!
                  228592
Seq. No.
                  LIB3196-010-P1-M1-H10
Seq. ID
                  BLASTX
Method
                  g2739008
NCBI GI
                  363
BLAST score
                  1.0e-34
E value
                  102
Match length
                  74
% identity
NCBI Description (AF022463) CYP78A3p [Glycine max]
                  228593
Seq. No.
                  LIB3196-010-P1-M1-H12
Seq. ID
                  BLASTX
Method
                  g2662343
NCBI GI
                  164
BLAST score
                   8.0e-12
E value
                   59
Match length
                   64
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                   228594
Seq. No.
                   LIB3196-010-P1-M1-H3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2995990
BLAST score
                   230
                   4.0e-19
E value
                   116
Match length
                   48
% identity
                   (AF053746) dormancy-associated protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2995992 (AF053747) dormancy-associated
                   protein [Arabidopsis thaliana]
                   228595
 Seq. No.
                   LIB3196-010-P1-M1-H4
 Seq. ID
Method
                   BLASTX
 NCBI GI
                   g542184
 BLAST score
                   166
                   1.0e-11
 E value
 Match length
                   94
                   37
 % identity
 NCBI Description globulin-1S, GLB1S - maize
                   228596
 Seq. No.
                   LIB3196-010-P1-M1-H8
 Seq. ID
```



```
Method
                   BLASTX
                   g2833389
NCBI GI
                   513
BLAST score
                   3.0e-52
E value
                   125
Match length
                   78
% identity
                   SOLUBLE GLYCOGEN (STARCH) SYNTHASE PRECURSOR (SS III)
NCBI Description
                   >gi 1200154_emb_CAA65065_ (X95759) glycogen (starch)
                   synthase [Solanum tuberosum]
                   228597
Seq. No.
                   LIB3196-010-P1-M1-H9
Seq. ID
                   BLASTX
Method
                   q126156
NCBI GI
BLAST score
                   431
                   8.0e-43
E value
                   109
Match length
                   82
% identity
                   LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
NCBI Description
                   >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134)
                   - upland cotton >gi_167373 (M16936) vicilin precursor
                    [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                   protein C134 [Saguinus oedipus]
                   228598
Seq. No.
                   LIB3196-011-P1-M1-A10
Seq. ID
                   BLASTX
Method
                    g2136315
NCBI GI
                    568
BLAST score
                    9.0e-59
E value
                    127
Match length
                    87
% identity
                    translation elongation factor Tu precursor - human
NCBI Description
                    >gi_704416 (L38995) elongation factor Tu [Homo sapiens]
                    >gi_4507733_ref_NP_003312.1_pTUFM_ Tu translation
                    elongation factor, mitochondrial
                    228599
 Seq. No.
                    LIB3196-011-P1-M1-A11
 Seq. ID
                    BLASTX
Method
                    q128378
NCBI GI
                    187
 BLAST score
                    4.0e-14
 E value
                    58
 Match length
                    59
 % identity
 NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN A (NS-LTP A)
                    (PHOSPHOLIPID TRANSFER PROTEIN) (PLTP)
                    >gi_82031_pir__S07142 nonspecific lipid transfer protein -
                    castor bean >gi_224909_prf__1204170A protein, nonspecific
                    lipid transfer [Ricinus communis]
                    228600
 Seq. No.
                    LIB3196-011-P1-M1-A9
```

Seq. ID

BLASTX Method q3687234 NCBI GI 247 BLAST score



```
4.0e-21
E value
                   92
Match length
                   51
% identity
                   (AC005169) putative copia-like transposable element
NCBI Description
                   [Arabidopsis thaliana] .
                   228601
Seq. No.
Seq. ID
                   LIB3196-011-P1-M1-B1
                   BLASTX
Method
NCBI GI
                   g4559342
BLAST score
                   428
                   2.0e-42
E value
Match length
                   120
                   67
% identity
                   (AC007087) putative copper methylamine oxidase [Arabidopsis
NCBI Description
                   thaliana]
                   228602
Seq. No.
                   LIB3196-011-P1-M1-B10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2072361
BLAST score
                   656
E value
                   4.0e-69
Match length
                   127
                   99
% identity
NCBI Description (AF001008) p38Beta2 MAP Kinase [Homo sapiens] >gi_2232138
                   (AF001174) p38beta2 MAP kinase [Homo sapiens]
                   >gi_2326554_emb_CAA74792_ (Y14440) stress activated protein
kinase-2b [Homo sapiens] >gi_3025677 (AF031135) p38beta2
                   MAP kinase [Homo sapiens]
                   >gi_4506083 ref_NP_002742.1_pPRKM11_ protein kinase
                   mitogen- activated
Seq. No.
                   228603
Seq. ID
                   LIB3196-011-P1-M1-B4
                   BLASTX
Method
NCBI GI
                   g2459421
BLAST score
                   368
E value
                   2.0e-35
Match length
                   102
% identity
                   67
NCBI Description (AC002332) putative calcium-binding EF-hand protein
                   [Arabidopsis thaliana]
Seq. No.
                   228604
                   LIB3196-011-P1-M1-B5
Seq. ID
Method
                . BLASTX
NCBI GI
                   g691752
BLAST score
                   321
                   8.0e-30
E value
Match length
                   121
% identity
                   51
NCBI Description (D29803) preproMP27-MP32 [Cucurbita sp.]
```

Seq. No. Seq. ID LIB3196-011-P1-M1-B6

228605

Method BLASTX

BLAST score

E value

301

2.0e-27



```
g3914435
NCBI GI
BLAST score
                  400
                  4.0e-39
E value
Match length
                  84
% identity
                  87
NCBI Description PROFILIN 1 > gi 3021375 emb CAA11756 (AJ223982) profilin
                  [Glycine max]
Seq. No.
                  228606
                  LIB3196-011-P1-M1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g181912
BLAST score
                  366
                  4.0e-35
E value
Match length
                  71
% identity
                  97
NCBI Description (M95586) E2A/HLF fusion protein [Homo sapiens]
                  228607
Seq. No.
                  LIB3196-011-P1-M1-B9
Seq. ID
Method
                  BLASTX
                  g72287
NCBI GI
BLAST score
                  382
E value
                  6.0e - 37
                  109
Match length
% identity
                  71
NCBI Description beta-globulin A precursor (clone 94) - upland cotton
                  (fragment) >qi 167377 (M16905) legumin precursor [Gossypium
                  hirsutum]
                  228608
Seq. No.
Seq. ID
                  LIB3196-011-P1-M1-C12
Method
                  BLASTX
NCBI GI
                  g3157943
BLAST score
                  313
                  7.0e-29
E value
Match length
                  110
                  57
% identity
NCBI Description (AC002131) Contains similarity to BAP31 protein gb X81816
                  from Mus musculus. [Arabidopsis thaliana]
Seq. No.
                  228609
Seq. ID
                  LIB3196-011-P1-M1-C3
Method
                  BLASTX
NCBI GI
                  q4455192
BLAST score
                  459
E value
                  5.0e-46
Match length
                  124
% identity
                  66
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  228610
                  LIB3196-011-P1-M1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827699
```



```
106
Match length
                   63
% identity
                   (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
                   228611
Seq. No.
                   LIB3196-011-P1-M1-D5
Seq. ID
                   BLASTX
Method
                   g207905
NCBI GI
                   202
BLAST score
                   6.0e-17
E value
                   119
Match length
                   50
% identity
                   (M18027) alpha globulin B [Artificial gene]
NCBI Description
                   228612
Seq. No.
                   LIB3196-011-P1-M1-D7
Seq. ID
                   BLASTX
Method
                   q476850
NCBI GI
                   637
BLAST score
                   6.0e-67
E value
                   128
Match length
                   99
% identity
                   heat shock cognate protein 70 - mouse >gi_309319 (M19141)
NCBI Description
                   heat shock protein 70 cognate [Mus musculus]
                   >gi_1661134_gb_AAB18391.1_ (U73744) heat shock 70 protein
                    [Mus musculus]
                    228613
Seq. No.
                   LIB3196-011-P1-M1-E2
Seq. ID
                    BLASTX
Method
                    g131392
NCBI GI
                    363
BLAST score
                    8.0e-47
E value
                    119
Match length
                    82
% identity
                    OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) (23 KD
NCBI Description
                    SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II)
                    >gi 81479_pir__S00005 photosystem II oxygen-evolving
                    complex protein 2 precursor - spinach
                    >gi_21265_emb_CAA29055_ (X05511) 23 kDa OEC protein
[Spinacia oleracea] >gi_225596_prf__1307179A luminal
                    protein 23kD [Spinacia oleracea]
                    228614
 Seq. No.
                    LIB3196-011-P1-M1-E3
 Seq. ID
                    BLASTX
Method
 NCBI GI
                    q2642215
 BLAST score
                    326
                    2.0e-30
 E value
                    77
 Match length
 % identity
 NCBI Description (AF030386) NOI protein [Arabidopsis thaliana]
                    228615
 Seq. No.
                    LIB3196-011-P1-M1-E4
 Seq. ID
```

BLASTX

g996057

Method NCBI GI



```
BLAST score
                  1.0e-60
E value
                  121
Match length
% identity
                  92
NCBI Description (X90872) associated to Golgi apparatus [Homo sapiens]
                  228616
Seq. No.
                  LIB3196-011-P1-M1-E8
Seq. ID
Method
                  BLASTX
                  q2995405
NCBI GI
BLAST score
                  453
                  3.0e-45
E value
                  115
Match length
                  70
% identity
NCBI Description (Y12432) polyprotein [Ananas comosus]
                  228617
Seq. No.
                  LIB3196-011-P1-M1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2506379
                  230
BLAST score
                   3.0e-19
E value
Match length
                   114
                   41
% identity
NCBI Description GTP-BINDING PROTEIN GUF1 (GTPASE GUF1)
                   >gi 1077352_pir__S50374 GTP-binding protein GUF1 - yeast
                   (Saccharomyces cerevisiae) >gi_596037 (U17243) Similar to
                   GTP binding proteins [Saccharomyces cerevisiae]
                   228618
Seq. No.
Seq. ID
                   LIB3196-011-P1-M1-F1
                   BLASTX
Method
NCBI GI
                   g543794
BLAST score
                   514
                   3.0e-52
E value
Match length
                   128
% identity
                   74
NCBI Description SERUM ALBUMIN PRECURSOR >gi 476379 pir ABHOS serum albumin
                   precursor - horse >gi_399672_emb_CAA52194 (X74045)
                   preproalbumin [Equus caballus]
Seq. No.
                   228619
                   LIB3196-011-P1-M1-F10
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g231536
BLAST score
                   565
E value
                   2.0e-58
Match length
                   121
                   88
 % identity
NCBI Description CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP)
                   (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL
```

AMINOPEPTIDASE) >gi\_99683\_pir\_\_S22399 leucyl aminopeptidase (EC 3.4.11.1) - Arabidopsis thaliana >gi\_16394\_emb\_CAA45040\_ (X63444) leucine aminopeptidase

[Arabidopsis thaliana] >gi\_4115380 (AC005967) putative

leucine aminopeptidase [Arabidopsis thaliana]



```
228620
Seq. No.
                  LIB3196-011-P1-M1-F3
Seq. ID
                  BLASTX
Method
                  q4406656
NCBI GI
                  439
BLAST score
                  1.0e-43
E value
                  109
Match length
                  81
% identity
                  (AF131820) Unknown [Homo sapiens]
NCBI Description
                  228621
Seq. No.
                  LIB3196-011-P1-M1-F4
Seq. ID
                  BLASTX
Method
                  g3287489
NCBI GI
                  632
BLAST score
                  3.0e-66
E value
                  125
Match length
                  100
% identity
                  (AF028832) Hsp89-alpha-delta-N [Homo sapiens]
NCBI Description
                  ,228622
Seq. No.
                  LIB3196-011-P1-M1-F5
Seq. ID
                   BLASTX
Method
                   g1620018
NCBI GI
                   595
BLAST score
                   6.0e-62
E value
                   125
Match length
% identity
                   95
                  (D87666) heat shock protein 90 [Homo sapiens]
NCBI Description
                   228623
Seq. No.
                   LIB3196-011-P1-M1-F7
Seq. ID
                   BLASTX
Method
                   g3249065
NCBI GI
                   142
BLAST score
                   5.0e-09
E value
Match length
                   54
                   57
% identity
                  (AC004473) Similar to HAK1 gb_U22945 high affinity
NCBI Description
                   potassium transporter from Schwanniomyces occidentalis.
                   [Arabidopsis thaliana]
                   228624
Seq. No.
                   LIB3196-011-P1-M1-F9
Seq. ID
Method
                   BLASTX
                   q1865677
NCBI GI
BLAST score
                   267
E value
                   7.0e-24
Match length
                   72
                   71
 % identity
                   (Y08568) trehalose-6-phosphate synthase [Arabidopsis
NCBI Description
                   thaliana]
 Seq. No.
                   228625
                   LIB3196-011-P1-M1-G1
 Seq. ID
```

BLASTX

g4204277

Method NCBI GI

NCBI Description



```
522
BLAST score
                   2.0e-53
E value
                   110
Match length
                   81
% identity
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   228626
Seq. No.
                   LIB3196-011-P1-M1-G2
Seq. ID
                   BLASTX
Method
                   g4204277
NCBI GI
                   210
BLAST score
                   3.0e-17
E value
                   54
Match length
                   69
% identity
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   228627
Seq. No.
                   LIB3196-011-P1-M1-G6
Seq. ID
                   BLASTX
Method
                   g119165
NCBI GI
                   422
BLAST score
                   9.0e-42
E value
                   110
Match length
                   76
% identity
                   ELONGATION FACTOR 1-GAMMA (EF-1-GAMMA)
NCBI Description
                   >gi_105918_pir__S22655 translation elongation factor eEF-1
                   gamma chain - human >gi_31102_emb_CAA45089_ (X63526)
                   homologue to elongation factor 1-gamma from A.salina [Homo
                   sapiens] >gi_31104_emb_CAA77630_ (Z11531) elongation
                   factor-1-gamma [Homo sapiens]
                   >gi_4503481_ref_NP_001395.1_pEEF1G_ eukaryotic translation
                   elongation factor 1 gamma
                   228628
 Seq. No.
                   LIB3196-011-P1-M1-H10
 Seq. ID
                   BLASTX
 Method
NCBI GI
                   g1174592
BLAST score
                   484
                   5.0e-49
E value
                   112
Match length
                   85
 % identity
                   TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
 NCBI Description
                   - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
                   sativum]
                   228629
 Seq. No.
                   LIB3196-011-P1-M1-H11
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q2493130
                   627
 BLAST score
                   1.0e-65
 E value
                   122
 Match length
 % identity
                   100
```

[Gossypium hirsutum]

VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B

SUBUNIT) >gi 459200 (U07053) vacuolar H+-ATPase subunit B



```
228630
Seq. No.
                  LIB3196-011-P1-M1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2995405
                  342
BLAST score
                  7.0e-36
E value
                  113
Match length
                   67
% identity
NCBI Description (Y12432) polyprotein [Ananas comosus]
                  228631
Seq. No.
                  LIB3196-012-P1-M1-A4
Seq. ID
                  BLASTX
Method
                   q1923256
NCBI GI
BLAST score
                   148
                   9.0e-14
E value
                   106
Match length
                   40
% identity
                  (U86782) 26S proteasome-associated padl homolog [Homo
NCBI Description
                   sapiens]
                   228632
Seq. No.
                   LIB3196-012-P1-M1-A9
Seq. ID
                   BLASTX
Method
                   g3158372
NCBI GI
                   392
BLAST score
                   2.0e-38
E value
                   80
Match length
                   54
% identity
NCBI Description (AF035383) polyubiquitin [Arabidopsis thaliana]
                   228633
Seq. No.
                   LIB3196-012-P1-M1-B12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4539292
BLAST score
                   306
E value
                   3.0e-28
Match length
                   68
                   82
 % identity
                   (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                   thaliana]
                   228634
 Seq. No.
                   LIB3196-012-P1-M1-B5
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q434759
                   191
 BLAST score
                   2.0e-16
 E value
                   92
 Match length
                   51
 % identity
 NCBI Description (D21163) similar to human elongation factor 2 mRNA (HSEF2).
                   [Homo sapiens]
                   228635
 Seq. No.
                   LIB3196-012-P1-M1-B6
 Seq. ID
```

BLASTX

g3024122

Method

NCBI GI

Match length

% identity

102

73



```
BLAST score
                  2.0e-41
E value
Match length
                  96
% identity
                  85
                  S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821
                   (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
Seq. No.
                  228636
                  LIB3196-012-P1-M1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3745821
                  455
BLAST score
                  2.0e-45
E value
Match length
                  89
                   94
% identity
NCBI Description Chain A, Tubulin Alpha-Beta Dimer, Electron Diffraction
                  228637
Seq. No.
Seq. ID
                  LIB3196-012-P1-M1-B8
                  BLASTX
Method
NCBI GI
                   q167367
BLAST score
                   628
E value
                   1.0e-68
                   130
Match length
                   99
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                   228638
Seq. No.
                   LIB3196-012-P1-M1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3790567
BLAST score
                   221
E value
                   4.0e-18
Match length
                   114
% identity
                   41
                  (AF078821) RING-H2 finger protein RHA1b [Arabidopsis
NCBI Description
                   thaliana]
                   228639
Seq. No.
                   LIB3196-012-P1-M1-D10
Seq. ID
                   BLASTX
Method
                   g3688172
NCBI GI
BLAST score
                   239
E value
                   2.0e-20
                   78
Match length
 % identity
NCBI Description (AL031804) putative protein [Arabidopsis thaliana]
                   228640
Seq. No.
Seq. ID
                   LIB3196-012-P1-M1-D7
                   BLASTX
Method
                   g3850818
NCBI GI
BLAST score
                   393
E value
                   2.0e-38
```



```
(Y18349) U2 snRNP auxiliary factor, small subunit [Oryza
NCBI Description
                   sativa]
                   228641
Seq. No.
                   LIB3196-012-P1-M1-E12
Seq. ID
                   BLASTX
Method
                   q116486
NCBI GI
                   420
BLAST score
E value
                   2.0e-41
                   83
Match length
                   98
% identity
                   CALPACTIN I LIGHT CHAIN (P10 PROTEIN) (P11) (CELLULAR
NCBI Description
                   LIGAND OF ANNEXIN II) >gi 89438 pir_B28489 calpactin I
                   light chain - bovine >gi_107251_pir__JC1139 calpactin I
                   light chain - human >gi 162785 (M16464) calpactin I light
                   chain [Bos taurus] >gi_179875 (M81457) calpactin I light
                   chain [Homo sapiens] >qi_180596 (M38591) cellular ligand of
                   annexin II [Homo sapiens]
                   >gi_4506761_ref_NP_002957.1_pS100A10_ S100 calcium-binding
                   protein A10 (annexin II ligand, calpactin I, light
                   polypeptide (p11))
                   228642
Seq. No.
                   LIB3196-012-P1-M1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g137578
BLAST score
                   367
                   3.0e - 35
E value
                   101
Match length
                   76
% identity
                   VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                   >gi_81545_pir__S06398 alpha-globulin type A precursor -
upland cotton >gi_167371 (M19378) vicilin precursor
                    [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                    [Artificial gene] >gi_226119_prf__1410330A vicilin gene A
                    [Saguinus oedipus]
                   228643
Seq. No.
                   LIB3196-012-P1-M1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2506477
                   558
BLAST score
E value
                    4.0e-62
                   129
Match length
                    96
% identity
```

GRG PROTEIN (ESP1 PROTEIN) (AMINO ENHANCER OF SPLIT) NCBI Description (AES-1/AES-2) >gi 435425 (U04241) homologous to Swiss-Prot

accession number P16371 [Homo sapiens] >gi\_3850562 (AC005944) GRG HUMAN; ESP1 PROTEIN; AMINO ENHANCER OF SPLIT; AES-1/AES-2; gp130 associated protein GAM [Homo

sapiens]

228644 Seq. No.

LIB3196-012-P1-M1-E6 Seq. ID

 ${\tt BLASTX}$ Method g126156 NCBI GI 444BLAST score



```
3.0e-44
E value
Match length
                  86
                  99
% identity
                  LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
NCBI Description
                  >gi 72288 pir _FWCNBB beta-globulin B precursor (clone 134)
                  - upland cotton >gi_167373 (M16936) vicilin precursor
                  [Gossypium hirsutum] >gi_1171335 (U43727) legumin B
                   [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                  protein C134 [Saguinus oedipus]
                  228645
Seq. No.
                  LIB3196-012-P1-M1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  a266691
                  319
BLAST score
                  1.0e-29
E value
                  62
Match length
                  100
% identity
NCBI Description OLEOSIN 16.4 KD >gi_167361 (L00934) 16.4 kDa oleosin
                   [Gossypium hirsutum]
                   228646
Seq. No.
                  LIB3196-012-P1-M1-E8
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1346342
                   426
BLAST score
E value
                   2.0e-48
                   115
Match length
                   89
% identity
                   KERATIN, TYPE I CYTOSKELETAL 17 (CYTOKERATIN 17) (K17) (CK
NCBI Description
                   17) (VERSION 2) >gi_186685 (M28439) keratin type 16 [Homo
                   sapiens]
                   228647
Seq. No.
                   LIB3196-012-P1-M1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3395436
                   218
BLAST score
                   9.0e-18
E value
Match length
                   67
                   61
% identity
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                   228648
Seq. No.
                   LIB3196-012-P1-M1-F10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1703052
BLAST score
                   480
                   2.0e-48
E value
                   123
Match length
                   76
 % identity
```

replication factor C (activator 1) 4 (37kD)

SUBUNIT) (A1 37 KD SUBUNIT) (RF-C 37 KD SUBUNIT) (RFC37) >gi 1498256 (M87339) replication factor C, 37-kDa subunit

[Homo sapiens] >gi\_4506491 ref NP\_002907.1\_pRFC4\_

NCBI Description ACTIVATOR 1 37 KD SUBUNIT (REPLICATION FACTOR C 37 KD



```
228649
Seq. No.
                  LIB3196-012-P1-M1-F12
Seq. ID
                  BLASTX
Method
                  q125105
NCBI GI
                  157
BLAST score
                  1.0e-10
E value
                  60
Match length
                  60
% identity
                  KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5)
NCBI Description
                  (58 KD_CYTOKERATIN) >gi_88051_pir_A29904 keratin K5, 58K
                  type II, epidermal (version 1) - human >gi_307082 (M21389)
                  keratin type II [Homo sapiens]
                  >gi_4557890_ref_NP_000415.1_pKRT5 keratin
                  228650
Seq. No.
                  LIB3196-012-P1-M1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2270994
                  164
BLAST score
                  6.0e-19
E value
                  77
Match length
                   68
% identity
                  (AF004809) Ca+2-binding EF hand protein [Glycine max]
NCBI Description
                  228651
Seq. No.
                  LIB3196-012-P1-M1-G2
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4530435
                   568
BLAST score
                   1.0e-58
E value
                   134
Match length
                   83
% identity
                  (AF117657) thyroid hormone receptor-associated protein
NCBI Description
                   complex component TRAP80 [Homo sapiens]
                   228652
Seq. No.
                   LIB3196-012-P1-M1-G7
Seq. ID
                   BLASTX
Method
                   g1922278
NCBI GI
                   213
BLAST score
                   1.0e-17
E value
Match length
                   48
                   83
% identity
NCBI Description (Z86091) TCTP protein [Fragaria x ananassa]
                   228653
Seq. No.
                   LIB3196-012-P1-M1-G8
Seq. ID
Method
                   BLASTX
                   q2244763
NCBI GI
                   440
BLAST score
                   9.0e-44
E value
                   114
Match length
                   72
 % identity
NCBI Description (Z97335) A6 anther-specific protein [Arabidopsis thaliana]
```

Seq. No. 228654

Seq. ID LIB3196-012-P1-M1-H12



```
BLASTX
Method
                   q131856
NCBI GI
                   529
BLAST score
                   3.0e-60
È`value
                   122
Match length
                   100
% identity
                   RAS-RELATED PROTEIN RAP-1B (GTP-BINDING PROTEIN SMG P21B)
NCBI Description
                   >gi_68951_pir__TVHUR1 transforming protein rap1b - human
>gi_108713_pir__A34655 transforming protein rap1b - bovine
                   >gi_163722 (M3\overline{31}41) GTP-binding protein (smg p21B) [Bos
                   taurus]
                   228655
Seq. No.
                   LIB3196-012-P1-M1-H6
Seq. ID
                   BLASTX
Method
                    g477138
NCBI GI
                    326
BLAST score
                    2.0e-30
E value
                    110
Match length
                    52
% identity
                    carcinoma-associated antigen GA733-1 precursor - human
NCBI Description
                    >gi_31591_emb_CAA31781_ (X13425) GA733-1 protein (AA 1-323)
                    [Homo sapiens]
                    228656
Seq. No.
                    LIB3196-012-P1-M1-H8
Seq. ID
                    BLASTX
Method
                    g2145023
NCBI GI
                    216
BLAST score
                    2.0e-17
E value
                    112
Match length
% identity
                    42
                   (U97700) 15.5 kDa oleosin [Sesamum indicum]
NCBI Description
                    228657
Seq. No.
                    LIB3196-013-P1-M1-A1
Seq. ID
Method
                    BLASTX
                    g2119106
NCBI GI
                    632
BLAST score
                    3.0e-66
E value
                    125
Match length
                    98
 % identity
                    ribosomal protein L3 - human (fragment) >gi 337580 (M90054)
NCBI Description
                    ribosomal protein L3 [Homo sapiens]
                    228658
 Seq. No.
                    LIB3196-013-P1-M1-A10
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2340052
                    145
 BLAST score
                    3.0e-11
 E value
 Match length
                    42
 % identity
 NCBI Description (L48990) troponin T [Mus musculus]
```

228659

LIB3196-013-P1-M1-A4

Seq. No.

Seq. ID

Seq. ID



```
BLASTX
Method
                  q3702323
NCBI GI
                  160
BLAST score
                  5.0e-11
E value
                  60
Match length
                  57
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                  228660
Seq. No.
                  LIB3196-013-P1-M1-A6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2244990
BLAST score
                  406
                  8.0e-40
E value
                  120
Match length
                  67
% identity
                  (Z97340) similarity to LIM homeobox protein -
NCBI Description
                  Caenorhabditis [Arabidopsis thaliana]
                  228661
Seq. No.
                  LIB3196-013-P1-M1-B1
Seq. ID
Method
                  BLASTX
                  g547753
NCBI GI
                  270
BLAST score
                  7.0e-24
E value
Match length
                  102
% identity
                  65
NCBI Description KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)
                  228662
Seq. No.
                  LIB3196-013-P1-M1-B12
Seq. ID
Method
                  BLASTX
                  q2829918
NCBI GI
                  190
BLAST score
                   2.0e-14
E value
Match length
                   56
% identity
                   71
NCBI Description (AC002291) similar to "tub" protein gp_U82468_2072162
                   [Arabidopsis thaliana]
                   228663
Seq. No.
                   LIB3196-013-P1-M1-B2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g126156
BLAST score
                   455
                   1.0e-45
E value
Match length
                   116
 % identity
                   79
NCBI Description LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
                   >gi 72288 pir FWCNBB beta-globulin B precursor (clone 134)
                   - upland cotton >gi 167373 (M16936) vicilin precursor
                   [Gossypium hirsutum] >gi_1171335 (U43727) legumin B
                   [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                   protein C134 [Saguinus oedipus]
                   228664
 Seq. No.
```

LIB3196-013-P1-M1-B6



Method BLASTX
NCBI GI g2498882
BLAST score 168
E value 8.0e-14
Match length 68
% identity 69
NCBI Description SPLICEOSO

on SPLICEOSOME ASSOCIATED PROTEIN 114 (SAP 114) (SF3A120)

>gi\_2146975\_pir\_\_S60735 splicing factor SF3a 120K chain human >gi\_899298\_emb\_CAA59494\_ (X85237) human splicing
factor [Homo sapiens] >gi\_3212998 (AC004997) spliceosome

associated protein 114 (SF3a) [Homo sapiens]

Seq. No. 228665 Seq. ID LIB3196-013-P1-M1-C4

Method BLASTX
NCBI GI g4193388
BLAST score 313
E value 7.0e-29
Match length 81
% identity 75

NCBI Description (AF091455) translationally controlled tumor protein [Hevea

brasiliensis]

Seq. No. 228666

Seq. ID LIB3196-013-P1-M1-D11

Method BLASTX
NCBI GI g1174448
BLAST score 197
E value 3.0e-15
Match length 56
% identity 66

NCBI Description TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR

(TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >gi\_547391 (L32016) alpha-subunit; putative

[Arabidopsis thaliana]

Seq. No. 228667

Seq. ID LIB3196-013-P1-M1-D7

Method BLASTX
NCBI GI g2511594
BLAST score 410
E value 3.0e-40
Match length 84
% identity 93

NCBI Description (Y13694) multicatalytic endopeptidase complex, proteasome

precursor, beta subunit [Arabidopsis thaliana]

>gi 2827525 emb CAA16533\_ (AL021633) multicatalytic

endopeptidase complex, proteasome precursor, beta subunit

[Arabidopsis thaliana] >gi\_3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]

Seq. No. 228668

Seq. ID LIB3196-013-P1-M1-D9

Method BLASTX
NCBI GI g2995384
BLAST score 170
E value 1.0e-12



NCBI Description (AB015234) uroplakin 1b [Homo sapiens]

% identity

```
Match length
                   44
% identity
                   75
                   (AJ004810) cytochrome P450 monooxygenase [Zea mays]
NCBI Description
                   228669
Seq. No.
                   LIB3196-013-P1-M1-E2
Seq. ID
Method
                   BLASTX
                   g133041
NCBI GI
                   548
BLAST score
                   2.0e-56
E value
Match length
                   106
                   100
% identity
                   60S ACIDIC RIBOSOMAL PROTEIN PO (L10E)
NCBI Description
                   >gi 71137 pir R5HUPO acidic ribosomal protein PO - human
                   >gi_19023\overline{2} (M17885) acidic ribosomal phosphoprotein (P0)
                   [Homo sapiens] >gi 2935618_gb_AAC05176_ (AC004263) 60S
                   ACIDIC RIBOSOMAL PROTEIN; match to P05388 (PID:g133041)
                   [Homo sapiens] >gi_4506667_ref_NP_000993.1_pRPLP0_
                   ribosomal protein, large, PO
                   228670
Seq. No.
                   LIB3196-013-P1-M1-E4
Seq. ID
Method
                   BLASTX
                   g125105
NCBI GI
                   480
BLAST score
                   2.0e-48
E value
                   96
"Match length
% identity
                   100
                   KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5)
NCBI Description
                   (58 KD CYTOKERATIN) >gi_88051_pir__A29904 keratin K5, 58K
                   type II, epidermal (version 1) - human >gi_307082 (M21389)
                   keratin type II [Homo sapiens]
                   >gi_4557890_ref_NP_000415.1_pKRT5_ keratin
                   228671
Seq. No.
                   LIB3196-013-P1-M1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2146797
BLAST score
                   483
                   8.0e-49
E value
                   121
Match length
% identity
                   protein disulfide-isomerase (EC 5.3.4.1) - Castor bean
NCBI Description
                   >gi_1134968 (U41385) protein disulphide isomerase PDI
                   [Ricinus communis] >gi_1587210_prf__2206331A protein
                   disulfide isomerase [Ricinus communis]
 Seq. No.
                   228672
 Seq. ID
                   LIB3196-013-P1-M1-F1
                   BLASTX
Method
NCBI GI
                   q3721858
 BLAST score
                   478
E value
                   3.0e-48
Match length
                   92
```



```
228673
Seq. No.
                   LIB3196-013-P1-M1-F10
Seq. ID
                   BLASTX
Method
                   g1346349
NCBI GI
                   612
BLAST score
                   6.0e-64
E value
                   124
Match length
                   99
% identity
                   KERATIN, TYPE II CYTOSKELETAL 6F (CYTOKERATIN 6F) (CK 6F)
NCBI Description
                   (K6F KERATIN) >gi_2119219_pir__I61771 keratin type II -
                   human >gi 908805 (L42612) keratin type II [Homo sapiens]
                   228674
Seq. No.
                   LIB3196-013-P1-M1-F12
Seq. ID
                   BLASTX
Method
                   g4567295
NCBI GI
                   318
BLAST score
                   2.0e-29
E value
                   106
Match length
                   51
% identity
                   (AC006918) putative pol polyprotein [Arabidopsis thaliana]
NCBI Description
                   228675
Seq. No.
                   LIB3196-013-P1-M1-F6
Seq. ID
                   BLASTX
Method
                   g2772564
NCBI GI
                   378
BLAST score
                   1.0e-36
E value
                   79
Match length
                   57
% identity
                   (AC004000) ADP/ATP carrier protein (adenine nucleotide
NCBI Description
                   translocator 2) [Homo sapiens]
                   228676
Seq. No.
                   LIB3196-013-P1-M1-G1
Seq. ID
                   BLASTX
Method
NCBI GI
                    q125080
BLAST score
                    487
                    3.0e-49
E value
                    99
Match length
                    98
 % identity
                   KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK
NCBI Description
                    14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal
                    - human >gi 386848 (J00124) keratin [Homo sapiens] >gi 4504913 ref NP 000517.1 pKRT14 keratin 14
                    (epidermolysis bullosa simplex, Dowling-Meara, Koebner)
 Seq. No.
                    228677
                    LIB3196-013-P1-M1-G10
 Seq. ID
                    BLASTX
 Method
                    g1596167
 NCBI GI
                    673
 BLAST score
                    4.0e-71
 E value
 Match length
                    125
                    100
 % identity
                   (D87953) RTP [Homo sapiens] >gi_3046386 (AF004162)
 NCBI Description
```

nickel-specific induction protein [Homo sapiens]



```
228678
Seq. No.
                   LIB3196-013-P1-M1-G11
Seq. ID
                   BLASTX
Method
                   q3603456
NCBI GI
                   610
BLAST score
                   1.0e-63
E value
                   121
Match length
                   34
% identity
                  (AF088848) polyubiquitin [Capsicum chinense]
NCBI Description
                   228679
Seq. No.
                   LIB3196-013-P1-M1-G2
Seq. ID
                   BLASTX
Method
                   g1731412
NCBI GI
BLAST score
                   467
                   6.0e-47
E value
                   123
Match length
                   6
% identity
                   ZINC FINGER PROTEIN 136 >gi_2136405_pir__B57785 zinc finger
NCBI Description
                   protein ZNF136 - human >gi_487785 (U09367) zinc finger
                   protein ZNF136 [Homo sapiens] >gi_1582216_prf__2118244B
                   ZNF136 protein [Homo sapiens]
                   >gi_4507987_ref_NP_003428.1_pZNF136_ zinc finger protein
                   136 (clone \overline{p}HZ-\overline{20})
                   228680
Seq. No.
                   LIB3196-013-P1-M1-G4
Seq. ID
                   BLASTX
Method
                   g423532
NCBI GI
                   594
BLAST score
                   8.0e-62
E value
                   123
Match length
                   97
% identity
                   plakoglobin - mouse (fragment)
NCBI Description
Seq. No.
                   228681
                   LIB3196-013-P1-M1-G5
Seq. ID
                   BLASTX
Method
                   q4580395
NCBI GI
                   191
BLAST score
E value
                    1.0e-14
                   102
Match length
                    48
% identity
                   (AC007171) putative kinesin-related protein [Arabidopsis
NCBI Description
                    thaliana]
                    228682
 Seq. No.
                    LIB3196-013-P1-M1-G7
 Seq. ID
                    BLASTX
Method
NCBI GI
                    g2194203
 BLAST score
                    396
                    1.0e-38
 E value
```

70

NCBI Description (U78310) pescadillo [Homo sapiens]

Match length

% identity



```
228683
Seq. No.
                   LIB3196-013-P1-M1-G8
Seq. ID
                   BLASTX
Method
                    g3334115
NCBI GI
                    283
BLAST score
                    2.0e-25
E value
                    73
Match length
                    78
% identity
                   ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                    (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664
                    (AF006489) adenine nucleotide translocator 1 [Gossypium
                    hirsutum]
                    228684
Seq. No.
                    LIB3196-013-P1-M1-H10
Seq. ID
                    BLASTX
Method
                    g2245098
NCBI GI
                    219
BLAST score
                    2.0e-18
E value
                    58
Match length
                    72
% identity
NCBI Description (Z97343) ribosomal protein [Arabidopsis thaliana]
                    228685
Seq. No.
                    LIB3196-013-P1-M1-H2
Seq. ID
                    BLASTX
Method
                    g121116
NCBI GI
BLAST score
                    616
                    2.0e-64
E value
                    125
Match length
                    34
% identity
NCBI Description GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR)
                    (ADF) (BREVIN) (AGEL) >gi_71649_pir__FAHUP gelsolin precursor, plasma - human >gi_736249_emb_CAA28000_ (X04412) plasma gelsolin [Homo sapiens] >gi_225304_prf__1211330A
                    gelsolin [Homo sapiens] >gi 4504165_ref NP 000168.1_pGSN_
                    qelsolin (amyloidosis, Finnish type)
                    228686
Seq. No.
                    LIB3196-014-P1-M1-A10
Seq. ID
                    BLASTX
Method
NCBI GI
                    q942596
                    581
BLAST score
                    2.0e-60
E value
                    119
Match length
% identity
NCBI Description (U30467) alpha-tubulin [Urechis caupo]
                    228687
Seq. No.
                    LIB3196-014-P1-M1-A11
Seq. ID
                    BLASTX
Method
NCBI GI
                    q2995405
BLAST score
                    239
                    2.0e-32
E value
Match length
                    119
```

NCBI Description (Y12432) polyprotein [Ananas comosus]

% identity

Seq. ID Method



```
228688
 Seq. No.
                     LIB3196-014-P1-M1-A2
 Seq. ID
                     BLASTX
 Method
 NCBI GI
                     g121116
 BLAST score
                     218
                     1.0e-17
 E value
                     44
 Match length
                     95
 % identity
                     GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR)
 NCBI Description
                     (ADF) (BREVIN) (AGEL) >gi_71649_pir__FAHUP gelsolin
                     precursor, plasma - human >gi_736249 emb_CAA28000 (X04412) plasma gelsolin [Homo sapiens] >gi_225304 prf_1211330A
                     gelsolin [Homo sapiens] >gi_4504165_ref_NP_000168.1_pGSN_
                     gelsolin (amyloidosis, Finnish type)
                     228689
 Seq. No.
                     LIB3196-014-P1-M1-A3
 Seq. ID
                     BLASTX
 Method
                     g3334115
 NCBI GI
                     378
 BLAST score
                     2.0e-36
 E value
                     94
 Match length
                     81
 % identity
                     ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
... NCBI Description
                      (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664
                      (AF006489) adenine nucleotide translocator 1 [Gossypium
                     hirsutum]
                     228690
 Seq. No.
                     LIB3196-014-P1-M1-A4
 Seq. ID
 Method
                     BLASTX
                     q125080
 NCBI GI
 BLAST score
                      559
 E value
                      9.0e-58
 Match length
                     112
  % identity
                      100
                     KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK
 NCBI Description
                      14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens]
                      >qi 4504913 ref NP 000517.1 pKRT14 keratin 14
                      (epidermolysis bullosa simplex, Dowling-Meara, Koebner)
  Seq. No.
                      228691
                      LIB3196-014-P1-M1-A6
  Seq. ID
                      BLASTX
  Method
  NCBI GI
                      q2495365
  BLAST score
                      597
  E value
                      4.0e-62
  Match length
                      126
                      93
  % identity
                     HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi 445127 prf_1908431B
  NCBI Description
                      heat shock protein HSP81-2 [Arabidopsis thaliana]
                      228692
 Seq. No.
```

LIB3196-014-P1-M1-A8

BLASTX



```
g1737218
NCBI GI
                  269
BLAST score
                  6.0e-24
E value
                  94
Match length
                  60
% identity
                  (U79959) vacuolar sorting receptor homolog [Arabidopsis
NCBI Description
                  thaliana]
                  228693
Seq. No.
                  LIB3196-014-P1-M1-B3
Seq. ID
                  BLASTX
Method
                  g207905
NCBI GI
                  290
BLAST score
                  4.0e-26
E value
                  87
Match length
                  66
% identity
                  (M18027) alpha globulin B [Artificial gene]
NCBI Description
                  228694
Seq. No.
                  LIB3196-014-P1-M1-B4
Seq. ID
                  BLASTX
Method
                  g207905
NCBI GI
                  184
BLAST score
                   1.0e-19
E value
                  81
Match length
                   67
% identity
                  (M18027) alpha globulin B [Artificial gene]
NCBI Description
                   228695
Seq. No.
                  LIB3196-014-P1-M1-C1
Seq. ID
                   BLASTX
Method
                   g3004948
NCBI GI
                   450
BLAST score
                   5.0e-45
E value
Match length
                   89
                   93
% identity
                  (AF037261) SH3-containing adaptor molecule-1 [Homo sapiens]
NCBI Description
Seq. No.
                   228696
                   LIB3196-014-P1-M1-C2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g430947
                   158
BLAST score
                   6.0e-11
E value
Match length
                   32
                   91
% identity
                  (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   228697
Seq. No.
                   LIB3196-014-P1-M1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1806146
BLAST score
                   495
                   3.0e-50
E value
                   108
Match length
```

% identity



```
(X97317) cdc2MsF [Medicago sativa]
NCBI Description
                   228698
Seq. No.
                   LIB3196-014-P1-M1-C4
Seq. ID
Method
                   BLASTX
                   g2351378
NCBI GI
                   315
BLAST score
                   2.0e-29
E value
                   66
Match length
                   89
% identity
                   (U54558) translation initiation factor eIF3 p66 subunit
NCBI Description
                   [Homo sapiens] >gi_4200328_emb_CAA18440_ (AL022313)
                   EIF3-P66 [Homo sapiens]
                   >gi_4503523_ref_NP_003744.1_pEIF3S7_ UNKNOWN
                   228699
Seq. No.
                   LIB3196-014-P1-M1-D1
Seq. ID
                   BLASTX
Method
                   q2244910
NCBI GI
BLAST score
                   169
                   6.0e-12
E value
                   72
Match length
                   46
% identity
                   (Z97339) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                   228700
Seq. No.
                   LIB3196-014-P1-M1-D3
Seq. ID
                   BLASTX
Method
                    g4204265
NCBI GI
                    293
BLAST score
                    2.0e-26
E value
                    122
Match length
                    54
% identity
                   (AC005223) 45643 [Arabidopsis thaliana]
NCBI Description
                    228701
Seq. No.
                    LIB3196-014-P1-M1-D6
Seq. ID
                    BLASTX
Method
NCBI GI
                    g71881
                    566
BLAST score
                    2.0e-58
E value
                    127
Match length
                    87
% identity
                    GTP-binding regulatory protein Gs alpha-S2 chain (adenylate
NCBI Description
                    cyclase-stimulating) - mouse >gi_51128_emb_CAA68695_
(Y00703) G-s-alpha protein (AA 1 - 394) [Mus musculus]
                    228702
Seq. No.
                    LIB3196-014-P1-M1-E11
Seq. ID
Method
                    BLASTX
                    q1170508
NCBI GI
                    209
BLAST score
E value
                    8.0e-17
                    43
Match length
% identity
                    91
NCBI Description EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8)
```

>gi 2119931 pir\_S60244 translation initiation factor



eIF-4A.8, anther-specific - common tobacco >gi\_475219\_emb\_CAA55639\_ (X79004) translation initiation factor (eIF-4A) [Nicotiana tabacum] >gi 475221\_emb\_CAA55640\_ (X79005) translation initiation

factor (eIF-4A) [Nicotiana tabacum]

Seq. No. 228703 Seq. ID LIB3196-014-P1-M1-E12

Method BLASTX
NCBI GI g1848212
BLAST score 487
E value 3.0e-49
Match length 95

Match length 95 % identity 47

NCBI Description (Y11209) protein disulfide-isomerase precursor [Nicotiana

tabacum]

Seq. No. 228704

Seq. ID LIB3196-014-P1-M1-E6

Method BLASTX
NCBI GI g1848212
BLAST score 173
E value 4.0e-25
Match length 108
% identity 39

NCBI Description (Y11209) protein disulfide-isomerase precursor [Nicotiana

tabacum]

Seq. No. 228705

Seq. ID LIB3196-014-P1-M1-E7

Method BLASTX
NCBI GI g2832906
BLAST score 499
E value 9.0e-51
Match length 99

% identity 94

NCBI Description (D89340) dipeptidyl peptidase III [Rattus norvegicus]

Seq. No. 228706

Seq. ID LIB3196-014-P1-M1-F12

Method BLASTX
NCBI GI g3882237
BLAST score 171
E value 4.0e-12
Match length 128
% identity 38

NCBI Description (AB018301) KIAA0758 protein [Homo sapiens]

Seq. No. 228707

Seq. ID LIB3196-014-P1-M1-F3

Method BLASTX
NCBI GI 94249649
BLAST score 221
E value 2.0e-20
Match length 106
% identity 52

NCBI Description (AF082889) GPI-anchored metastasis-associated protein

% identity

94



## homolog [Homo sapiens]

```
228708
Seq. No.
                  LIB3196-014-P1-M1-F5
Seq. ID
                  BLASTX
Method
                  g728837
NCBI GI
                  211
BLAST score
                  4.0e-17
E value
                  175
Match length
                  18
% identity
NCBI Description ALU SUBFAMILY SQ WARNING ENTRY !!!!
                  228709
Seq. No.
                  LIB3196-014-P1-M1-F6
Seq. ID
                  BLASTX
Method
                  g478811
NCBI GI
                  236
BLAST score
                  4.0e-20
E value
                  60
Match length
                  20
% identity
                  polyubiquitin - bovine >gi_645_emb_CAA79146_ (Z18245)
NCBI Description
                  polyubiquitin [Bos taurus]
                  228710
Seq. No.
                  LIB3196-014-P1-M1-G10
Seq. ID
                  BLASTX
Method
                  g3242717
NCBI GI
BLAST score
                  275
                   2.0e-24
E value
                  127
Match length
                   43
% identity
NCBI Description (AC003040) putative APG protein [Arabidopsis thaliana]
                   228711
Seq. No.
                  LIB3196-014-P1-M1-G11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g418507
                   231
BLAST score
                   3.0e-19
E value
                   102
Match length
                   46
% identity
NCBI Description S-ADENOSYLMETHIONINE: 2-DEMETHYLMENAQUINONE
                   METHYLTRANSFERASE >gi_541097_pir__S40872 hypothetical
                   protein f161 - Escherichia coli >gi_305032 (L19201)
                   ORF_f161 [Escherichia coli] >gi_1336002 (U56082)
                   S-adenosylmethionine: 2-demethylmenaquinone
                   methyltransferase [Escherichia coli] >gi_1790364 (AE000467)
                   menaquinone biosynthesis, unknown [Escherichia coli]
                   228712
Seq. No.
Seq. ID
                   LIB3196-014-P1-M1-G2
Method
                   BLASTX
NCBI GI
                   g2129579
                   693
BLAST score
                   2.0e-73
E value
Match length
                   128
```



```
Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400)
NCBI Description
                  Dwarf1 [Arabidopsis thaliana]
                  228713
Seq. No.
                  LIB3196-014-P1-M1-G4
Seq. ID
Method
                  BLASTX
                  q207905
NCBI GI
BLAST score
                  414
E value
                  1.0e-40
                  130
Match length
                  68
% identity
                  (M18027) alpha globulin B [Artificial gene]
NCBI Description
                  228714
Seq. No.
                  LIB3196-014-P1-M1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2497464
BLAST score
                  164
                  4.0e-14
E value
Match length
                  93
% identity
                  56
                  RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT (RAB
NCBI Description
                  GERANYL-GERANYLTRANSFERASE ALPHA SUBUNIT) (RAB GG
                  TRANSFERASE) (RAB GGTASE)
                  228715
Seq. No.
                  LIB3196-014-P1-M1-G8
Seq. ID
                  BLASTX
Method
                  q2497938
NCBI GI
BLAST score
                  482
E value
                  1.0e-50
Match length
                  123
                  83
% identity
                  AQUAPORIN 3 >gi 1854374 dbj BAA19237 (AB001325) aquaporin
NCBI Description
                   3 [Homo sapiens]
Seq. No.
                   228716
Seq. ID
                  LIB3196-014-P1-M1-G9
Method
                  BLASTX
NCBI GI
                   g1362754
BLAST score
                   390
E value
                   2.0e-38
Match length
                  118
                   82
% identity
NCBI Description aquaporin 3 - human
Seq. No.
                   228717
                   LIB3196-014-P1-M1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q401322
BLAST score
                   676
E value
                   2.0e-71
Match length
                   131
                   99
% identity
                  VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
NCBI Description
                   SUBUNIT) >gi 167313 (L03186) vacuolar H+-ATPase catalytic
```

subunit [Gossypium hirsutum]

% identity



```
Seq. No.
                   228718
                   LIB3196-014-P1-M1-H12
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g1688076
 BLAST score
                   430
 E value
                   2.0e-42
 Match length
                   88
 % identity
                   51
                   (U46571) tetratricopeptide repeat protein [Homo sapiens]
 NCBI Description
                   >gi_4507713_ref_NP_003306.1_pTTC2_ tetratricopeptide repeat
                   domain
                   228719
 Seq. No.
 Seq. ID
                   LIB3196-014-P1-M1-H2
 Method
                   BLASTX
 NCBI GI
                   g3915742
 BLAST score
                   581
                   3.0e-60
 E value
 Match length
                   122
                   90
 % identity
                   LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319
 NCBI Description
                    (M69188) legumin A [Gossypium hirsutum]
                   >gi 444320 prf 1906369A legumin A:ISOTYPE=D alloallele
                   [Gossypium hirsutum]
                   228720
 Seq. No.
 Seq. ID
                   LIB3196-014-P1-M1-H3
 Method
                   BLASTX
 NCBI GI
                   g1762945
 BLAST score
                   245
 E value
                    7.0e-21
                   70
 Match length
 % identity
                    64
                   (U66269) ORF; able to induce HR-like lesions [Nicotiana
 NCBI Description
                    tabacum]
                    228721
 Seq. No.
                   LIB3196-014-P1-M1-H4
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g4493521
                    158
 BLAST score
 E value
                    6.0e-11
                    42
 Match length
                    71
 % identity
                   (AL022476) dJ323M22.1 (human ortholog of chicken P52 and
 NCBI Description
                   mouse H74) [Homo sapiens]
                    228722
 Seq. No.
                    LIB3196-014-P1-M1-H5
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g386850
 BLAST score
                    639
                    5.0e-67
 E value
Match length
                    132
```

NCBI Description (M19723) keratin K5 [Homo sapiens]



```
228723
 Seq. No.
                    LIB3196-014-P1-M1-H6
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g2136102
                    175
 BLAST score
                    1.0e-12
 E value
                    76
 Match length
                    51
 % identity
                    retinoblastoma 1 - human >gi_536845 (M26460) retinoblastoma
 NCBI Description
                    1 [Homo sapiens]
                    228724
 Seq. No.
                    LIB3196-014-P1-M1-H7
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g2995405
 BLAST score
                    263
                    7.0e-26
 E value
                    113
 Match length
                    59
 % identity
 NCBI Description (Y12432) polyprotein [Ananas comosus]
                    228725
Seq. No.
                    LIB3196-015-P1-M1-A10
Seq. ID
                    BLASTX
 Meťhod
                    q1169534
 NCBI GI
 BLAST score
                    519
                     5.0e-53
 E value
                    112
 Match length
                     89
 % identity
 NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                    (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir__S39203 phosphopyruvate hydratase (EC 4.2.1.11) - castor bean
                     >gi_433609_emb_CAA82232 (Z28386) enolase [Ricinus
                     communis]
 Seq. No.
                     228726
                     LIB3196-015-P1-M1-A11
 Seq. ID
 Method
                     BLASTX
 NCBI GI
                     q4512671
 BLAST score
                     234
 E value
                     1.0e-19
 Match length
                     82
  % identity
 NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]
  Seq. No.
                     228727
                     LIB3196-015-P1-M1-A6
  Seq. ID
 Method
                     BLASTX
  NCBI GI
                     g125105
  BLAST score
                     633
  E value
                     2.0e-66
 Match length
                     127
  % identity
                     98
                   KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5)
  NCBI Description
                     (58 KD CYTOKERATIN) >gi_88051_pir__A29904 keratin K5, 58K
```

type II, epidermal (version 1) - human >gi\_307082 (M21389)



keratin type II [Homo sapiens] >gi\_4557890\_ref\_NP\_000415.1\_pKRT5\_ keratin

228728 Seq. No. LIB3196-015-P1-M1-A9 Seq. ID BLASTX Method g226120 NCBI GI 331 BLAST score 5.0e-31 E value 80 Match length 84 % identity NCBI Description vicilin gene B [Saguinus oedipus] 228729 Seq. No. LIB3196-015-P1-M1-B10 Seq. ID BLASTX Method q1778145 NCBI GI 439 BLAST score 2.0e-46 E value Match length 108 92 % identity (U66402) phosphate/phosphoenolpyruvate translocator NCBI Description precursor [Nicotiana tabacum] 228730 Seq. No.

LIB3196-015-P1-M1-B11 Seq. ID

BLASTX Method g115427 NCBI GI 461 BLAST score 2.0e-46 E value 108 Match length 80 % identity

PLACENTAL-CADHERIN PRECURSOR (P-CADHERIN) NCBI Description

>gi 319934\_pir\_\_IJHUCP cadherin 3 precursor - human >gi 35323 emb CAA45177 (X63629) p-cadherin [Homo sapiens] >gi 226518\_prf\_\_1516312A Ca dependent cell adhesion protein [Homo sapiens] >gi 4502723\_ref\_NP\_001784.1\_pCDH3\_ cadherin 3, P-cadherin (placental) (NOTE:redefinition of symbol)

228731 Seq. No.

LIB3196-015-P1-M1-B3 Seq. ID

BLASTX Method NCBI GI g623590 187 BLAST score 4.0e-14 E value 40 Match length 85 % identity

NCBI Description (L29275) putative [Nicotiana tabacum]

228732 Seq. No.

LIB3196-015-P1-M1-B5 Seq. ID

BLASTX Method NCBI GI q3643595 298 BLAST score 4.0e-27 E value Match length 106 55 % identity

32737

E value

Match length

% identity

5.0e-45

108 79



```
NCBI Description (AC005395) putative oleosin protein [Arabidopsis thaliana]
                   228733
Seq. No.
                   LIB3196-015-P1-M1-B7
Seq. ID
                   BLASTX
Method
                   g2766165
NCBI GI
                   435
BLAST score
                   2.0e-43
E value
                   82
Match length
                   96
% identity
NCBI Description (AB008430) CDEP [Homo sapiens]
                   228734
Seq. No.
                   LIB3196-015-P1-M1-C3
Seq. ID
                   BLASTX
Method
                   g3319958
NCBI GI
BLAST score
                   166
                   6.0e-12
E value
                   82
Match length
                   8
% identity
                   (AJ228139) VAKTI precursor [Homo sapiens]
NCBI Description
                   228735
Seq. No.
                   LIB3196-015-P1-M1-C5
Seq. ID
                   BLASTX
Method
                   q1304668
NCBI GI
BLAST score
                   494
                    4.0e-50
E value
                    96
Match length
                    96
% identity
                   (U42376) RIG-E precursor [Homo sapiens] >gi_1465747
NCBI Description
                    (U56145) thymic shared antigen-1/stem cell antigen-2 [Homo
                    sapiens] >gi_1519440 (U66711) 9804 [Homo sapiens]
                    >gi_4454267_emb_CAA92321_ (Z68179) retinoic acid induced
gene E [Homo sapiens] >gi_4505049_ref_NP_002337.1_pLY6E_
                    lymphocyte antigen 6 complex, locus E
                    228736
Seq. No.
                    LIB3196-015-P1-M1-C6
Seq. ID
                    BLASTX
Method
NCBI GI
                    g229506
BLAST score
                    156
                    6.0e-11
E value
                    36
Match length
                    83
 % identity
NCBI Description aldolase C [Oryctolagus cuniculus]
 Seq. No.
                    228737
                    LIB3196-015-P1-M1-D10
 Seq. ID
                    BLASTX
 Method
                    q3297816
 NCBI GI
                    450
 BLAST score
```

NCBI Description (AL031032) putative protein [Arabidopsis thaliana]



```
228738
Seq. No.
                  LIB3196-015-P1-M1-D5
Seq. ID
                  BLASTX
Method
                  q1262890
NCBI GI
BLAST score
                  507
                  1.0e-51
E value
                  117
Match length
                  81
% identity
                  (U35627) MHC class I B [Papio hamadryas anubis]
NCBI Description
                  228739
Seq. No.
                  LIB3196-015-P1-M1-D7
Seq. ID
                  BLASTX
Method
                  g225581
NCBI GI
                  142
BLAST score
E value
                  2.0e-09
                  52
Match length
                   60
% identity
NCBI Description storage protein C94 [Saguinus oedipus]
                  228740
Seq. No.
                  LIB3196-015-P1-M1-D8
Seq. ID
                  BLASTX
Method
                  g2583108
NCBI GI
BLAST score
                  205
                   3.0e-16
E value
Match length
                  107
                   45
% identity
                  (AC002387) putative surface protein [Arabidopsis thaliana]
NCBI Description
                   228741
Seq. No.
                   LIB3196-015-P1-M1-E2
Seq. ID
                   BLASTX
Method
                   g4417306
NCBI GI
                   156
BLAST score
E value
                   2.0e-10
Match length
                   105
                   31
% identity
                  (AC006446) putative Athila retroelement ORF1 protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   228742
                   LIB3196-015-P1-M1-E9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1173444
BLAST score
                   454
E value
                   2.0e-45
Match length
                   126
                   70
% identity
                   SKD1 PROTEIN >gi 1083520 pir S48696 suppressor protein
NCBI Description
                   SKD1 - mouse >qi 557876 (U10119) SKD1 [Mus musculus]
                   228743
Seq. No.
                   LIB3196-015-P1-M1-F1
```

Seq. ID

BLASTX Method NCBI GI g3687389 BLAST score 482

32739

% identity

100



```
1.0e-48
E value
                  114
Match length
                   81
% identity
                  (Y16124) putative cullin protein [Lycopersicon esculentum]
NCBI Description
                  228744
Seq. No.
                  LIB3196-015-P1-M1-F10
Seq. ID
                  BLASTX
Method
                   g3901014
NCBI GI
BLAST score
                   235
                   9.0e-20
E value
                   55
Match length
                   76
% identity
                   (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                   sylvatica]
                   228745
Seq. No.
                   LIB3196-015-P1-M1-F2
Seq. ID
                   BLASTX
Method
                   g2935291
NCBI GI
BLAST score
                   535
                   1.0e-54
E value
                   108
Match length
                   97
% identity
                   (AF035531) syntaxin 10 [Homo sapiens]
NCBI Description
                   >gi_4507285_ref_NP_003756.1_pSTX10_ UNKNOWN
                   228746
Seq. No.
                   LIB3196-015-P1-M1-F3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2842494
BLAST score
                   346
                   9.0e-33
E value
                   107
Match length
                   62
% identity
NCBI Description
                   (AL021749) prohibitin-like protein [Arabidopsis thaliana]
                   >gi 4097688 (U66591) prohibitin 1 [Arabidopsis thaliana]
                   >gi 4097694 (U66594) prohibitin 1 [Arabidopsis thaliana]
                   228747
Seq. No.
                   LIB3196-015-P1-M1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q167367
BLAST score
                   626
                   1.0e-65
E value
Match length
                   123
% identity
                   95
                  (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                   228748
Seq. No.
                   LIB3196-015-P1-M1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131786
BLAST score
                   534
                   6.0e-55
E value
                   103
Match length
```

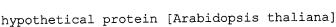


RAS-RELATED PROTEIN RAB-1A (YPT1-RELATED PROTEIN) NCBI Description >gi 68968\_pir TVMSYP GTP-binding protein ypt1 - mouse >gi 2144599 pir TVHUYP GTP-binding protein Rab1 - human >gi 2144600 pir TVDGYP GTP-binding protein Rab1 - dog >gi\_55457\_emb\_CAA68284\_ (Y00094) Ypt1 protein (AA 1-205) [Mus musculus] >gi\_550060 (M28209) GTP-binding protein [Homo sapiens] >gi\_763158\_emb\_CAA33760\_ (X15744) GTP-binding protein [Mus musculus] Seq. No. 228749 LIB3196-015-P1-M1-G12 Seq. ID Method BLASTX NCBI GI q730773 384 BLAST score 3.0e-37 E value Match length 71 100 % identity SPLICING FACTOR, ARGININE/SERINE-RICH 1 (PRE-MRNA SPLICING NCBI Description FACTOR SF2, P33 SUBUNIT) (ALTERNATIVE SPLICING FACTOR ASF-1) >gi\_105293\_pir\_\_A40040 alternative splicing factor ASF-1 - human >gi\_179075 (M72709) alternative [Homo sapiens] >gi 338047 (M69040) SF2p33 [Homo sapiens] 228750 Seq. No. LIB3196-015-P1-M1-G7 Seq. ID BLASTX Method g2582665 NCBI GI 256 BLAST score 2.0e-22 E value 88 Match length 59 % identity NCBI Description (Z82983) thi [Citrus sinensis] 228751 Seq. No. LIB3196-015-P1-M1-G9 Seq. ID Method BLASTX NCBI GI q133841 232 BLAST score 2.0e-19 E value Match length 51 % identity CHLOROPLAST 30S RIBOSOMAL PROTEIN S18 >gi\_71016\_pir\_\_R3NT18 NCBI Description ribosomal protein S18 - common tobacco chloroplast >gi\_11851\_emb\_CAA77371\_ (Z00044) ribosomal protein S18 [Nicotiana tabacum] >gi\_225220\_prf\_\_1211235BB ribosomal protein S18 [Nicotiana tabacum] Seq. No. 228752 LIB3196-015-P1-M1-H1 Seq. ID Method BLASTX NCBI GI q4512685 BLAST score 180

3.0e-13 E value 70 Match length 49

% identity (AC006931) hypothetical protein [Arabidopsis thaliana] NCBI Description >gi 4559325 gb AAD22987.1\_AC007087\_6 (AC007087)





```
228753
Seq. No.
                  LIB3196-015-P1-M1-H11
Seq. ID
                  BLASTX
Method
                  g417745
NCBI GI
                  638
BLAST score
                  6.0e-67
E value
                  125
Match length
                  98
% identity
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                  HYDROLASE) (ADOHCYASE) >gi_170773 (L11872)
                  S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]
                  228754
Seq. No.
                  LIB3196-015-P1-M1-H12
Seq. ID
                  BLASTX
Method
                  g3236242
NCBI GI
                  364
BLAST score
                  7.0e-35
E value
                  93
Match length
                  80
% identity
                  (AC004684) putative ribosomal protein L36 [Arabidopsis
NCBI Description
                  thaliana]
                  228755
Seq. No.
                  LIB3196-015-P1-M1-H4
Seq. ID
Method
                  BLASTX
                  g2143868
NCBI GI
                   422
BLAST score
                   1.0e-41
E value
Match length
                   86
                   97
% identity
NCBI Description NAB1 - rat >gi_915282 (U17253) NAB1 [Rattus norvegicus]
                   228756
Seq. No.
                   LIB3196-015-P1-M1-H5
Seq. ID
Method
                   BLASTX
                   q2505876
NCBI GI
BLAST score
                   258
                   2.0e-22
E value
Match length
                   99
                   55
% identity
NCBI Description (Y12776) MYB-related protein [Arabidopsis thaliana]
                   228757
Seq. No.
                   LIB3196-016-P1-M1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g218157
                   207
BLAST score
                   6.0e-17
E value
Match length
                   50
 % identity
                   80
NCBI Description (D13512) cytoplasmic aldolase [Oryza sativa]
                   228758
 Seq. No.
                   LIB3196-016-P1-M1-A10
 Seq. ID
```



```
BLASTX
Method
                    q2119204
NCBI GI
                    382
BLAST score
                    6.0e-37
E value
                    86
Match length
                    92
% identity
                    vimentin - human >gi 37850 emb CAA39600 (X56134) vimentin
NCBI Description
                    [Homo sapiens]
                    228759
Seq. No.
                    LIB3196-016-P1-M1-A11
Seq. ID
                    BLASTX
Method
                    q3746127
NCBI GI
                    323
BLAST score
                    4.0e-30
E value
Match length
                    65
                    91
% identity
                   (U76253) E25B protein [Mus musculus]
NCBI Description
                    228760
Seq. No.
                    LIB3196-016-P1-M1-A12
Seq. ID
                    BLASTX
Method
                    g3746127
NCBI GI
                    130
BLAST score
                    2.0e-17
E value
Match length
                    60
% identity
                    83
NCBI Description (U76253) E25B protein [Mus musculus]
                    228761
Seq. No.
                    LIB3196-016-P1-M1-A2
Seq. ID
Method
                    BLASTX
NCBI GI
                    q3041684
                    238
BLAST score
                    4.0e-20
E value
Match length
                    78
% identity
                    69
NCBI Description EPITHELIAL MEMBRANE PROTEIN-1 (EMP-1) (TUMOR-ASSOCIATED
                    MEMBRANE PROTEIN) (CL-20) (B4B PROTEIN)
                    >gi_1460068_emb_CAA90627_ (Z50751) B4B [Homo sapiens]
>gi_1542883_emb_CAA69217_ (Y07909) progression associated
protein [Homo sapiens] >gi_1932786 (U77085) epithelial
                    membrane protein [Homo sapiens] >gi 2506160 (U43916) TMP
                     [Homo sapiens] >gi 4503559 ref NP 001414.1_pEMP1_
                    epithelial membrane protein
Seq. No.
                    228762
                    LIB3196-016-P1-M1-A3
Seq. ID
Method
                    BLASTX
NCBI GI
                     q3335359
BLAST score
                    210
E value
                     9.0e-17
Match length
                    125
% identity
                     43
NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]
```

Seq. No. 228763

NCBI GI

BLAST score



```
LIB3196-016-P1-M1-A8
Seq. ID
                  BLASTX
Method
                  a179950
NCBI GI
BLAST score
                  509
                  5.0e-52
E value
                  98
Match length
                  96
% identity
NCBI Description
                  (K02400) catalase [Homo sapiens]
                  228764
Seq. No.
                  LIB3196-016-P1-M1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q82426
                  537
BLAST score
                   4.0e-55
E value
Match length
                  112
                   45
% identity
                  ubiquitin precursor - barley (fragment)
NCBI Description
                  >gi_755763_emb_CAA27751_ (X04133) ubiquitin polyprecursor
                   (171 aa) [Hordeum vulgare]
                   228765
Seq. No.
                   LIB3196-016-P1-M1-B2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q388891
BLAST score
                   631
                   4.0e-66
E value
                   122
Match length
                   100
% identity
NCBI Description (L12711) transketolase [Homo sapiens]
                   228766
Seq. No.
                   LIB3196-016-P1-M1-B3
Seq. ID
                   BLASTX
Method
                   g107458
NCBI GI
BLAST score
                   680
E value
                   8.0e-72
                   126
Match length
                   100
% identity
NCBI Description protein kinase (EC 2.7.1.37) cdc2/cdc28-like - human
Seq. No.
                   228767
                   LIB3196-016-P1-M1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3790102
BLAST score
                   389
E value
                   9.0e-38
                   85
Match length
% identity
                   82
                  (AF095521) pyrophosphate-dependent phosphofructokinase
NCBI Description
                   alpha subunit [Citrus X paradisi]
                   228768
Seq. No.
                   LIB3196-016-P1-M1-B6
Seq. ID
                   BLASTX
Method
```

32744

g3790102 366



```
E value
                   5.0e-35
                   87
Match length
                   77
% identity
                   (AF095521) pyrophosphate-dependent phosphofructokinase
NCBI Description
                   alpha subunit [Citrus X paradisi]
                   228769
Seq. No.
                   LIB3196-016-P1-M1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3643595
                   396
BLAST score
E value
                   1.0e-38
Match length
                   111
                   68
% identity
                  (AC005395) putative oleosin protein [Arabidopsis thaliana]
NCBI Description
                   228770
Seq. No.
                   LIB3196-016-P1-M1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3355311
BLAST score
                   189
                   2.0e-18
E value
                   59
Match length
                   90
% identity
                   (AJ009737) eukaryotic translation initiation factor 6 [Beta
NCBI Description
                   vulgaris]
                   228771
Seq. No.
                   LIB3196-016-P1-M1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3176098
                   376
BLAST score
                   3.0e-36
E value
Match length
                   109
                   70
% identity
NCBI Description
                  (Y15036) annexin [Medicago truncatula]
                   228772
Seq. No.
                   LIB3196-016-P1-M1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1001355
BLAST score
                   304
E value
                   8.0e-28
Match length
                   106
                   58
% identity
                  (D64006) auxin-induced protein [Synechocystis sp.]
NCBI Description
                   228773
Seq. No.
                   LIB3196-016-P1-M1-C12
Seq. ID
                   BLASTX
Method
                   q1001355
NCBI GI
                   250
BLAST score
E value
                   2.0e-21
                   103
Match length
                   52
 % identity
```

NCBI Description (D64006) auxin-induced protein [Synechocystis sp.]



```
228774
  Seq. No.
                     LIB3196-016-P1-M1-C6
  Seq. ID
Method
                     BLASTX
  NCBI GI
                     q266690
                     169
  BLAST score
                      6.0e-12
  E value
                     78
  Match length
                      47
  % identity
                     OLEOSIN 18.2 KD >gi_167363 (L00935) 18.2 kDa oleosin [Gossypium hirsutum] >gi_167365 (L00936) 18.2 kDa oleosin
  NCBI Description
                      [Gossypium hirsutum]
                     228775
  Seq. No.
                     LIB3196-016-P1-M1-C8
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g3738257
                     327
  BLAST score
                      1.0e-30
  E value
  Match length
                     72
                      90
  % identity
                     (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
  NCBI Description
                     nigra]
                      228776
  Seq. No.
  Seq. ID
                     LIB3196-016-P1-M1-D12
  Method
                     BLASTX
                      q3094014
  NCBI GI
                      153
  BLAST score
                      4.0e-10
  E value
  Match length
                      41
  % identity
                      73
  NCBI Description (AF060862) unknown [Homo sapiens]
                      228777
   Seq. No.
   Seq. ID
                      LIB3196-016-P1-M1-D2
  Method
                      BLASTX
   NCBI GI
                      g285957
   BLAST score
                      174
                      2.0e-12
  E value
                      133
  Match length
   % identity
                      31
  NCBI Description (D14689) KIAA0023 [Homo sapiens]
                      228778
   Seq. No.
   Seq. ID
                      LIB3196-016-P1-M1-D3
   Method
                      BLASTX
   NCBI GI
                      g3914480
   BLAST score
                      389
   E value
                      1.0e-37
                      77
  Match length
   % identity
                      94
                     PROTEASE M PRECURSOR (NEUROSIN) (ZYME) (SP59) >gi_1518788
   NCBI Description
                      (U62801) protease M [Homo sapiens]
                      >gi_1805493_dbj_BAA11306_ (D78203) neurosin [Homo sapiens]
                      >gi_2318115 (AF013988) serine protease [Homo sapiens]
                      >gi_4506155_ref_NP_002765.1 pPRSS9 protease, serine, 9
```

(neurosin)



```
228779
Seq. No.
                   LIB3196-016-P1-M1-D4-
Seq. ID
                   BLASTX
Method
                   g2369714
NCBI GI
                   497
BLAST score
                   2.0e-50
E value
                   107
Match length
                   88
% identity
                   (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
Seq. No.
                   228780
                   LIB3196-016-P1-M1-D5
Seq. ID
                   BLASTX
Method
NCBI GI
                   .q3202042
BLAST score
                   355
                   9.0e - 34
E value
Match length
                   104
% identity
                   67
                   (AF069324) 26S proteasome regulatory subunit S5A
NCBI Description
                   [Mesembryanthemum crystallinum]
Seq. No.
                   228781
                   LIB3196-016-P1-M1-D7
Seq. ID
                   BLASTX
Method
                   q2498490
NCBI GI
                   649
BLAST score
E value
                   3.0e-68
                   129
Match length
                   97
% identity
                   VIRAL INTEGRATION SITE PROTEIN INT-6 >gi_1854579 (L35556)
NCBI Description
                   Int-6 [Mus musculus] >gi_2114363 (U62962) similar to mouse Int-6 [Homo sapiens] >gi_2351382 (U54562) eIF3-p48 [Homo
                   sapiens] >gi_2688818 (U85947) Int-6 [Homo sapiens]
                   >gi 2695701 (U94175) mammary tumor-associated protein INT6
                    [Homo sapiens] >gi_4503521_ref_NP_001559.1_pEIF3S6_ murine
                   mammary tumor integration site 6 (oncogene homolog)
                    228782
Seq. No.
                   LIB3196-016-P1-M1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                    q4544372
                    190
BLAST score
                    2.0e-14
E value
                    92
Match length
                    38
% identity
                   (AC006920) putative reverse transcriptase [Arabidopsis
NCBI Description
                    thaliana]
Seq. No.
                    228783
                    LIB3196-016-P1-M1-E1
Seq. ID
                    BLASTX
Method
NCBI GI
                    q81857
BLAST score
                    333
```

3.0e - 31

74

86

E value

Match length % identity



IgE-dependent histamine-releasing factor homolog - alfalfa NCBI Description (fragment) >gi\_19658\_emb\_CAA45349\_ (X63872) translationally controlled tumor protein [Medicago sativa] 228784 Seq. No. LIB3196-016-P1-M1-E12 Seq. ID Method BLASTX g2072977 NCBI GI 183 BLAST score 1.0e-13 E value Match length 117 45 % identity (U93574) putative p150 [Homo sapiens] NCBI Description 228785 Seq. No. LIB3196-016-P1-M1-E3 Seq. ID Method BLASTX NCBI GI q3288675 BLAST score 363 1.0e-34 E value Match length 100 74 % identity (D88575) TP55 [Homo sapiens] >gi\_3769373 (AF027866) megsin NCBI Description [Homo sapiens] >gi\_4505149\_ref\_NP\_003775.1\_pMEGSIN\_ UNKNOWN 228786 Seq. No. LIB3196-016-P1-M1-E4 Seq. ID BLASTX Method NCBI GI q3687237 203 BLAST score 6.0e-16 E value Match length 100 50 % identity (AC005169) putative Cys3His zinc-finger protein NCBI Description [Arabidopsis thaliana] 228787 Seq. No. Seq. ID LIB3196-016-P1-M1-E5 Method BLASTX NCBI GI q127621 482 BLAST score 1.0e-48 E value Match length 92 98 % identity NCBI Description MYC PROTO-ONCOGENE PROTEIN (C-MYC) >gi\_86684 pir\_\_JU0449 c-myc protein - chimpanzee >gi 176653 (M38057) [Chimpanzee

c-myc proto-oncogene, complete cds.], gene products [Pan

troglodytes]

228788 Seq. No.

LIB3196-016-P1-M1-E6 Seq. ID

Method BLASTX NCBI GI q283985 BLAST score 492 8.0e-50 E value Match length 129 77 % identity

BLAST score

E value

536

5.0e-55



```
amphiglycan - human >gi_28680_emb_CAA47406_ (X67016)
NCBI Description
                  amphiglycan [Homo sapiens]
                  >gi_4506861_ref_NP_002990.1_pSDC4_ syndecan 4 (amphiglycan,
                  ryudocan)
                  228789
Seq. No.
                  LIB3196-016-P1-M1-E7
Seq. ID
                  BLASTX
Method
                  g1350762
NCBI GI
                  305
BLAST score
                  6.0e-28
E value
                  80
Match length
                  74
% identity
                  60S RIBOSOMAL PROTEIN L6 (TAX-RESPONSIVE ENHANCER ELEMENT
NCBI Description
                  BINDING PROTEIN 107) (TAXREB107) (NEOPLASM-RELATED PROTEIN
                  C140) >gi_2136251_pir__I51803 TAXREB107 - human
                  >gi 433416_dbj_BAA04491_ (D17554) TAXREB107 [Homo sapiens]
                  228790
Seq. No.
                  LIB3196-016-P1-M1-E8
Seq. ID
                  BLASTX
Method
                  g1620898
NCBI GI
BLAST score
                  538
                  2.0e-55
E value
                  109
Match length
                   97
% identity
                  (D87957) protein involved in sexual development [Homo
NCBI Description
                  sapiens]
                  228791
Seq. No.
                  LIB3196-016-P1-M1-E9
Seq. ID
                  BLASTX
Method
                   g1666236
NCBI GI
                   179
BLAST score
                   4.0e-13
E value
                   107
Match length
                   31
% identity
NCBI Description (U76261) unknown [Hordeum vulgare]
                   228792
Seq. No.
                   LIB3196-016-P1-M1-F1
Seq. ID
Method
                   BLASTX
                   q1488368
NCBI GI
                   679
BLAST score
                   1.0e-71
E value
                   129
Match length
                   89
% identity
                   (S80993) MG1=high molecular weight mucin {C-terminal}
NCBI Description
                   [human, sublingual gland, Peptide Partial, 196 aa] [Homo
                   sapiens]
                   228793
Seq. No.
                   LIB3196-016-P1-M1-F10
Seq. ID
                   BLASTX
Method
                   g1743354
NCBI GI
```



```
Match length
                   130
% identity
                   (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
NCBI Description
                   228794
Seq. No.
                   LIB3196-016-P1-M1-F11
Seq. ID
Method
                   BLASTX
                   q82207
NCBI GI
BLAST score
                   403
                   2.0e-39
E value
Match length
                   120
% identity
                   71
NCBI Description hypothetical protein 1708 - common tobacco chloroplast
                   228795
Seq. No.
                   LIB3196-016-P1-M1-F12
Seq. ID
Method
                   BLASTX
                   q1362804
NCBI GI
                   572
BLAST score
E value
                   4.0e-59
                   124
Match length
                    91
% identity
                   giantin - human >gi_405715_emb_CAA53052_ (X75304) giantin
NCBI Description
                    [Homo sapiens]
                    228796
Seq. No.
                   LIB3196-016-P1-M1-F7
Seq. ID
Method
                   BLASTX
                    g266691
NCBI GI
                    272
BLAST score
E value
                    4.0e-24
Match length
                    96
                    62
% identity
NCBI Description OLEOSIN 16.4 KD >gi_167361 (L00934) 16.4 kDa oleosin
                    [Gossypium hirsutum]
Seq. No.
                    228797
                    LIB3196-016-P1-M1-G4
Seq. ID
Method
                    BLASTX
NCBI GI
                    g113116
BLAST score
                    160
                    5.0e-11
E value
Match length
                    82
% identity
                    43
NCBI Description ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME)
                    >gi_111396_pir__A35007 ATP citrate (pro-S)-lyase (EC 4.1.3.8) - rat >gi_203490 (J05210) ATP citrate-lyase
                    [Rattus norvegicus]
                    228798
Seq. No.
Seq. ID
                    LIB3196-016-P1-M1-G5
Method
                    BLASTX
                    g1350762
NCBI GI
                    389
BLAST score
E value
                    1.0e-37
                    96
Match length
```

77

% identity



NCBI Description 60S RIBOSOMAL PROTEIN L6 (TAX-RESPONSIVE ENHANCER ELEMENT BINDING PROTEIN 107) (TAXREB107) (NEOPLASM-RELATED PROTEIN C140) >gi\_2136251\_pir\_\_151803 TAXREB107 - human

>gi 433416 dbj BAA04491 (D17554) TAXREB107 [Homo sapiens]

Seq. No. 228799

Seq. ID LIB3196-016-P1-M1-G9

Method BLASTX
NCBI GI g3668089
BLAST score 364
E value 6.0e-35
Match length 112
% identity 58

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 228800

Seq. ID LIB3196-016-P1-M1-H10

Method BLASTX
NCBI GI g91300
BLAST score 207
E value 8.0e-23
Match length 110
% identity 57

NCBI Description signal recognition particle 54K protein - mouse

Seq. No. 228801

Seq. ID LIB3196-016-P1-M1-H9

Method BLASTX
NCBI GI 94335724
BLAST score 174
E value 1.0e-12
Match length 121
% identity 39

NCBI Description (AC006248) putative RING-H2 finger protein [Arabidopsis

thaliana]

Seq. No. 228802

Seq. ID LIB3196-017-P1-M1-A1

Method BLASTX
NCBI GI g730832
BLAST score 169
E value 5.0e-12
Match length 53
% identity 57

NCBI Description 8.4 KD SULFUR-RICH PROTEIN PRECURSOR (SE60 PROTEIN)

(PROBABLE PROTEINASE INHIBITOR P322) >gi\_99949\_pir\_\_S24965 probable proteinase inhibitor (Bowman-Birk) p322 - soybean >gi\_18748 emb\_CAA78359 (Z13956) a protein similar to

>gi\_18748\_emb\_CAA78359\_ (Z13956) a protein similar to potato tuber protein p322 homolgous to Bowman-Birk

Proteinase Inhibitor [Glycine max]

Seq. No. 228803

Seq. ID LIB3196-017-P1-M1-A11

Method BLASTX
NCBI GI g1703146
BLAST score 590
E value 2.0e-61



```
116
Match length
                   100
% identity
                   ACTIN-LIKE PROTEIN 2 (ACTIN-LIKE PROTEIN ACTL)
NCBI Description
                   >gi 1079382 pir__JC4039 actin-like protein - chicken
                   >gi 806554 emb CAA52151 (X73971) actin-like protein
                   [Gallus gallus]
                   228804
Seq. No.
                   LIB3196-017-P1-M1-A12
Seq. ID
Method
                   BLASTX
                   g1239957
NCBI GI
BLAST score
                   276
                   1.0e-24
E value
                   109
Match length
                   59
% identity
                   (L38487) estrogen receptor-related protein [Homo sapiens]
NCBI Description
                   228805
Seq. No.
                   LIB3196-017-P1-M1-A4
Seq. ID
                   BLASTX
Method
                   g2809244
NCBI GI
                   192
BLAST score
                   1.0e-14
E value
                   87
Match length
                   47
% identity
                   (AC002560) F21B7.13 [Arabidopsis thaliana]
NCBI Description
                   228806
Seq. No.
                   LIB3196-017-P1-M1-A6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1703463
BLAST score
                   335
                   1.0e-31
E value
Match length
                   83
                   83
% identity
NCBI Description
                   POTASSIUM-TRANSPORTING ATPASE ALPHA-LIKE CHAIN (PROTON
                    PUMP) (NON-GASTRIC H+/K+ ATPASE ALPHA SUBUNIT) >gi_404017
                    (U02076) ATP-driven ion pump [Homo sapiens] >gi 1237010
                    (L42563) non-gastric H+, K+-ATPase [Homo sapiens]
                   >gi_1588308_prf__2208325A H/K-ATPase [Homo sapiens]
>gi_4502275_ref_NP_001667.1_pATP1AL1_ ATPase, Na+/K+
                    transporting, alpha polypeptide-like
                    228807
Seq. No.
Seq. ID
                    LIB3196-017-P1-M1-A9
Method
                    BLASTX
NCBI GI
                    g3337356
BLAST score
                    514
E value
                    2.0e-52
Match length
                    116
```

% identity 94

(AC004481) putative protein transport protein SEC61 alpha NCBI Description

subunit [Arabidopsis thaliana]

228808 Seq. No.

Seq. ID LIB3196-017-P1-M1-B1

Method BLASTX



```
NCBI GI
                   q3789925
                   232
BLAST score
                   2.0e-19
E value
Match length
                   90
% identity
                   51
                   (AF086625) phosphoinositide-dependent protein kinase PDK1
NCBI Description
                   [Mus musculus]
                   228809
Seq. No.
                   LIB3196-017-P1-M1-B10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3821280
                   415
BLAST score
                   4.0e-41
E value
Match length
                   86
                   88
% identity
                   (AJ009952) asparagine synthetase type II [Phaseolus
NCBI Description
                   vulgaris]
Seq. No.
                   228810
                   LIB3196-017-P1-M1-B11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g547299
BLAST score
                   550
                   1.0e-56
E value
Match length
                   99
                   100
% identity
                   beta 2-microglobulin, beta 2-M [Papio hamadryas=baboons,
NCBI Description
                   26CB-1, Peptide, 99 aa]
                   228811
Seq. No.
                   LIB3196-017-P1-M1-B12
Seq. ID
                   BLASTX
Method
                   g3004502
NCBI GI
                   631
BLAST score
                   4.0e-66
E value
                   121
Match length
                    97
% identity
                   (U97276) quiescin [Homo sapiens]
NCBI Description
                   >gi 4506361_ref_NP_002817.1_pQSCN6_ quiescin Q6
                    228812
Seq. No.
                   LIB3196-017-P1-M1-B2
Seq. ID
                   BLASTX
Method
                   g1346190
NCBI GI
                    447
BLAST score
                    2.0e-44
E value
Match length
                    89
                    96
% identity
NCBI Description GLUTAMATE--CYSTEINE LIGASE CATALYTIC SUBUNIT
                    (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS HEAVY
                    CHAIN) >gi_87540_pir__JH0611 glutamate--cysteine ligase (EC 6.3.2.2) heavy chain - human >gi_183039 (M90656)
                    gamma-glutamylcysteine synthetase [Homo sapiens]
                    >gi 4557625 ref_NP_001489.1_pGLCLC_ glutamate-cysteine
```

ligase



```
228813
Seq. No.
                   LIB3196-017-P1-M1-B5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2160166
                   246
BLAST score
                   4.0e-21
E value
                   108
Match length
                   48
% identity
                  (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                   228814
Seq. No.
                   LIB3196-017-P1-M1-B7
Seq. ID
                   BLASTX
Method
                   q2098705
NCBI GI
BLAST score
                   178
                   3.0e-13
E value
                   91
Match length
                   43
% identity
NCBI Description (U82973) pectinesterase [Citrus sinensis]
                   228815
Seq. No.
                   LIB3196-017-P1-M1-C10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q207905
BLAST score
                   522
                   2.0e-53
E value
                   103
Match length
                   99
% identity
NCBI Description (M18027) alpha globulin B [Artificial gene]
Seq. No.
                   228816
                   LIB3196-017-P1-M1-C12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2589011
BLAST score
                   563
                   3.0e-58
E value
Match length
                   119
                   53
% identity
                   (AB008549) type 1 procollagen C-proteinase enhancer protein
NCBI Description
                   [Homo sapiens] >gi 3135316 (AF053356) PCOLCE [Homo sapiens]
                   >qi 4322387 gb AAD16041_ (AF083655) procollagen
                   C-proteinase enhancer protein [Homo sapiens]
                   228817
Seq. No.
                   LIB3196-017-P1-M1-C3
Seq. ID
Method
                   BLASTX
                   g122007
NCBI GI
                   416
BLAST score
                    6.0e-41
E value
                   106
Match length
                   78
 % identity
NCBI Description HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley
                   >gi 20448 emb \overline{\text{CAA}37828} (X\overline{53}831) H2A histone protein (AA 1
                    - 149) [Petroselinum crispum]
```

228818 TJB3196-017-P1

Seq. ID LIB3196-017-P1-M1-C9

Seq. No.



```
BLASTX
Method
                   g137580
NCBI GI
                   173
BLAST score
                   7.0e-13
E value
                   36
Match length
                   97
% identity
                   VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72)
NCBI Description
                   >gi_72286_pir__FWCNAB alpha-globulin B precursor (clone
                   C72) - upland cotton >gi_167375 (M16891) vicilin precursor
                   [Gossypium hirsutum]
                   228819
Seq. No.
                   LIB3196-017-P1-M1-D1
Seq. ID
Method
                   BLASTX
                   q3901014
NCBI GI
                   280
BLAST score
                   5.0e-25
E value
                   62
Match length
                   79
% identity
                   (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                   sylvatica]
                   228820
Seq. No.
                   LIB3196-017-P1-M1-D12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g586120
                   231
BLAST score
                   3.0e-19
E value
                   102
Match length
                   49
% identity
                   TRICHOHYALIN >gi_539701 pir__A45973 trichohyalin - human
NCBI Description
                   >gi 292836 (L09190) trichohyalin [Homo sapiens]
                   228821
Seq. No.
                   LIB3196-017-P1-M1-D5
Seq. ID
                   BLASTX
Method
NCBI GI
                   a126156
BLAST score
                    432
                    7.0e-43
E value
                    106
Match length
% identity
                    79
                   LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
NCBI Description
                    >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134)
                    - upland cotton >gi 167373 (M16936) vicilin precursor
                    [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                    protein C134 [Saguinus oedipus]
Seq. No.
                    228822
                    LIB3196-017-P1-M1-D6
Seq. ID
Method
                    BLASTX
NCBI GI
                    q3834307
BLAST score
                    322
                    6.0e-30
E value
Match length
                    121
```

32755

NCBI Description (AC005679) Strong similarity to gene T10I14.120 gi\_2832679

50

% identity



putative protein from Arabidopsis thaliana BAC gb\_AL021712. ESTs gb\_N65887 and gb\_N65627 come from this gene. [Arabidopsis thaliana]

Seq. No. 228823 LIB3196-017-P1-M1-D8 Seq. ID Method BLASTX NCBI GI g2262170 BLAST score 344 E value 2.0e-32 122 Match length 57 % identity

NCBI Description (AC002329) predicted glycosyl hydrolase [Arabidopsis

thaliana]

Seq. No. 228824

Seq. ID LIB3196-017-P1-M1-D9

Method BLASTX
NCBI GI g126156
BLAST score 215
E value 6.0e-19
Match length 65
% identity 78

NCBI Description LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)

>gi\_72288\_pir\_\_FWCNBB beta-globulin B precursor (clone 134)
- upland cotton >gi\_167373 (M16936) vicilin precursor
[Gossypium hirsutum] >gi\_1171335 (U43727) legumin B
[Gossypium hirsutum] >gi\_225582\_prf\_\_1306412C storage

protein C134 [Saguinus oedipus]

Seq. No. 228825

Seq. ID LIB3196-017-P1-M1-E1

Method BLASTX
NCBI GI g130770
BLAST score 561
E value 6.0e-58
Match length 121
% identity 88

NCBI Description PHOSPHATIDYLINOSITOL TRANSFER PROTEIN ALPHA ISOFORM (PTDINS

TRANSFER PROTEIN ALPHA) (PTDINSTP) (PI-TP-ALPHA)

>gi\_2135910\_pir\_\_I53775 phosphatidylinositol transfer
protein - human >gi\_189939 (M73704) phosphatidylinositol

transfer protein [Homo sapiens]

Seq. No. 228826

Seq. ID LIB3196-017-P1-M1-E11

Method BLASTX
NCBI GI g1174592
BLAST score 573
E value 2.0e-59
Match length 114
% identity 100

NCBI Description TUBULIN ALPHA-1 CHAIN >gi\_2119270\_pir\_\_S60233 alpha-tubulin

- garden pea >gi 525332 (U12589) alpha-tubulin [Pisum

sativum]

Seq. No. 228827



```
Seq. ID
                  LIB3196-017-P1-M1-E2
Method
                  BLASTX
NCBI GI
                  q4063760
BLAST score
                  179
                  4.0e-13
E value
Match length
                  55
                  58
% identity
NCBI Description
                  (AC005561) putative POL3 protein [Arabidopsis thaliana]
                  228828
Seq. No.
Seq. ID
                  LIB3196-017-P1-M1-E3
Method
                  BLASTX
                  q2160517
NCBI GI
BLAST score
                  325
E value
                  3.0e-30
Match length
                  89
                  79
% identity
NCBI Description
                 (U42408) ladinin [Homo sapiens]
                  228829
Seq. No.
                  LIB3196-017-P1-M1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1946355
BLAST score
                  152
                  5.0e-10
E value
Match length
                  109
                   35
% identity
                  (U93215) maize transposon MuDR mudrA protein isolog
NCBI Description
                   [Arabidopsis thaliana] >gi_2880040 (AC002340) maize
                  transposon MuDR mudrA-like protein [Arabidopsis thaliana]
Seq. No.
                   228830
                  LIB3196-017-P1-M1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2833280
BLAST score
                   621
E value
                   6.0e-65
Match length
                  128
% identity
                   92
                  NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR
NCBI Description
                   (COMPLEX I-39KD) (CI-39KD)
                   228831
Seq. No.
Seq. ID
                  LIB3196-017-P1-M1-F10
Method
                  BLASTX
NCBI GI
                  g683553
BLAST score
                  179
E value
                   3.0e-13
Match length
                   44
                   77
% identity
NCBI Description
                  (Z48450) oleosin-like protein [Citrus sinensis]
                   >gi 1582679 prf 2119230A oleosin homolog [Citrus sinensis]
                   228832
Seq. No.
Seq. ID
                  LIB3196-017-P1-M1-F3
Method
                  BLASTX
NCBI GI
                   g3413706
```

E value

Match length

% identity

9.0e-38



```
460
BLAST score
                  4.0e-46
E value
                  117
Match length
                  68
% identity
                  (AC004747) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  228833
Seq. No.
                  LIB3196-017-P1-M1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3335375
BLAST score
                  606
E value
                  3.0e-63
Match length
                  117
                  97
% identity
                  (AC003028) putative amidase [Arabidopsis thaliana]
NCBI Description
                  228834
Seq. No.
                  LIB3196-017-P1-M1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1362107
BLAST score
                  177
                   5.0e-13
E value
Match length
                  44
                  82
% identity
NCBI Description GUT8-2a protein - common tobacco
Seq. No.
                   228835
                  LIB3196-017-P1-M1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4191319
BLAST score
                   162
                   3.0e-11
E value
Match length
                   31
                   100
% identity
                  (AF044670) 33 kDa Vamp-associated protein; VAP-33 [Homo
NCBI Description
                   sapiens] >gi 4240456 (AF086627) VAMP-associated protein A
                   [Homo sapiens]
Seq. No.
                   228836
                   LIB3196-017-P1-M1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2119228
BLAST score
                   188
E value
                   3.0e-14
Match length
                   67
% identity
                   60
NCBI Description keratin K4a - human (fragment) >gi 313159 emb CAA47914_
                   (X67683) keratin K4a [Homo sapiens]
Seq. No.
                   228837
                   LIB3196-017-P1-M1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2583135
                   389
BLAST score
```



NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]

>gi\_3822216 (AF074948) FIL [Arabidopsis thaliana]

>gi\_4322477\_gb\_AAD16053\_ (AF087015) abnormal floral organs
protein [Arabidopsis thaliana]

Seq. No.

228838

Seq. ID

LIB3196-017-P1-M1-G9

Method

BLASTX

NCBI GI

RLAST score

285

NCBI GI g117501
BLAST score 285
E value 8.0e-26
Match length 54
% identity 96

NCBI Description CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60)

(52 KD RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A)

>gi\_87015\_pir\_\_A37047 calreticulin precursor - human

 $>gi_179882$  (M84739) calreticulin [Homo sapiens]  $>gi_337487$ 

(M32294) Ro ribonucleoprotein autoantigen (Ro/SS-A) precursor [Homo sapiens] >gi 1905911 (AD000092)

calreticulin [Homo sapiens]

Seq. No. 228839

Seq. ID LIB3196-017-P1-M1-H1

Method BLASTX
NCBI GI g224293
BLAST score 375
E value 3.0e-36
Match length 76
% identity 100

NCBI Description histone H4 [Triticum aestivum]

Seq. No. 228840

Seq. ID LIB3196-017-P1-M1-H10

Method BLASTX
NCBI GI g2894607
BLAST score 359
E value 3.0e-34
Match length 101
% identity 65

NCBI Description (AL021889) NAM (no apical meristem) - like protein

[Arabidopsis thaliana]

Seq. No. 228841

Seq. ID LIB3196-017-P1-M1-H11

Method BLASTX
NCBI GI g2384671
BLAST score 407
E value 4.0e-40
Match length 91
% identity 85

NCBI Description (AF012657) putative potassium transporter AtKT2p

[Arabidopsis thaliana]

Seq. No. 228842

Seq. ID LIB3196-017-P1-M1-H5

Method BLASTX NCBI GI g683553



```
272
BLAST score
                   4.0e-24
E value
                   104
Match length
                   57
% identity
                   (Z48450) oleosin-like protein [Citrus sinensis]
NCBI Description
                   >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]
                   228843
Seq. No.
                   LIB3196-017-P1-M1-H6
Seq. ID
                   BLASTX
Method
                   g4580472
NCBI GI
                   545
BLAST score
                   5.0e-56
E value
                   114
Match length
                   86
% identity
                   (AC006081) DNA binding protein; similar to CDC27 and nuclear
NCBI Description
                   scaffold proteins [Arabidopsis thaliana]
                    228844
Seq. No.
                   LIB3196-017-P1-M1-H8
Seq. ID
                    BLASTX
Method
                    g113287
NCBI GI
                    551
BLAST score
                    9.0e-57
E value
                    105
Match length
                    100
% identity
                   ACTIN, ALPHA SKELETAL MUSCLE (ALPHA-ACTIN 1)
NCBI Description
                    >gi_71610_pir__ATHU actin, skeletal muscle - human
                   >gi_71612_pir__ATRT actin, skeletal muscle - rat
                    >gi_71613_pir__ATCH actin alpha, skeletal muscle - chicken
                    >gi_90264_pir__A24904 actin, skeletal muscle - mouse
                    >gi_55577_emb_CAA24529_ (V01218) actin [Rattus norvegicus] >gi_63029_emb_CAA24753_ (V01507) a-actin [Gallus gallus]
                    >gi_17802\overline{9} (J\overline{0}0068) alpha-actin [Homo sapiens] >gi_309088
                    (M1\overline{2}866) actin [Mus musculus] >gi 337746 (M20543)
                    alpha-skeletal actin precursor [Homo sapiens] >gi_387081
                    (M12347) alpha-actin [Mus musculus] >gi_790202 (U16368)
                    skeletal alpha actin [Sus scrofa] >gi_223503_prf__0809315A
                    actin [Rattus norvegicus]
                    >gi_4501881_ref_NP_001091.1_pACTA1_ actin, alpha 1,
                    skeletal muscle
Seq. No.
                    228845
                    LIB3196-018-P1-M1-A10
Seq. ID
                    BLASTX
Method
                    q1076510
NCBI GI
BLAST score
                    446
E value
                    2.0e-44
Match length
                    107
% identity
                    peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean
NCBI Description
                    >gi_829119_emb_CAA52414_ (X74403) cyclophilin [Phaseolus
                    vulgaris]
```

Seq. No. 228846

Seq. ID LIB3196-018-P1-M1-A12

Method BLASTX



```
NCBI GI
                  g3786007
                  276
BLAST score
                  1.0e-24
E value
                  104
Match length
                  59
% identity
                  (AC005499) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  228847
Seq. No.
                  LIB3196-018-P1-M1-A2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3688191
BLAST score
                  196
                  3.0e-15
E value
Match length
                  63
                  63
% identity
                  (AJ010090) MAP3K alpha protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                   228848
Seq. No.
                  LIB3196-018-P1-M1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g137578
BLAST score
                   497
                   2.0e-50
E value
Match length
                   118
                   79
% identity
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                   >gi_81545_pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                   [Artificial gene] >gi 226119 prf 1410330A vicilin gene A
                   [Saguinus oedipus]
                   228849
Seq. No.
                   LIB3196-018-P1-M1-A6
Seq. ID
                   BLASTX
Method
                   g2244754
NCBI GI
                   465
BLAST score
                   1.0e-46
E value
                   97
Match length
                   84
% identity
                  (Z97335) heat shock transcription factor homolog
NCBI Description
                   [Arabidopsis thaliana]
                   228850
Seq. No.
                   LIB3196-018-P1-M1-B11
Seq. ID
                   BLASTX
Method
                   g2879792
NCBI GI
                   129
BLAST score
                   2.0e-16
E value
                   88
Match length
```

60 % identity (AL021813) SPAC23A1.04c, possible glycosyl hydrolase, NCBI Description len:756aa, similar eg. to C. elegans Q18679, (586aa), fasta

scores, opt:566, E():0, (48.0% identity in 452 aa overlap), also similar to YHR204W, YH04\_YEAST, P38888, hypothet



```
Seq. No.
                   228851
                   LIB3196-018-P1-M1-B2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q226407
BLAST score
                   290
                   3.0e-26
E value
Match length
                   121
% identity
                   46
                   retrotransposon del1-46 [Lilium henryi]
NCBI Description
                   228852
Seq. No.
                   LIB3196-018-P1-M1-B4
Seq. ID
Method
                   BLASTX
                   g2224931
NCBI GI
                   312
BLAST score
                   9.0e-29
E value
Match length
                   119
% identity
                   57
                   (AF004215) ethylene-insensitive3-like3 [Arabidopsis
NCBI Description
                   thaliana]
                   228853
Seq. No.
                   LIB3196-018-P1-M1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1375485
BLAST score
                   631
                   4.0e-66
E value
Match length
                   119
% identity
                   100
                  (U43077) CDC37 homolog [Homo sapiens] >gi_1421821 (U63131)
NCBI Description
                   CDC37 homolog [Homo sapiens]
                   228854
Seq. No.
                   LIB3196-018-P1-M1-C5
Seq. ID
                   BLASTX
Method
                   g280816
NCBI GI
                   441
BLAST score
                   7.0e-44
E value
                   86
Match length
                   99
% identity
NCBI Description keratin 13, type I, cytoskeletal, short form - human
                   >gi_30377_emb_CAA36673_ (X52426) cytokeratin 13 [Homo sapiens] >gi_3603253 (AF049259) keratin 13 [Homo sapiens]
                   >gi 4504911 ref NP 002265.1 pKRT13 keratin
                   228855
Seq. No.
                   LIB3196-018-P1-M1-C7
Seq. ID
                   BLASTX
Method
                   g3445207
NCBI GI
BLAST score
                    306
                    3.0e-28
E value
                   99
Match length
                    64
% identity
NCBI Description (AC004786) unknown protein [Arabidopsis thaliana]
```

Seq. No. 228856

Seq. ID LIB3196-018-P1-M1-C8



Method BLASTX
NCBI GI g3096949
BLAST score 262
E value 2.0e-25
Match length 98
% identity 62

NCBI Description (Y16328) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana] >gi\_3894399 (AF067798) cyclic nucleotide-gated cation channel [Arabidopsis thaliana]

Seq. No. 228857

Seq. ID LIB3196-018-P1-M1-C9

Method BLASTX
NCBI GI g1070592
BLAST score 590
E value 2.0e-61
Match length 114
% identity 100

NCBI Description ubiquitin / ribosomal protein CEP52 - human

>gi\_37565\_emb\_CAA40313\_ (X56998) ubiquitin-52 amino acid
fusion protein [Homo sapiens] >gi\_37567\_emb\_CAA40312\_
(X56997) ubiquitin-52 amino acid fusion protein [Homo
sapiens] >gi\_37569\_emb\_CAA40314\_ (X56999) ubiquitin-52
amino acid fusion protein [Homo sapiens] >gi\_600538

(M24508) ubiquitin [Artificial sequence]

>gi\_1050758\_emb\_CAA57958\_ (X82636) ubiquitin/ribosomal
protein L40 [Rattus norvegicus] >gi 1628608 (U72496)

ubiquitin/ribosomal fusion protein [Sus scrofa] >gi\_3288887 (AC005253) ubiquitin-52 amino acid fusion protein [Homo sapiens] >gi\_4139066 (AF081142) ubiquitin/ribosomal protein

CEP52 fusion protein [Cricetulus sp.]

>gi\_4262555\_gb\_AAD14688\_ (AF118402) ubiquitin/60S ribosomal

fusion protein [Mus musculus]

>gi\_4507761\_ref\_NP\_003324.1\_pUBA52\_ ubiquitin A-52 residue

ribosomal protein fusion product

Seq. No. 228858

Seq. ID LIB3196-018-P1-M1-D10

Method BLASTX
NCBI GI g125077
BLAST score 238
E value 4.0e-20
Match length 52
% identity 94

NCBI Description KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK

13) >gi\_71526\_pir\_\_KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi\_34033 emb CAA32786 (X14640) keratin

13 [Homo sapiens]

Seq. No. 228859

Seq. ID LIB3196-018-P1-M1-D2

Method BLASTX
NCBI GI g123101
BLAST score 316
E value 2.0e-29
Match length 80
% identity 81

BLAST score

Match length

% identity

E value

453

88 53

3.0e-45



NCBI Description NONHISTONE CHROMOSOMAL PROTEIN HMG-14 >gi\_107207\_pir\_\_A33310 nonhistone chromosomal protein HMG-14 - human >gi\_306863 (J02621) high mobility group protein 14 [Homo sapiens] >gi 386779 (M21339) high mobility group protein 14 [Homo sapiens] >gi 3171155 (AF064861) HMG-14 [Homo sapiens] 228860 Seq. No. LIB3196-018-P1-M1-D4 Seq. ID Method BLASTX NCBI GI g2392771 BLAST score 321 E value 6.0e-30 94 Match length % identity 65 (AC002534) putative kinesin-like protein [Arabidopsis NCBI Description thaliana] 228861 Seq. No. LIB3196-018-P1-M1-D5 Seq. ID Method BLASTX NCBI GI g2088654 BLAST score 526 E value 7.0e-54Match length 117 % identity 88 NCBI Description (AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana] 228862 Seq. No. LIB3196-018-P1-M1-D7 Seq. ID Method BLASTX g435480 NCBI GI BLAST score 313 E value 5.0e-29 Match length 78 % identity 78 NCBI Description (X76679) MAL-b [Homo sapiens] 228863 Seq. No. Seq. ID LIB3196-018-P1-M1-E10 Method BLASTX NCBI GI q3063396 BLAST score 432 E value 7.0e-43Match length 99 -% identity 82 NCBI Description (AB012947) vcCyP [Vicia faba] Seq. No. 228864 Seq. ID LIB3196-018-P1-M1-E4 Method BLASTX NCBI GI q115502



NCBI Description CALMODULIN-RELATED PROTEIN NB-1 (CALMODULIN-LIKE PROTEIN) (CLP) >gi\_71690\_pir\_\_MCHUNB calmodulin~related protein NB-1 - human >gi\_29650\_emb\_CAA31809\_ (X13461) hGH6 calmodulin-like protein [Homo sapiens] >gi\_189081 (M58026) NB-1 [Homo sapiens] 228865 Seq. No. LIB3196-018-P1-M1-E5 Seq. ID BLASTX Method g2245020 NCBI GI 526 BLAST score 7.0e-54 E value 120 Match length % identity 81 (Z97341) growth regulator homolog [Arabidopsis thaliana] NCBI Description 228866 Seq. No. LIB3196-018-P1-M1-F1 Seq. ID BLASTX Method q3851636 NCBI GI 471 BLAST score 2.0e-47 E value Match length 107 % identity 82 (AF098519) unknown [Avicennia marina] >gi\_4128206 NCBI Description (AF056316) 40S ribosome protein S7 [Avicennia marina] Seq. No. 228867 LIB3196-018-P1-M1-F10 Seq. ID BLASTX Method g2119180 NCBI GI 519 BLAST score E value 5.0e-53 118 Match length 94 % identity NCBI Description S-laminin - human (fragment) >gi\_288401\_emb\_CAA51288\_ (X72760) S-laminin [Homo sapiens] 228868 Seq. No. LIB3196-018-P1-M1-F11 Seq. ID Method BLASTX g2137594 NCBI GI BLAST score 168 7.0e-12 E value 46 Match length 65 % identity neuropsin - mouse >gi\_1020091\_dbj\_BAA06451\_ (D30785) NCBI Description neuropsin [Mus musculus] >gi\_\overline{1582323\_prf}\_\overline{2118319A} neuropsin [Mus musculus] 228869 Seq. No. Seq. ID LIB3196-018-P1-M1-F7

Method BLASTX g114682 NCBI GI 162 BLAST score 2.0e-11 E value Match length 59



```
% identity
                  ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)
                  >gi_100471_pir__A35227 H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, mitochondrial - sweet
                  potato >qi 168270 (J05397) F-1-ATPase delta subunit
                  precursor (EC 3.6.1.3) [Ipomoea batatas]
                  228870
Seq. No.
                  LIB3196-018-P1-M1-G10
Seq. ID
                  BLASTX
Method
                  q419482
NCBI GI
BLAST score
                  185
                  7.0e-14
E value
                  111
Match length
                  43
% identity
NCBI Description pol polyprotein - human endogenous virus S71
Seq. No.
                   228871
Seq. ID
                  LIB3196-018-P1-M1-G11
                   BLASTX
Method
                   q2190550
NCBI GI
                   456
BLAST score
E value
                   1.0e-45
                   122
Match length
% identity
                  (AC001229) ESTs gb T45673, gb N37512 come from this gene.
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   228872
                   LIB3196-018-P1-M1-G12
Seq. ID
                   BLASTX
Method
                   g2119204
NCBI GI
BLAST score
                   194
E value
                   6.0e-15
Match length
                   62
                   66
% identity
                  vimentin - human >gi_37850_emb_CAA39600_ (X56134) vimentin
NCBI Description
                   [Homo sapiens]
Seq. No.
                   228873
                   LIB3196-018-P1-M1-G2
Seq. ID
                   BLASTX
Method
                   q3355465
NCBI GI
BLAST score
                   382
                   5.0e-37
E value
                   114
Match length
                   62
% identity
                  (AC004218) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   228874
Seq. No.
                   LIB3196-018-P1-M1-G3
Seq. ID
```

Method BLASTX
NCBI GI g2605714

BLAST score 243 E value 1.0e-20



```
63
Match length
                  79
% identity
                  (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
NCBI Description
                  thaliana]
                  228875
Seq. No.
                  LIB3196-018-P1-M1-G4
Seq. ID
                  BLASTX
Method
                  g2507389
NCBI GI
                  617
BLAST score
                  2.0e-64
E value
                  124
Match length
                  94
% identity
                  SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
:NCBI Description
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi 1848137 emb CAA62998_ (X91902) serine
                  hydroxymethyltransferase [Oryctolagus cuniculus]
                   228876
Seq. No.
                  LIB3196-018-P1-M1-G5
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2119340
BLAST score
                   666
                   3.0e-70
E value
                   127
Match length
                   98
% identity
                  calponin - human >gi_1526432_dbj_BAA12090_ (D83735) neutral
NCBI Description
                   calponin [Homo sapiens]
                   228877
Seq. No.
                  LIB3196-018-P1-M1-G7
Seq. ID
                   BLASTX
Method
                   g1174637
NCBI GI
                   175
BLAST score
E value
                   1.0e-12
                   37
Match length
% identity
                   97
NCBI Description TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE (TER ATPASE) (15S
                   MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN)
                   (VCP) >gi_1083817_pir__A55190 transitional endoplasmic
                   reticulum ATPase - rat >qi 641973 (U11760) transitional
                   endoplasmic reticulum ATPase [Rattus norvegicus]
                   >gi 1093322_prf__2103265A transitional endoplasmic
                   reticulum ATPase [Rattus norvegicus]
                   228878
Seq. No.
Seq. ID
                   LIB3196-018-P1-M1-H1
Method
                   BLASTX
NCBI GI
                   q477094
                   243
BLAST score
                   1.0e-20
E value
```

115 Match length % identity 47

NCBI Description STE11 protein kinase homolog NPK1 - common tobacco

Seq. No. 228879

LIB3196-018-P1-M1-H4 Seq. ID



```
Method
                   BLASTX
NCBI GI
                   g1906828
                   390
BLAST score
                   7.0e-38
E value
                   123
Match length
                   70
% identity
NCBI Description
                   (Y11828) heat shock protein [Arabidopsis thaliana]
                   228880
Seq. No.
                   LIB3196-018-P1-M1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g114181
BLAST score
                   183
                   1.0e-13
E value
Match length
                   84
                   49
 % identity
                   3-DEHYDROQUINATE SYNTHASE >gi 68385 pir SYECQ
NCBI Description
                   3-dehydroquinate synthase (EC 4.6.1.3) - Escherichia coli
                   >gi_40968_emb_CAA27495_ (X03867) 3-dehydroquinate synthase
                   (aa 1-362) [Escherichia coli] >gi_41225_emb_CAA79666
                   (Z19601) ORF, aroB. Millar G., Coggins J.R.; FEBS Lett.
                   200:11-17(1986) [Escherichia coli] >gi_606323 (U18997)
                   3-dehydroquinate synthase [Escherichia coli] >gi_1789791
                   (AE000414) 3-dehydroquinate synthase [Escherichia coli]
 Seq. No.
                   228881
                   LIB3196-019-P1-M1-A1
 Seq. ID
Method
                   BLASTX
NCBI GI
                   q4432854
BLAST score
                   146
                   3.0e-09
E value
                   57
Match length
                   47
 % identity
                  (AC006300) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   228882
 Seq. No.
                   LIB3196-019-P1-M1-A10
 Seq. ID
Method
                   BLASTX
NCBI GI
                   q547753
 BLAST score
                   576
                   1.0e-59
 E value
Match length
                   120
 % identity
                   96
NCBI Description KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)
                   228883
 Seq. No.
                   LIB3196-019-P1-M1-A12
 Šėq. ID
Method
                   BLASTX
                   g81546
 NCBI GI
 BLAST score
                   547
 E value
                   2.0e-56
Match length
                   106
% identity
                   100
 NCBI Description alpha-globulin type B precursor (tandem 1) - upland cotton
                   (fragment)
```

Seq. No. 228884

Seq. No.

Seq. ID

228889

LIB3196-019-P1-M1-B6



```
Seq. ID
                   LIB3196-019-P1-M1-A3
                   BLASTX
Method
NCBI GI
                   q1843527
BLAST score
                   330
                   5.0e-31
E value
Match length
                   91
                   76
% identity
NCBI Description
                  (U73747) annexin [Gossypium hirsutum]
                   228885
Seq. No.
Seq. ID
                   LIB3196-019-P1-M1-B10
Method
                   BLASTX
NCBI GI
                   g3123271
BLAST score
                   446
E value
                   2.0e-44
Match length
                   104
                   81
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S6 >gi 2224751 emb CAA74381 (Y14052)
                   ribosomal protein S6 [Arabidopsis thaliana]
                   228886
Seq. No.
                   LIB3196-019-P1-M1-B2
Seq. ID
Method
                 · BLASTX
NCBI GI
                   q88052
BLAST score
                   548
E value
                   1.0e-56
Match length
                   108
                   100
% identity
NCBI Description keratin K5, 58K type II, epidermal (version 2) - human
                   (fragment)
                   228887
Seq. No.
                   LIB3196-019-P1-M1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3738302
BLAST score
                   494
E value
                   4.0e-50
Match length
                   115
% identity
                   81
                   (AC005309) tubby-like protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4249398 (AC006072) putative tubby protein [Arabidopsis
                   thaliana]
                   228888
Seq. No.
Seq. ID
                   LIB3196-019-P1-M1-B5
Method
                   BLASTX
NCBI GI
                   g3184186
BLAST score
                   332
E value
                   4.0e-31
                   115
Match length
% identity
                   61
                   (AB004788) BNIP3L [Homo sapiens] >gi_3342915 (AF079221)
NCBI Description
                   BCL2/adenovirus E1B 19kDa-interacting protein 3a [Homo
                   sapiens] >gi 4138826 (AF067396) NIX [Homo sapiens]
```



BLASTX Method g280816 NCBI GI 627 BLAST score 1.0e-65 E value Match length 126 98 % identity

keratin 13, type I, cytoskeletal, short form - human NCBI Description >gi\_30377\_emb\_CAA36673\_ (X52426) cytokeratin 13 [Homo sapiens]  $\overline{gi}_{3603253}$  ( $\overline{A}F049259$ ) keratin 13 [Homo sapiens]

>gi 4504911\_ref\_NP\_002265.1\_pKRT13\_ keratin

228890 Seq. No.

LIB3196-019-P1-M1-B7 Seq. ID

Method BLASTX g3876053 NCBI GI BLAST score 167 9.0e-12 E value 105 Match length 33 % identity

(Z69789) cDNA EST EMBL:D66552 comes from this gene; cDNA NCBI Description

EST EMBL: D70371 comes from this gene; cDNA EST EMBL: C11164 comes from this gene; cDNA EST EMBL:C13175 comes from this gene; cDNA EST yk270e3.3 comes from this gene; cDNA  $\dots$ >gi\_3878811\_emb\_CAA93682\_ (Z69794) cDNA EST EMBL:D66552 comes from this gene; cDNA EST EMBL: D70371 comes from this gene; cDNA EST EMBL:C11164 comes from this gene; cDNA EST EMBL: C13175 comes from this gene; cDNA EST yk270e3.3 comes

from this gene; cDNA

228891 Seq. No.

LIB3196-019-P1-M1-C1 Seq. ID

Method BLASTX NCBI GI q547753 392 BLAST score 3.0e-38 E value Match length 87

% identity 90

NCBI Description KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)

228892 Seq. No.

LIB3196-019-P1-M1-C10 Seq. ID

Method BLASTX NCBI GI q1778838 BLAST score 560 7.0e-58E value Match length 122 % identity

NCBI Description (U83113) INS-1 winged-helix homolog [Homo sapiens]

228893 Seq. No.

Seq. ID LIB3196-019-P1-M1-C12

BLASTX Method NCBI GI q4263790 BLAST score 524 E value 1.0e-53 Match length 113 % identity 91



(AC006068) putative ch-TOG protein [Arabidopsis thaliana] NCBI Description Seq. No. 228894 LIB3196-019-P1-M1-C3 Seq. ID BLASTX Method q3901014 NCBI GI BLAST score 234 1.0e-19 E value Match length 55 76 % identity (AJ130886) metallothionein-like protein class II [Fagus NCBI Description sylvatica] 228895 Seq. No. LIB3196-019-P1-M1-C4 Seq. ID Method BLASTX q2605714 NCBI GI BLAST score 222 3.0e-18 E value Match length 57 81 % identity (AF026275) beta-tonoplast intrinsic protein [Arabidopsis NCBI Description thaliana] 228896 Seq. No. LIB3196-019-P1-M1-C8 Seq. ID Method BLASTX NCBI GI g2245104 BLAST score 150 8.0e-10 E value 105 Match length 34 % identity (Z97343) LTR retrotransposon [Arabidopsis thaliana] NCBI Description 228897 Seq. No. LIB3196-019-P1-M1-D1 Seq. ID BLASTX Method g3947448 NCBI GI 279 BLAST score E value 6.0e-25 115 Match length 50 % identity (AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA NCBI Description EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene [Caenorhabdi... >gi\_3947543\_emb\_CAA88952\_ (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene [Caenorhabditi 228898 Seq. No. LIB3196-019-P1-M1-D10 Seq. ID

Method BLASTX NCBI GI g125080 BLAST score 148



E value 1.0e-09 Match length 58 % identity 57

NCBI Description KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK

14) >gi\_2144816\_pir\_\_KRHUE keratin, 50K type I cytoskeletal

- human >gi 386848 (J00124) keratin [Homo sapiens] >qi 4504913 ref NP 000517.1 pKRT14 keratin 14

(epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No. 228899

Seq. ID LIB3196-019-P1-M1-D11

Method BLASTX
NCBI GI g3201554
BLAST score 232
E value 1.0e-19
Match length 88
% identity 56

NCBI Description (AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No. 228900

Seq. ID LIB3196-019-P1-M1-D12

Method BLASTX
NCBI GI g464986
BLAST score 416
E value 5.0e-41
Match length 77
% identity 97

% identity

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN

LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi\_421857\_pir\_\_S32674 ubiquitin--protein ligase (EC

6.3.2.19) UBC9 - Arabidopsis thaliana

>gi\_297884\_emb\_CAA78714\_ (Z14990) ubiquitin conjugating
enzyme homolog [Arabidopsis thaliana] >gi\_349211 (L00639)

ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi\_600391\_emb\_CAA51201\_ (X72626) ubiquitin conjugating

enzyme E2 [Arabidopsis thaliana]

>gi\_4455355\_emb\_CAB36765.1\_ (AL035524) ubiquitin-protein

ligase UBC9 [Arabidopsis thaliana]

Seq. No. 228901

Seq. ID LIB3196-019-P1-M1-D2

Method BLASTX
NCBI GI g1710840
BLAST score 542
E value 9.0e-56
Match length 118
% identity 84

NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE

HYDROLASE) (ADOHCYASE) (CYTOKININ BINDING PROTEIN CBP57)
>gi\_441217\_dbj\_BAA03709\_(D16138) S-adenosyl-L-homocystein
hydrolase [Nicotiana sylvestris] >gi\_1857024\_dbj\_BAA08142\_
(D45204) S-adenosyl-L-homocysteine hydrolase [Nicotiana

tabacum] >gi\_2588781\_dbj\_BAA23164\_ (D49804)

S-adenosyl-L-homocysteine hydrolase [Nicotiana tabacum]

Seq. No. 228902

Seq. ID LIB3196-019-P1-M1-D5

NCBI Description



```
Method
                  BLASTX
NCBI GI
                  g124224
                  462
BLAST score
                  2.0e-46
E value
                  103
Match length
                  87
% identity
                  INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)
NCBI Description
                   >gi_100345_pir__S21060 translation initiation factor eIF-5A
                   - common tobacco >gi 19887_emb_CAA45105_ (X63543)
                   eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]
Seq. No.
                   228903
                  LIB3196-019-P1-M1-D7
Seq. ID
                  BLASTX
Method
                   q3868758
NCBI GI
BLAST score
                   400
                   4.0e-39
E value
Match length
                  73
                   96
% identity
                  (D89802) elongation factor 1B gamma [Oryza sativa]
NCBI Description
                   228904
Seq. No.
                  LIB3196-019-P1-M1-E1
Seq. ID
                   BLASTX
Method
                  ~g1363944
NCBI GI
                   480
BLAST score
                   2.0e-48
E value
                   97
Match length
                   97
% identity
                  type I keratin 16 - human >gi_1195531_bbs_172338 (S79867)
NCBI Description
                   type I keratin 16, K16 [human, epidermal keratinocytes,
                   Peptide, 473 aa] [Homo sapiens]
                   228905
Seq. No.
                   LIB3196-019-P1-M1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3915742
BLAST score
                   577
                   7.0e-60
E value
                   112
Match length
                   98
% identity
                  LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi 167319
NCBI Description
                   (M69188) legumin A [Gossypium hirsutum]
                   >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele
                   [Gossypium hirsutum]
                   228906
Seq. No.
Seq. ID
                   LIB3196-019-P1-M1-E11
Method
                   BLASTX
NCBI GI
                   q49868
BLAST score
                   625
                   2.0e-65
E value
Match length
                   124
% identity
                   100
```

(X03765) put. beta-actin (aa 27-375) [Mus musculus]

>gi 387083 (M12481) cytoplasmic beta-actin [Mus musculus]



Seq. No. 228907 LIB3196-019-P1-M1-E12 Seq. ID Method BLASTX NCBI GI g3880433 BLAST score 259 2.0e-22 E value Match length 95 % identity 28 (Z66521) similar to mitochondrial RNA splicing MSR4 like NCBI Description protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans] Seq. No. 228908 LIB3196-019-P1-M1-E3 Seq. ID BLASTX-Method q4056469 NCBI GI BLAST score 274 2.0e-24 E value Match length 85 74 % identity (AC005990) Strong similarity to gb\_M95166 ADP-ribosylation NCBI Description factor from Arabidopsis thaliana. ESTs gb\_Z25826, gb R90191, gb N65697, gb AA713150, gb\_T46332, gb\_AA040967, gb AA712956, gb T46403, gb T46050, gb AI100391 and gb\_Z25043 come from t 228909 Seq. No. Seq. ID LIB3196-019-P1-M1-E5 Method BLASTX g3859591 NCBI GI 199 BLAST score 2.0e-15 E value 87 Match length % identity 43 (AF104919) No definition line found [Arabidopsis thaliana] NCBI Description 228910 Seq. No. LIB3196-019-P1-M1-E6 Seq. ID Method BLASTX g3915742 NCBI GI 554 BLAST score 4.0e-57 E value 117 Match length % identity 91 NCBI Description LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi\_167319 (M69188) legumin A [Gossypium hirsutum] >gi\_444320\_prf\_\_1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum] 228911 Seq. No. LIB3196-019-P1-M1-E9 Seq. ID Method BLASTX NCBI GI q3915742

Method BLASTX
NCBI GI g3915742
BLAST score 513
E value 2.0e-52
Match length 110
% identity 89



```
LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi 167319
NCBI Description
                   (M69188) legumin A [Gossypium hirsutum]
                   >gi_444320 prf__1906369A legumin A:ISOTYPE=D alloallele
                   [Gossypium hirsutum]
                   228912
Seq. No.
                   LIB3196-019-P1-M1-F1
Seq. ID
Method
                   BLASTX
                   q2618721
NCBI GI
BLAST score
                   168
                   6.0e-12
E value
                   102
Match length
% identity
                   50
                   (U49072) IAA16 [Arabidopsis thaliana]
NCBI Description
                   228913
Seq. No.
                   LIB3196-019-P1-M1-F4
Seq. ID
                   BLASTX
Method
NCBI GI
                    q1346347
                    594
BLAST score
                    8.0e-62
E value
                    124
Match length
                    97
% identity
                   KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D)
NCBI Description
                    (K6D KERATIN) >gi_2119225_pir__161769 keratin type II -
                    human (fragment) \overline{>}gi_9148\overline{3}3 (\overline{L4}2610) keratin type II [Homo
                    sapiens]
Seq. No.
                    228914
                    LIB3196-019-P1-M1-F6
Seq. ID
                    BLASTX
Method
                    g2582665
NCBI GI
                    216
BLAST score
                    1.0e-17
E value
                    76
Match length
                    58
% identity
NCBI Description (Z82983) thi [Citrus sinensis]
                    228915
Seq. No.
                    LIB3196-019-P1-M1-F8
Seq. ID
                    BLASTX
Method
                    g137578
NCBI GI
BLAST score
                    224
                    3.0e-25
E value
                    93
Match length
                    64
% identity
NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
                    >gi_81545_pir__S06398 alpha-globulin type A precursor -
                    upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                    [Artificial gene] >gi_226119_prf__1410330A vicilin gene A
```

[Saguinus oedipus]
Seq. No. 228916

Seq. ID LIB3196-019-P1-M1-G1

Method BLASTX NCBI GI g110630

% identity



```
BLAST score
                   632
                   3.0e-66
E value
                  126
Match length
                  100
% identity
NCBI Description lamin B - mouse >gi_293689 (M35153) lamin B [Mus musculus]
                  228917
Seq. No.
                  LIB3196-019-P1-M1-G11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g133500
                   283
BLAST score
                   2.0e-25
E value
                   52
Match length
                   100
% identity
NCBI Description RETINOIC ACID RECEPTOR GAMMA-2 (RAR-GAMMA-2)
                   228918
Seq. No.
                   LIB3196-019-P1-M1-G2
Seq. ID
Method
                   BLASTX
                   q3075398
NCBI GI
                   170
BLAST score
                   4.0e-12
E value
                   71
Match length
                   51
% identity
                  (AC004484) unknown protein [Arabidopsis thaliana]
NCBI Description
                   228919
Seq. No.
Seq. ID
                   LIB3196-019-P1-M1-G5
                   BLASTX
Method
NCBI GI
                   g72287
                   386
BLAST score
                   2.0e-37
E value
                   108
Match length
                   71
% identity
                   beta-globulin A precursor (clone 94) - upland cotton
NCBI Description
                   (fragment) >gi_167377 (M16905) legumin precursor [Gossypium
                   hirsutum]
                   228920
Seq. No.
                   LIB3196-019-P1-M1-G6
Seq. ID
                   BLASTX
Method
                   g4008006
NCBI GI
                   276
BLAST score
                   2.0e-24
E value
Match length
                   120
 % identity
                   47
                   (AF084034) receptor-like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   228921
 Seq. No.
                   LIB3196-019-P1-M1-G9
 Seq. ID
                   BLASTX
 Method
                   g2224911
 NCBI GI
                   192
 BLAST score
                   8.0e-15
 E value
                   89
 Match length
                   46
```



```
(U93048) somatic embryogenesis receptor-like kinase [Daucus
NCBI Description
                  carota]
                  228922
Seq. No.
                  LIB3196-019-P1-M1-H5
Seq. ID
                  BLASTX
Method
                  q1710008
NCBI GI
BLAST score
                  402
                  2.0e-39
E value
                  117
Match length
                  73
% identity
                  GTP-BINDING NUCLEAR PROTEIN RAN1B >gi 1370205_emb_CAA98188_
NCBI Description
                  (Z73960) RAN1B [Lotus japonicus]
                  228923
Seq. No.
                  LIB3196-019-P1-M1-H6
Seq. ID
Method
                  BLASTX
                  q71532
NCBI GI
BLAST score
                  511
                   4.0e-52
E value
                   111
Match length
                   93
% identity
                  keratin, type II cytoskeletal - human (fragment)
NCBI Description
                   >gi 34069_emb_CAA24760_ (V01516) keratin [Homo sapiens]
                   >gi 386847 (J\overline{0}0269) keratin [Homo sapiens]
                   228924
Seq. No.
                   LIB3196-019-P1-M1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1703129
BLAST score
                   433
                   5.0e-43
E value
Match length
                   86
                   98
% identity
                  ACTIN 11 >gi_2129522_pir__$68109 actin 11 - Arabidopsis
NCBI Description
                   thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis
                   thaliana]
Seq. No.
                   228925
                   LIB3196-020-P1-M1-A2
Seq. ID
Method
                   BLASTX
                   g1346344
NCBI GI
                   588
BLAST score
                   5.0e-61
E value
Match length
                   129
                   95
% identity
                  KERATIN, TYPE II CYTOSKELETAL 6A (CYTOKERATIN 6A) (CK 6A)
NCBI Description
                   (K6A KERATIN) >gi_2119221_pir__A57398 keratin type II -
                   human >gi 908779 (L42583) keratin type II [Homo sapiens]
Seq. No.
                   228926
```

Seq. ID LIB3196-020-P1-M1-A5

Method BLASTX
NCBI GI g2982453
BLAST score 540
E value 2.0e-55
Match length 118



```
% identity
                  (AL022223) fructose-bisphosphate aldolase-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  228927
Seq. No.
                  LIB3196-020-P1-M1-A6
Seq. ID
                  BLASTX
Method
                  q4176522
NCBI GI
                  159
BLAST score
                  8.0e-11
E value
                  116
Match length
                  28
% identity
                  (AL035263) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                  228928
Seq. No.
                  LIB3196-020-P1-M1-A8
Seq. ID
                  BLASTX
Method
                  g4539307
NCBI GI
                  183
BLAST score
                  1.0e-13
E value
                   62
Match length
                   58
% identity
                  (AL049480) putative acidic ribosomal protein [Arabidopsis
NCBI Description
                  thaliana]
                   228929
Seq. No.
                  LIB3196-020-P1-M1-A9
Seq. ID
                  BLASTX
Method
                   g2134803
NCBI GI
BLAST score
                   677
                   2.0e-71
E value
                   134
Match length
                   99
% identity
NCBI Description band-6-protein - human >gi_535015_emb_CAA55881_ (X79293)
                   band-6-protein [Homo sapiens]
                   228930
Seq. No.
                   LIB3196-020-P1-M1-B1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2995405
                   124
BLAST score
E value
                   9.0e-15
                   99
Match length
                   47
% identity
NCBI Description (Y12432) polyprotein [Ananas comosus]
                   228931
Seq. No.
                   LIB3196-020-P1-M1-B11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1732411
BLAST score
                   644
                   1.0e-67
E value
Match length
                   125
% identity
                   99
NCBI Description (U47924) isopeptidase T [Homo sapiens]
```

228932

Seq. No.



```
LIB3196-020-P1-M1-B12
Seq. ID
                  BLASTX
Method
                  g441457
NCBI GI
                  520
BLAST score
                  4.0e-53
E value
                  96
Match length
                  99
% identity
                  (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                  esculentum]
                  228933
Seq. No.
                  LIB3196-020-P1-M1-B2
Seq. ID
                  BLASTX
Method
                  g116850
NCBI GI
                  588
BLAST score
                  5.0e-61
E value
                  114
Match length
                  100
% identity
                  COFILIN, NON-MUSCLE ISOFORM >gi 89176 pir A29240 cofilin -
NCBI Description
                  pig >gi_164425 (M20866) cofilin [Sus scrofa]
                  228934
Seq. No.
                  LIB3196-020-P1-M1-B3
Seq. ID
                  BLASTX
Method
                  g3970854
NCBI GI
                  396
BLAST score
                  1.0e-38
E value
                  126
Match length
                  63
% identity
NCBI Description (AB015332) HRIHFB2018 [Homo sapiens]
                  228935
Seq. No.
                  LIB3196-020-P1-M1-B7
Seq. ID
                  BLASTX
Method
                  q3269284
NCBI GI
BLAST score
                  347
                  8,0e-33
E value
                  109
Match length
                  67
% identity
NCBI Description (AL030978) histone H2A- like protein [Arabidopsis thaliana]
                  228936
Seq. No.
Seq. ID
                  LIB3196-020-P1-M1-B8
                  BLASTX
Method
                  q125887
NCBI GI
BLAST score
                   272
                   5.0e-24
E value
                   119
Match length
                   50
% identity
NCBI Description ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
                   >gi 82092_pir S04765 LAT52 protein precursor - tomato
                   >gi 295812 emb CAA33854 (X15855) LAT52 [Lycopersicon
```

Seq. No. 228937

Seq. ID LIB3196-020-P1-M1-B9

esculentum]

Method BLASTX



NCBI GI g137578
BLAST score 442
E value 4.0e-44
Match length 83
% identity 100

NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)

>gi\_81545\_pir\_\_S06398 alpha-globulin type A precursor 
upland cotton >gi\_167371 (M19378) vicilin precursor

[Gossypium hirsutum] >gi\_207906 (M18027) alpha globulin A

[Gossypium hirsutum] >gi\_207906 (M18027) alpha globulin A [Artificial gene] >gi\_226119\_prf\_\_1410330A vicilin gene A

[Saguinus oedipus]

Seq. No. 228938

Seq. ID LIB3196-020-P1-M1-C1

Method BLASTX
NCBI GI g113944
BLAST score 586
E value 8.0e-61
Match length 118
% identity 44

NCBI Description ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9)

(P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN)

>gi 71756 pir LUHU annexin I - human

>gi\_34388\_emb\_CAA29338\_ (X05908) lipocortin (AA 1-346)
[Homo sapiens] >gi\_224956\_prf\_ 1204261A lipocortin [Homo sapiens] >gi\_4502101\_ref\_NP\_000691.1\_pANX1\_ annexin I

(lipocortin I)

Seq. No. 228939

Seq. ID LIB3196-020-P1-M1-C3
Method BLASTX
NCBI GI g133841
BLAST score 351

BLAST score 351 E value 3.0e-33 Match length 78 % identity 91

NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S18 >gi\_71016\_pir\_\_R3NT18

ribosomal protein S18 - common tobacco chloroplast >gi\_11851\_emb\_CAA77371\_ (Z00044) ribosomal protein S18 [Nicotiana tabacum] >gi\_225220\_prf\_\_1211235BB ribosomal

protein S18 [Nicotiana tabacum]

Seq. No. 228940

Seq. ID LIB3196-020-P1-M1-C4

Method BLASTX
NCBI GI g4115933
BLAST score 281
E value 4.0e-25
Match length 87
% identity 70

NCBI Description (AF118223) contains similarity to human RNA polymerase II

complex component SRB7 (GB:U52960) [Arabidopsis thaliana]

Seq. No. 228941

Seq. ID LIB3196-020-P1-M1-C5

Method BLASTX NCBI GI 91408471



```
447
BLAST score
                   1.0e-44
E value
                   101
Match length
                   79
% identity
                   (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                   thaliana] >gi 3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
                   228942
Seq. No.
                   LIB3196-020-P1-M1-C8
Seq. ID
                   BLASTX
Method
                   q4415917
NCBI GI
                   390
BLAST score
                   7.0e-38
E value
                   123
Match length
                    58
% identity
                    (AC006282) putative protein containing zinc finger domain
NCBI Description
                    [Arabidopsis thaliana]
                    228943
Seq. No.
                   LIB3196-020-P1-M1-D11
Seq. ID
                   BLASTX
Method
                    q2911047
NCBI GI
BLAST score
                    402
                    2.0e-39
E value
                    100
Match length
                    73
% identity
                   (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                    228944
Seq. No.
Seq. ID
                    LIB3196-020-P1-M1-D12
                    BLASTX
Method
                    q4455787
NCBI GI
                    148
BLAST score
                    5.0e-10
E value
                    51
Match length
                    47
% identity
                   (AL035536) putative DNA polymerase accessory protein
NCBI Description
                    [Schizosaccharomyces pombe]
Seq. No.
                    228945
                    LIB3196-020-P1-M1-D2
Seq. ID
Method
                    BLASTX
                    q399132
NCBI GI
BLAST score
                    451
                    5.0e-45
E value
                    89
Match length
                    97
% identity
                   BTG1 PROTEIN (B-CELL TRANSLOCATION GENE 1 PROTEIN)
NCBI Description
                    >gi 86982 pir S20947 BTG1 protein - human
                    >gi_2137175_pir__I48272 btg1 protein - mouse
                    >gi_29509 emb_CAA43435_ (X61123) BTG1 [Homo sapiens] >gi_50188_emb_CAA78902_ (Z16410) btg1 [Mus musculus]
                    >gi_29330\overline{6} (L\overline{1}6846) BT\overline{G}1 [Mus musculus]
                    >gi_4502473_ref_NP_001722.1_pBTG1_ B-cell translocation
```

protein



Seq. No.

```
LIB3196-020-P1-M1-D5
Seq. ID
                  BLASTX
Method
                  g3901014
NCBI GI
                  235
BLAST score
                  1.0e-19
E value
                  55
Match length
% identity
                  (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                  sylvatica]
                  228947
Seq. No.
                  LIB3196-020-P1-M1-D8
Seq. ID
                  BLASTX
Method
                  g1000207
NCBI GI
BLAST score
                  624
                  2.0e-65
E value
                  120
Match length
                  99
% identity
                  (U33920) semaphorin [Homo sapiens]
NCBI Description
                  228948
Seq. No.
                  LIB3196-020-P1-M1-D9
Seq. ID
                  BLASTX
Method
                   q125105
NCBI GI
                   625
BLAST score
                   2.0e-65
E value
                   130
Match length
                   95
% identity
                   KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5)
NCBI Description
                   (58 KD CYTOKERATIN) >gi_88051_pir__A29904 keratin K5, 58K
                   type II, epidermal (version 1) - human >gi_307082 (M21389)
                   keratin type II [Homo sapiens]
                   >gi 4557890_ref_NP_000415.1_pKRT5_ keratin
                   228949
Seq. No.
                   LIB3196-020-P1-M1-E10
Seq. ID
                   BLASTX
Method
                   q1351111
NCBI GI
                   431
BLAST score
                   9.0e-43
E value
                   86
Match length
                   97
% identity
                   SIGNAL RECOGNITION PARTICLE 9 KD PROTEIN (SRP9)
NCBI Description
                   >gi_1362938_pir__A57292 signal recognition particle protein
                   SRP9 - human >gi_897851 (U20998) signal recognition
                   particle subunit 9 [Homo sapiens]
                   >gi_4507217_ref_NP_003124.1_pSRP9_ signal recognition
                   particle 9kD
                   228950
 Seq. No.
                   LIB3196-020-P1-M1-E11
 Seq. ID
                   BLASTX
Method
                   g4454706
 NCBI GI
 BLAST score
                   378
                   2.0e-36
 E value
 Match length
                   91
```

Match length



```
% identity
NCBI Description (AF070665) HSPC009 [Homo sapiens]
                  228951
Seq. No.
                  LIB3196-020-P1-M1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q100196
BLAST score
                  498
                  1.0e-50
E value
Match length
                  110
% identity
NCBI Description chlorophyll a/b-binding protein (cab-11) - tomato
Seq. No.
                  228952
Seq. ID
                  LIB3196-020-P1-M1-E3
Method
                  BLASTX
NCBI GI
                  g1711507
BLAST score
                  227
                  7.0e-19
E value
                  68
Match length
% identity
                  60
                  SIGNAL RECOGNITION PARTICLE 19 KD PROTEIN (SRP19)
NCBI Description
                  >gi 624221 (U19030) signal recognition particle 19 kDa
                  protein subunit SRP19 [Oryza sativa]
                  228953
Seq. No.
Seq. ID
                  LIB3196-020-P1-M1-E4
                  BLASTX
Method
NCBI GI
                  q2760345
BLAST score
                   381
                   4.0e-37
E value
Match length
                  88
                  22
% identity
NCBI Description (U84967) ubiquitin [Arabidopsis thaliana]
                  228954
Seq. No.
Seq. ID
                  LIB3196-020-P1-M1-E6
Method
                  BLASTX
                  q137578
NCBI GI
BLAST score
                   463
                   2.0e-46
E value
Match length
                  103
                   50
% identity
NCBI Description
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
                  >gi_81545_pir__S06398 alpha-globulin type A precursor -
                  upland cotton >gi 167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi 207906 (M18027) alpha globulin A
                   [Artificial gene] >gi 226119 prf 1410330A vicilin gene A
                   [Saguinus oedipus]
Seq. No.
                  228955
Seq. ID
                  LIB3196-020-P1-M1-E8
Method
                  BLASTX
NCBI GI
                  q541849
BLAST score
                  212
E value
                  5.0e-17
```

NCBI GI

BLAST score

q118926

206



```
% identity
                  anthranilate synthase (EC 4.1.3.27) beta chain -
NCBI Description
                  Arabidopsis thaliana >gi_403434 (L22585) anthranilate
                  synthase beta subunit [Arabidopsis thaliana]
                  228956
Seq. No.
                  LIB3196-020-P1-M1-F1
Seq. ID
                  BLASTX
Method
                  q4263710
NCBI GI
BLAST score
                  517
E value
                  8.0e-53
                  106
Match length
                  67
% identity
NCBI Description (AC006223) putative pur-alpha transcriptional activator
                  protein [Arabidopsis thaliana]
                  228957
Seq. No.
                  LIB3196-020-P1-M1-F11
Seq. ID
                  BLASTX
Method
                  q3015538
NCBI GI
                  375
BLAST score
                  3.0e-36
E value
                  111
Match length
% identity
                  69
                  (U93181) nuclear dual-specificity phosphatase [Homo
NCBI Description
                  sapiens]
                  228958
Seq. No.
                  LIB3196-020-P1-M1-F2
Seq. ID
                  BLASTX
Method
                   g3420900
NCBI GI
BLAST score
                   188
                   3.0e-14
E value
                   98
Match length
                   40
 % identity
NCBI Description (AF081125) ER lumen protein retaining receptor
                   [Caenorhabditis elegans]
                   228959
 Seq. No.
                   LIB3196-020-P1-M1-F3
 Seq. ID
                   BLASTX
 Method
                   g130582
 NCBI GI
 BLAST score
                   186
                   6.0e-14
 E value
                   74
 Match length
                   50
 % identity
 NCBI Description RETROVIRUS-RELATED POL POLYPROTEIN FROM TRANSPOSON TNT 1-94
                   [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
                   >gi 100342 pir__S04273 hypothetical protein - common
                   tobacco >gi_20045_emb_CAA32025_ (X13777) ORF [Nicotiana
                   tabacum]
                   228960
 Seq. No.
 Seq. ID
                   LIB3196-020-P1-M1-F4
                   BLASTX
 Method
```



E value 2.0e-16

Match length 43

NCBI Description DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR >gi\_320600\_pir\_\_E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi\_167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi\_227781\_prf\_\_1710351E abscisic acid responsive protein E [Craterostigma plantagineum]

228961 Seq. No. LIB3196-020-P1-M1-F5 Seq. ID BLASTX Method g135005 NCBI GI 173 BLAST score 2.0e-12 E value 76 Match length 39 % identity

NCBI Description STRICTOSIDINE SYNTHASE PRECURSOR >gi\_82067\_pir\_\_S01325

strictosidine synthase (EC 4.3.3.2) - serpentwood

>gi\_21127\_emb\_CAA44208\_ (X62334) strictosidine synthase
[Rauvolfia serpentina] >gi\_21129\_emb\_CAA68725\_ (Y00756)

strictosidine synthase [Rauvolfia serpentina]

>gi\_226162\_prf\_\_1413232A strictosidine synthase [Rauvolfia

serpentina]

Seq. No. 228962

Seq. ID LIB3196-020-P1-M1-F6

Method BLASTX
NCBI GI g122007
BLAST score 419
E value 3.0e-41
Match length 111
% identity 76

NCBI Description HISTONE H2A >gi\_100161\_pir\_\_S11498 histone H2A - parsley

>gi\_20448\_emb\_C $\overline{A}$ A37828 $\overline{A}$  (X $\overline{A}$ 3831) H2A histone protein (AA 1

- 149) [Petroselinum crispum]

Seq. No. 228963

Seq. ID LIB3196-020-P1-M1-F9

Method BLASTX
NCBI GI g3913414
BLAST score 457
E value 9.0e-46
Match length 122
% identity 75

NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME 2 (ADOMETDC 2)

(SAMDC 2) (SAMDC16) >gi\_1155242 (U38527)

S-adenosylmethionine decarboxylase 2 [Dianthus

caryophyllus]

Seq. No. 228964

Seq. ID LIB3196-020-P1-M1-G1

Method BLASTX
NCBI GI g88044
BLAST score 580
E value 3.0e-60

BLAST score

E value

297 4.0e-27



```
Match length
                   121
                   96
% identity
                   keratin 4, type II, cytoskeletal - human (fragment)
NCBI Description
                   >gi 34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA)
                    [Homo sapiens]
                   228965
Seq. No.
                   LIB3196-020-P1-M1-G5
Seq. ID
                   BLASTX
Method
                    g126156
NCBI GI
                    584
BLAST score
                    1.0e-60
E value
                    117
Match length
                    99
% identity
                   LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
NCBI Description
                    >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134)
                    - upland cotton >gi_167373 (M16936) vicilin precursor
                    [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                    protein C134 [Saguinus oedipus]
                    228966
Seq. No.
                    LIB3196-020-P1-M1-G6
Seq. ID
Method
                    BLASTX
                    g547713
NCBI GI
                    283
BLAST score
                    2.0e-25
E value
Match length
                    78
                    62
% identity
                   EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E)
NCBI Description
                    (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-(ISO)4F 25 KD
                    SUBUNIT) (EIF-(ISO)4F P28 SUBUNIT) >gi_322866_pir__B44452
                    translation initiation factor eIF-4F isozyme form subunit
                    p28 - wheat >gi_170751 (M95818) initiation factor (iso)4F
                    p28 subunit [Triticum aestivum]
                    228967
Seq. No.
                    LIB3196-020-P1-M1-G9
Seq. ID
                    BLASTX
Method
                    a547751
NCBI GI
                    650
BLAST score
                    2.0e-68
E value
                    132
Match length
% identity
                    KERATIN, TYPE I CYTOSKELETAL 17 (CYTOKERATIN 17) (K17) (CK
NCBI Description
                    17) (39.1) (VERSION 1) >gi_422802_pir__S30433 keratin 17,
                    cytoskeletal - human >gi_30379_emb_CAA79626_ (Z19574)
                    cytokeratin 17 [Homo sapiens] >gi_34075_emb_CAA44451_(X62571) keratin related product [Homo sapiens]
                    >gi 4557701 ref NP_000413.1_pKRT17_ keratin
                    228968
 Seq. No.
                    LIB3196-020-P1-M1-H10
 Seq. ID
                    BLASTX
 Method
                    q3694872
 NCBI GI
```



```
Match length
                   64
                   83
% identity
                   (AF092547) profilin [Ricinus communis]
NCBI Description
                   228969
Seq. No.
                   LIB3196-020-P1-M1-H11
Seq. ID
                   BLASTX
Method
                   g3334157
NCBI GI
                   199
BLAST score
                   1.0e-20
E value
                   63
Match length
                   78
% identity
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                   >gi 1220142 emb CAA59468_ (X85185) cyclophilin
                   [Catharanthus roseus]
                   228970
Seq. No.
                   LIB3196-020-P1-M1-H3
Seq. ID
                   BLASTX
Method
                   g126156
NCBI GI
                   195
BLAST score
                    5.0e-15
E value
                    95
Match length
                    53
% identity
                   LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
NCBI Description
                    >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134)
                    - upland cotton >gi_167373 (M16936) vicilin precursor
                    [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                    protein C134 [Saguinus oedipus]
Seq. No.
                    228971
                    LIB3196-020-P1-M1-H4
Seq. ID
                    BLASTX
Method
NCBI GI
                    q416662
BLAST score
                    316
                    3.0e-29
E value
                    127
Match length
                    53
% identity
                    21 KD SEED PROTEIN PRECURSOR >gi_99954 pir_S16252 trypsin
NCBI Description
                    inhibitor homolog - soybean >gi 21909 emb CAA39860
                    (X56509) 21 kDa seed protein [Theobroma cacao]
                    228972
 Seq. No.
                    LIB3196-020-P1-M1-H9
 Seq. ID
Method
                    BLASTX
 NCBI GI
                    g2465540
 BLAST score
                    248
                    3.0e-21
 E value
                    55
Match length
 % identity
                    (AF005632) phosphodiesterase I/nucleotide pyrophosphatase
NCBI Description
```

Seq. No. 228973

Seq. ID LIB3196-021-P1-M1-A1

beta [Homo sapiens]



```
Method
                  BLASTX
                  g4539459
NCBI GI
                  245
BLAST score
                  7.0e-21
E value
                  53
Match length
                  72
% identity
NCBI Description (AL049500) putative protein [Arabidopsis thaliana]
                  228974
Seq. No.
                  LIB3196-021-P1-M1-A10
Seq. ID
                  BLASTX
Method
                  g2914703
NCBI GI
                  312
BLAST score
                  9.0e-29
E value
                  122
Match length
                  52
% identity
                  (AC003974) unknown protein [Arabidopsis thaliana]
NCBI Description
                  228975
Seq. No.
                  LIB3196-021-P1-M1-A3
Seg. ID
                  BLASTX
Method
                   g4263522
NCBI GI
BLAST score
                   322
                   6.0e - 30
E value
                   126
Match length
                   45
% identity
                  (AC004044) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   228976
Seq. No.
                   LIB3196-021-P1-M1-A4
Seq. ID
                   BLASTX
Method
                   g4510364
NCBI GI
                   170
BLAST score
                   4.0e-12
E value
                   100
Match length
                   46
% identity
                  (AC007017) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   228977
Seq. No.
                   LIB3196-021-P1-M1-A5
Seq. ID
                   BLASTX
Method
                   q232190
NCBI GI
                   347
BLAST score
                   8.0e-33
E value
                   78
Match length
                   85
 % identity
                   GLUTATHIONE PEROXIDASE HOMOLOG 6P229 >gi_100291 pir_s20501
 NCBI Description
                   glutathione peroxidase homolog - wood tobacco
                   >gi_19739_emb_CAA42780_ (X60219) homologous to animal
                   glutathione peroxidases [Nicotiana sylvestris]
                   228978
 Seq. No.
                   LIB3196-021-P1-M1-A6
 Seq. ID
                   BLASTX
 Method
                   g266690
 NCBI GI
                   401
 BLAST score
```

4.0e-39

E value



```
109
Match length
                   75
% identity
                  OLEOSIN 18.2 KD >gi_167363 (L00935) 18.2 kDa oleosin
NCBI Description
                   [Gossypium hirsutum] >gi_167365 (L00936) 18.2 kDa oleosin
                   [Gossypium hirsutum]
                   228979
Seq. No.
Seq. ID
                  LIB3196-021-P1-M1-A8
                  BLASTX
Method
NCBI GI
                  g4415931
BLAST score
                  176
E value
                   4.0e-13
Match length
                   53
% identity
                   64
NCBI Description
                  (AC006418) unknown protein [Arabidopsis thaliana]
                  >gi 4559393 gb AAD23053.1 AC006526 18 (AC006526) unknown
                  protein [Arabidopsis thaliana]
                  228980
Seq. No.
                  LIB3196-021-P1-M1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g88052
BLAST score
                   553
E value
                   3.0e-57
Match length
                  110
% identity
                   100
NCBI Description keratin K5, 58K type II, epidermal (version 2) - human
                   (fragment)
                   228981
Seq. No.
Seq. ID
                   LIB3196-021-P1-M1-B2
Method
                  BLASTX
NCBI GI
                   g3220164
BLAST score
                  155
E value
                   3.0e-10
Match length
                  53
                   91
% identity
NCBI Description (AF029777) hGCN5 [Homo sapiens]
                  228982
Seq. No.
Seq. ID
                  LIB3196-021-P1-M1-B3
Method
                  BLASTX
NCBI GI
                   q4539660
BLAST score
                   445
E value
                   3.0e-44
Match length
                  127
% identity
NCBI Description (AF061282) polyprotein [Sorghum bicolor]
                  228983
Seq. No.
                  LIB3196-021-P1-M1-B4
Seq. ID
```

Method BLASTX
NCBI GI g1169475
BLAST score 697
E value 7.0e-74
Match length 132
% identity 100



```
NCBI Description ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION
                    FACTOR TU) (EF-TU) >gi 556301 (M22432) elongation factor Tu
                    [Mus musculus]
                    228984
 Seq. No.
 Seq. ID
                    LIB3196-021-P1-M1-B6
 Method
                   BLASTX
 NCBI GI
                    q4204308
 BLAST score
                    217
 E value
                    1.0e-17
                    39
 Match length
 % identity
                    92
 NCBI Description (AC003027) lcl prt seq No definition line found
                    [Arabidopsis thaliana]
 Seq. No.
                    228985
 Seq. ID
                    LIB3196-021-P1-M1-B8
 Method
                    BLASTX
                    q3915742
 NCBI GI
 BLAST score
                    468
 E value
                    3.0e-47
 Match length
                    95
                    94
 % identity
 NCBI Description LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319
                    (M69188) legumin A [Gossypium hirsutum]
                    >gi 444320 prf 1906369A legumin A:ISOTYPE=D alloallele
                    [Gossypium hirsutum]
 Seq. No.
                    228986
 Seq. ID
                    LIB3196-021-P1-M1-C1
 Method
                    BLASTX
 NCBI GI
                    g119172
 BLAST score
                    349
 E value
                    4.0e-33
 Match length
                    84
 % identity
                    87
.. NCBI Description ELONGATION FACTOR 2 (EF-2) >gi 2144947 pir_ EFHU2
                    translation elongation factor eEF-2 - human
                    >gi 31106 emb CAA35829 (X51466) elongation factor 2 [Homo
                    sapiens] >gi_31108_emb_CAA77750_ (Z11692) human elongation
                    factor 2 [Homo sapiens] >gi 4503483 ref NP 001952.1 pEEF2
                    eukaryotic translation elongation factor
  Seq. No.
                    228987
  Seq. ID
                    LIB3196-021-P1-M1-C10
 Method
                    BLASTX
 NCBI GI
                    q131770
 BLAST score
                    333
  E value
                    3.0e-31
 Match length
                    91
  % identity
                    66
 NCBI Description 40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
```

[Dictyostelium discoideum]

(VEGETATIVE SPECIFIC PROTEIN V12) >gi\_70880\_pir\_\_R3D024 ribosomal protein S9.e - slime mold (Dictyostelium

discoideum) >gi\_7353\_emb\_CAA29844\_ (X06636) rp1024 protein



```
228988
Seq. No.
Seq. ID
                  LIB3196-021-P1-M1-C2
Method
                  BLASTX
NCBI GI
                  g226120
BLAST score
                  683
                  3.0e-72
E value
                  130
Match length
% identity
                  100
NCBI Description vicilin gene B [Saguinus oedipus]
                  228989
Seq. No.
Seq. ID
                  LIB3196-021-P1-M1-C3
Method
                  BLASTX
NCBI GI
                  q3643609
BLAST score
                  238
                  4.0e-20
E value
Match length
                  103
                  56
% identity
                 (AC005395) putative Cys3His zinc finger protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  228990
                  LIB3196-021-P1-M1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g207384
BLAST score
                  286
                  1.0e-25
E value
Match length
                  87
                   69
% identity
NCBI Description (M15202) tropomyosin T class IIa beta-1 [Rattus norvegicus]
                  228991
Seq. No.
Seq. ID
                  LIB3196-021-P1-M1-C5
                  BLASTX
Method
NCBI GI
                  g2224907
BLAST score
                   382
E value
                   6.0e-37
Match length
                   129
% identity
                  (U78294) 15S-lipoxygenase [Homo sapiens]
NCBI Description
                   >gi 4557309 ref NP 001132.1 pALOX15B arachidonate
                   15-lipoxygenase, second type
                   228992
Seq. No.
                  LIB3196-021-P1-M1-D11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2160166
BLAST score
                   386
                   1.0e-37
E value
Match length
                   93
% identity
                   77
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
                   228993
Seq. No.
Seq. ID
                  LIB3196-021-P1-M1-D12
```

Method BLASTX NCBI GI g3327392



```
BLAST score
E value
                  5.0e-09
Match length
                  79
                  44
% identity
NCBI Description
                  (AC004483) reverse-transcriptase-like protein [Arabidopsis
                  thalianal
Seq. No.
                  228994
Seq. ID
                  LIB3196-021-P1-M1-D5
                  BLASTX
Method
NCBI GI
                  g2135344
BLAST score
                  695
E value
                  1.0e-73
Match length
                  133
% identity
                  50
NCBI Description HER3 protein precursor - human >gi_306841 (M34309) HER3
                  protein precursor [Homo sapiens]
                  >gi_4503597_ref_NP_001973.1_pERBB3 v-erb-b2 avian
                  erythroblastic leukemia viral oncogene homolog
                  228995
Seq. No.
                  LIB3196-021-P1-M1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3877645
BLAST score
                  142
                  8.0e-09
E value
Match length
                  68
% identity
                  43
NCBI Description (283230) cDNA EST yk355g3.5 comes from this gene
                  [Caenorhabditis elegans]
Seq. No.
                  228996
Seq. ID
                  LIB3196-021-P1-M1-D8
Method
                  BLASTX
NCBI GI
                  g1706571
                  373
BLAST score
E value
                  7.0e-36
                  127
Match length
% identity
                  56
NCBI Description EPITHELIAL CHLORIDE CHANNEL PROTEIN (CALCIUM-ACTIVATED
                  CHLORIDE CHANNEL) > gi 1184066 (U36445) calcium-activated
                  chloride channel [Bos taurus]
Seq. No.
                  228997
Seq. ID
                  LIB3196-021-P1-M1-E11
Method
                  BLASTX
NCBI GI
                  g2499488
BLAST score
                  569
                  6.0e-59
E value
Match length
                  112
% identity
                  91
NCBI Description PYROPHOSPHATE -- FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
                  ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                   (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                   (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849)
```

[Ricinus communis]

pyrophosphate-dependent phosphofructokinase alpha subunit

Match length



```
Seq. No.
                   228998
                   LIB3196-021-P1-M1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q137578
BLAST score
                   511
E value
                   4.0e-52
Match length
                   124
% identity
                   84
                   VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                   >gi_81545_pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi 167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi 207906 (M18027) alpha globulin A
                   [Artificial gene] >gi 226119 prf 1410330A vicilin gene A
                   [Saguinus oedipus]
                   228999
Seq. No.
Seq. ID
                   LIB3196-021-P1-M1-E5
                   BLASTX
Method
NCBI GI
                   q121283
BLAST score
                   613
E value
                   5.0e-64
Match length
                   125
% identity
NCBI Description GLUCOSYLCERAMIDASE PRECURSOR (BETA-GLUCOCEREBROSIDASE)
                   (ACID BETA-GLUCOSIDASE) (D-GLUCOSYL-N-ACYLSPHINGOSINE
                   GLUCOHYDROLASE) >gi_183028 (M19285) glucocerebrosidase [Homo sapiens] >gi_4503935_ref_NP_000148.1_pGBA_
                   glucosidase, beta; acid (includes glucosylceramidase)
                   229000
Seq. No.
Seq. ID
                   LIB3196-021-P1-M1-E6
Method
                   BLASTX
NCBI GI
                   g125080
BLAST score
                   624
                   3.0e-65
E value
                   126
Match length
% identity
NCBI Description
                   KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK
                   14) >qi 2144816 pir KRHUE keratin, 50K type I cytoskeletal
                   - human >gi 386848 (J00124) keratin [Homo sapiens]
                   >gi 4504913 ref NP 000517.1 pKRT14 keratin 14
                   (epidermolysis bullosa simplex, Dowling-Meara, Koebner)
Seq. No.
                   229001
Seq. ID
                   LIB3196-021-P1-M1-E7
Method
                   BLASTX
NCBI GI
                   q3915742
BLAST score
                   348
                   5.0e-33
E value
```

% identity 80

NCBI Description LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi\_167319 (M69188) legumin A [Gossypium hirsutum]

>gi\_444320\_prf\_\_1906369A legumin A:ISOTYPE=D alloallele

[Gossypium hirsutum]



```
Seq. No.
                   229002
                  LIB3196-021-P1-M1-E8
Seq. ID
Method
                   BLASTX
                   q4098124
NCBI GI
                   389
BLAST score
                   7.0e-38
E value
Match length
                   106
% identity
                   62
NCBI Description (U73522) AMSH [Homo sapiens]
                   229003
Seq. No.
                   LIB3196-021-P1-M1-E9
Seq. ID
                   BLASTX
Method
                   q3608171
NCBI GI
BLAST score
                   531
                   2.0e-54
E value
Match length
                   126
                   83
% identity
                   (D86306) proton-translocating inorganic pyrophosphatase
NCBI Description
                   [Cucurbita moschata]
                   229004
Seq. No.
                   LIB3196-021-P1-M1-F1
Seq. ID
                   BLASTX
Method
                   g2498017
NCBI GI
                   512
BLAST score
                   4.0e-52
E value
Match length
                   133
% identity
                   77
                   HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT
NCBI Description
                   INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1
                   ALPHA) >gi_2135434_pir__I38972 hypoxia-inducible factor 1
                   alpha - human >gi_{8813\overline{46}} (U22431) hypoxia-inducible factor
                   1 alpha [Homo sapiens] >gi_1144013 (U29165) ARNT
                   interacting protein [Homo sapiens]
                   >gi_1097959_prf__2114407A hypoxia-inducible factor 1 [Homo
                   sapiens] >gi_4504385_ref_NP_001521.1_pHIF1A_
hypoxia-inducible factor 1, alpha subunit (basic
                   helix-loop-helix transcription factor)
                   229005
Seq. No.
                   LIB3196-021-P1-M1-F10
Seq. ID
                   BLASTX
Method
                   g4415947
NCBI GI
                   267
BLAST score
                   1.0e-23
E value
                   99
Match length
                   53
 % identity
NCBI Description (AC006418) putative laccase [Arabidopsis thaliana]
                    229006
 Seq. No.
                   LIB3196-021-P1-M1-F3
 Seq. ID
                   BLASTX
Method
 NCBI GI
                    q3421134
```

398

112

7.0e - 39

BLAST score

Match length

E value



```
% identity
                  (AF045666) arginine decarboxylase [Theobroma cacao]
NCBI Description
                  229007
Seq. No.
                  LIB3196-021-P1-M1-F6
Seq. ID
                  BLASTX
Method
                  g2224569
NCBI GI
                  229
BLAST score
                  6.0e-19
E value
                  71
Match length
                  55
% identity
                  (AB002312) KIAA0314 [Homo sapiens]
NCBI Description
                  229008
Seq. No.
                  LIB3196-021-P1-M1-F7
Seq. ID
                  BLASTX
Method
                  g3150035
NCBI GI
                  191
BLAST score
                  9.0e-15
E value
                  61
Match length
                  64
% identity
                  (U37100) aldose reductase-like peptide [Homo sapiens]
NCBI Description
                  229009
Seq. No.
                  LIB3196-021-P1-M1-F8
Seq. ID
                  BLASTX
Method
                   q2505870
NCBI GI
BLAST score
                   303
                   1.0e-27
E value
                   125
Match length
                   57
% identity
                  (Y12227) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   229010
Seq. No.
                   LIB3196-021-P1-M1-F9
Seq. ID
                   BLASTX
Method
                   g137578
NCBI GI
                   395
BLAST score
                   1.0e-38
E value
                   98
Match length
                   44
% identity
                   VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                   >gi_81545_pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi 207906 (M18027) alpha globulin A
                   [Artificial gene] >gi 226119 prf 1410330A vicilin gene A
                   [Saguinus oedipus]
                   229011
Seq. No.
Seq. ID
                   LIB3196-021-P1-M1-G1
                   BLASTX
Method
                   q2499488
NCBI GI
BLAST score
                   550
                   1.0e-56
E value
Match length
                   109
                   91
% identity
NCBI Description PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
```



229012

ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi\_483547\_emb\_CAA83682\_ (Z32849) pyrophosphate-dependent phosphofructokinase alpha subunit [Ricinus communis]

Seq. ID LIB3196-021-P1-M1-G11
Method BLASTX
NCBI GI g3986758
BLAST score 374
E value 5.0e-36
Match length 71
% identity 100

Seq. No.

Seq. No.

NCBI Description (AF109905) CLCP [Mus musculus]

229013

Seq. ID LIB3196-021-P1-M1-G12
Method BLASTX
NCBI GI g3193316
BLAST score 573
E value 2.0e-59
Match length 125
% identity 85

NCBI Description (AF069299) contains similarity to nucleotide sugar

epimerases [Arabidopsis thaliana]

 Seq. No.
 229014

 Seq. ID
 LIB3196-021-P1-M1-G5

 Method
 BLASTX

 NCBI GI
 q4406703

NCBI GI g4406703 BLAST score 368 E value 3.0e-35 Match length 71 % identity 97

NCBI Description (AF131856) Unknown [Homo sapiens]

Seq. No. 229015

Seq. ID LIB3196-021-P1-M1-G7

Method BLASTX
NCBI GI g2578033
BLAST score 175
E value 1.0e-12
Match length 39
% identity 87

NCBI Description (X97016) omega-6 desaturase [Gossypium hirsutum]

Seq. No. 229016

Seq. ID LIB3196-021-P1-M1-G8

Method BLASTX
NCBI GI g3775993
BLAST score 545
E value 5.0e-56
Match length 123
% identity 86

NCBI Description (AJ010460) RNA helicase [Arabidopsis thaliana]



```
229017
Seq. No.
                   LIB3196-021-P1-M1-G9
Seq. ID
Method
                   BLASTX
                   q1723614
NCBI GI
                   152
BLAST score
                   3.0e-10
E value
Match length
                   84
                   45
% identity
                   RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE D
NCBI Description
                   (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)
                   >gi 2121009_pir__S60168 hypothetical protein X - Zymomonas
                   mobilis >gi_1143378_dbj_BAA09443_ (D50832) homologue of E.
                   coli ClpB5' ORF [Zymomonas mobilis]
Seq. No.
                   229018
                   LIB3196-021-P1-M1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2745974
                   558
BLAST score
                   1.0e-57
E value
                   131
Match length
                   83
% identity
                  (U84004) putative tumor suppressor [Homo sapiens]
NCBI Description
                   229019
Seq. No.
                   LIB3196-021-P1-M1-H12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2431771
BLAST score
                   212
                   5.0e-17
E value
                   104
Match length
                   44
% identity
NCBI Description (U62753) acidic ribosomal protein P2b [Zea mays]
                   229020
Seq. No.
                   LIB3196-021-P1-M1-H5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g136452
                   341
BLAST score
                   4.0e-32
E value
                   105
Match length
                   62
% identity
NCBI Description STEM-SPECIFIC PROTEIN TSJT1 >gi 100383 pir S13551
                   stem-specific protein - common tobacco >gi_20037_emb_CAA36525_ (X52283) stem specific, weakly
                   expressed in other organs [Nicotiana tabacum]
                   229021
Seq. No.
                   LIB3196-021-P1-M1-H7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g126041
BLAST score
                   419
                    2.0e-41
E value
                   87
Match length
                    99
% identity
```

>gi 1070432 pir DEHULH L-lactate dehydrogenase (EC

NCBI Description L-LACTATE DEHYDROGENASE H CHAIN (LDH-B)



1.1.1.27) chain H - human >gi\_34329\_emb\_CAA68701\_ (Y00711) lactate dehydrogenase B (AA 1 - 334) [Homo sapiens] >gi\_1200083\_emb\_CAA32033\_ (X13794) lactate dehydrogenase B [Homo sapiens] >gi\_4557032\_ref\_NP\_002291.1\_pLDHB\_ lactate dehydrogenase B

Seq. No. 229022 LIB3196-021-P1-M1-H8 Seq. ID Method BLASTX g280816 NCBI GI BLAST score 342 E value 2.0e-32 Match length 66 98 % identity

NCBI Description keratin 13, type I, cytoskeletal, short form - human >gi\_30377\_emb\_CAA36673\_ (X52426) cytokeratin 13 [Homo sapiens] >gi\_3603253 (AF049259) keratin 13 [Homo sapiens]

>gi 4504911 ref NP 002265.1 pKRT13\_ keratin

 Seq. No.
 229023

 Seq. ID
 LIB3196-021-P1-M1-H9

 Method
 BLASTX

 NCBI GI
 g1707032

 BLAST score
 143

 E value
 5.0e-09

E value 5.0 Match length 81% identity 41

NCBI Description (U80445) coded for by C. elegans cDNA ykl3g5.3; coded for

by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA

yk65h8

Seq. No. 229024
Seq. ID LIB3196-022-P1-M1-A1

Method BLASTX
NCBI GI g346219
BLAST score 240
E value 3.0e-20
Match length 127
% identity 50

NCBI Description keratin K4a - human (fragment)

Seq. No. 229025

Seq. ID LIB3196-022-P1-M1-A11

Method BLASTX
NCBI GI g226120
BLAST score 484
E value 6.0e-49
Match length 93
% identity 100

NCBI Description vicilin gene B [Saguinus oedipus]

Seq. No. 229026

Seq. ID LIB3196-022-P1-M1-A2

Method BLASTX NCBI GI g2467274



```
202
BLAST score
                   7.0e-16
E value
                   65 -
Match length
                   63
% identity
                   (Z99759) rna binding protein [Schizosaccharomyces pombe]
NCBI Description
                   229027
Seq. No.
                   LIB3196-022-P1-M1-A6
Seq. ID
                   BLASTX
Method
                   g2369714
NCBI GI
                   625
BLAST score
                   2.0e-65
E value
                   121
Match length
                   98
% identity
                   (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                   229028
Seq. No.
                   LIB3196-022-P1-M1-A8
Seq. ID
                   BLASTX
Method
                   q4467804
NCBI GI
                   445
BLAST score
                   3.0e-44
E value
                   117
Match length
                   76
% identity
                   (AL031678) TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3
NCBI Description
                   PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3).)
                   [Homo sapiens]
                   229029
Seq. No.
                   LIB3196-022-P1-M1-B10
Seq. ID
                   BLASTX
Method
                   g115833
NCBI GI
                    374
BLAST score
                    5.0e-36
E value
                    100
Match length
                    74
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR
NCBI Description
                    (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll a/b-binding protein Cab10A - tomato >gi_170394 (M32605)
                    a-binding protein [Lycopersicon esculentum]
Seq. No.
                    229030
                    LIB3196-022-P1-M1-B12
Seq. ID
                    BLASTX
Method
                    q3367523
NCBI GI
BLAST score
                    371
E value
                    1.0e-35
Match length
                    105
% identity
                    66
                    (AC004392) ESTs gb AA728658 and gb N95943 come from this
NCBI Description
                    gene. [Arabidopsis thaliana]
Seq. No.
                    229031
                    LIB3196-022-P1-M1-B3
Seq. ID
                    BLASTX
Method
```

q4490741

170

NCBI GI

BLAST score



```
3.0e-22
E value
                  102
Match length
% identity
                  58
NCBI Description (AL035708) hypothetical protein [Arabidopsis thaliana]
                  229032
Seq. No.
                  LIB3196-022-P1-M1-B4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4539327
BLAST score
                   400
E value
                   3.0e - 39
                  111
Match length
% identity
NCBI Description (AL035679) putative proton pump [Arabidopsis thaliana]
Seq. No.
                   229033
                  LIB3196-022-P1-M1-B7
Seq. ID
                  BLASTX
Method
                   g2352906
NCBI GI
BLAST score
                   342
                   3.0e - 32
E value
                   82
Match length
                   83
% identity
                  (AF011794) cell cycle progression restoration 8 protein
NCBI Description
                   [Homo sapiens]
                   229034
Seq. No.
                   LIB3196-022-P1-M1-B8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3702342
BLAST score
                   243
                   1.0e-20
E value
                   109
Match length
                   48
% identity
NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]
                   229035
Seq. No.
                   LIB3196-022-P1-M1-C10
Seq. ID
                   BLASTX
Method
                   g1208427
NCBI GI
BLAST score
                   329
                   9.0e - 31
E value
                   88
Match length
                   44
 % identity
NCBI Description (D83485) ER-60 protease [Homo sapiens]
                   229036
 Seq. No.
                   LIB3196-022-P1-M1-C3
 Seq. ID
                   BLASTX
Method
                   q1710017
 NCBI GI
                   562
 BLAST score
                   5.0e-58
 E value
                   112
 Match length
                   97
 % identity
 NCBI Description RAS-RELATED PROTEIN RAB-18 >gi_478319_pir__JN0874
                   ras-related GTP-binding protein Rab18 - mouse >gi_388325
```

(L04966) Rab18 [Mus musculus] >gi\_515041\_emb\_CAA56583

BLAST score

E value

519

5.0e-53



## (X80333) rab18 [Mus musculus]

```
229037
Seq. No.
                  LIB3196-022-P1-M1-C4
Seq. ID
Method
                  BLASTX
                  g125105
NCBI GI
                  529
BLAST score
                  7.0e-59
E value
                  127
Match length
                  95
% identity
                  KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5)
NCBI Description
                  (58 KD CYTOKERATIN) >gi_88051_pir__A29904 keratin K5, 58K
                  type II, epidermal (version 1) - human >gi_307082 (M21389)
                  keratin type II [Homo sapiens]
                  >gi_4557890_ref_NP_000415.1_pKRT5_ keratin
                  229038
Seq. No.
                  LIB3196-022-P1-M1-C5
Seq. ID
                  BLASTX
Method
                  g2498864
NCBI GI
                  255
BLAST score
                   4.0e-22
E value
                   72
Match length
                   33
% identity
                  RRP5 PROTEIN HOMOLOG (KIAA0185) >gi 1136430 dbj_BAA11502
NCBI Description
                   (D80007) similar to hypothetical protein YM9959.11C of
                   S.cerevisiae. [Homo sapiens]
                   229039
Seq. No.
                   LIB3196-022-P1-M1-C8
Seq. ID
                   BLASTX
Method
                   g3297823
NCBI GI
                   213
BLAST score
                   4.0e-17
E value
                   75
Match length
                   63
% identity
                  (AL031032) putative protein [Arabidopsis thaliana]
NCBI Description
                   229040
Seq. No.
                   LIB3196-022-P1-M1-C9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3915742
                   488
BLAST score
                   2.0e-54
E value
Match length
                   120
% identity
                   91
NCBI Description LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319
                   (M69188) legumin A [Gossypium hirsutum]
                   >qi 444320 prf 1906369A legumin A:ISOTYPE=D alloallele
                   [Gossypium hirsutum]
                   229041
Seq. No.
                   LIB3196-022-P1-M1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g225580
```



Match length 121 % identity 85

NCBI Description storage protein C72 [Saguinus oedipus]

Seq. No. 229042

Seq. ID LIB3196-022-P1-M1-D4

Method BLASTX
NCBI GI g1173187
BLAST score 530
E value 2.0e-54
Match length 105
% identity 95

NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi\_1362041\_pir\_\_S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden

strawberry >gi 643074 (U19940) putative 40S ribosomal

protein s12 [Fragaria x ananassa]

Seq. No. 229043

Seq. ID LIB3196-022-P1-M1-D6

Method BLASTX
NCBI GI g1695719
BLAST score 629
E value 6.0e-66
Match length 123
% identity 99

NCBI Description (D89342) luminal binding protein [Arabidopsis thaliana]

Seq. No. 229044

Seq. ID LIB3196-022-P1-M1-D7

Method BLASTX
NCBI GI g1737218
BLAST score 460
E value 4.0e-46
Match length 101
% identity 76

NCBI Description (U79959) vacuolar sorting receptor homolog [Arabidopsis

thaliana]

Seq. No. 229045

Seq. ID LIB3196-022-P1-M1-D9

Method BLASTX
NCBI GI g2500380
BLAST score 514
E value 2.0e-52
Match length 94
% identity 100

NCBI Description 60S RIBOSOMAL PROTEIN L44 >gi\_2119128\_pir\_\_JC4923 ribosomal

protein RL44 - upland cotton >gi 1553129 (U64677) ribosomal

protein L44 isoform a [Gossypium hirsutum] >gi\_1553131 (U64678) ribosomal protein L44 isoform b [Gossypium

hirsutum]

Seq. No. 229046

Seq. ID LIB3196-022-P1-M1-E1

Method BLASTX NCBI GI g3319958 BLAST score 567



1.0e-58

E value

```
Match length
                   112
% identity
                   10
NCBI Description
                  (AJ228139) VAKTI precursor [Homo sapiens]
                  229047
Seq. No.
                  LIB3196-022-P1-M1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                   q88052
BLAST score
                   337
E value
                   1.0e-31
Match length
                   122
                   55
% identity
NCBI Description
                  keratin K5, 58K type II, epidermal (version 2) - human
                   (fragment)
                   229048
Seq. No.
                  LIB3196-022-P1-M1-E3
Seq. ID
Method
                  BLASTX
                  g3510264
NCBI GI
BLAST score
                   218
E value
                   9.0e-18
Match length
                   115
% identity
                   41
                  (AC005310) hypothetical protein, 5' partial [Arabidopsis
NCBI Description
                   thalianal
                   229049
Seq. No.
                  LIB3196-022-P1-M1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2982453
BLAST score
                   512
E value
                   3.0e-52
Match length
                   116
% identity
                   86
NCBI Description
                  (AL022223) fructose-bisphosphate aldolase-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   229050
                   LIB3196-022-P1-M1-E8
Seq. ID
Method
                   BLASTX
                   g178052
NCBI GI
BLAST score
                   654
E value
                   8.0e-69
Match length
                   125
% identity
                   100
NCBI Description
                  (M95178) alpha-actinin [Homo sapiens]
                   >gi 4501891 ref NP 001093.1 pACTN1 actinin, alpha
Seq. No.
                   229051
                  LIB3196-022-P1-M1-F1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3882211
BLAST score
                   628
E value
                   9.0e-66
Match length
                   127
% identity
                   97
```

NCBI GI

E value

BLAST score

g2586125

3.0e-44

444



```
NCBI Description (AB018288) KIAA0745 protein [Homo sapiens]
                  229052
                          C_{ij}
Seq. No.
                  LIB3196-022-P1-M1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1707855
BLAST score
                  499
E value
                  1.0e-50
Match length
                  113
                  79
% identity
NCBI Description
                  (Y09292) obtusifoliol 14-alpha-demethylase [Triticum
                  aestivum]
                  229053
Seq. No.
Seq. ID
                  LIB3196-022-P1-M1-F12
Method
                  BLASTX
NCBI GI
                  q1363944
BLAST score
                   592
E value
                   1.0e-61
Match length
                  119
                   99
% identity
                  type I keratin 16 - human >gi_1195531_bbs_172338 (S79867)
NCBI Description
                   type I keratin 16, K16 [human, epidermal keratinocytes,
                   Peptide, 473 aa] [Homo sapiens]
                   229054
Seq. No.
                  LIB3196-022-P1-M1-F3
Seq. ID
Method
                  BLASTX
                   g2135234
NCBI GI
                   224
BLAST score
E value
                   8.0e-27
Match length
                   126
% identity
                  gene PP2A protein - human >gi 1000888 (L42373) protein
NCBI Description
                   phosphatase 2A B56-alpha [Homo sapiens]
                   >gi 1585671 prf 2201437A phospholipase
                   2A:SUBUNIT=regulatory:ISOTYPE=alpha [Homo sapiens]
Seq. No.
                   229055
                   LIB3196-022-P1-M1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2559012
BLAST score
                   548
E value
                   2.0e-56
Match length
                   114
% identity
                   100
NCBI Description
                   (AF026293) chaperonin containing t-complex polypeptide 1,
                   beta subunit; CCT-beta [Homo sapiens] >gi_4090929
                   (AF026166) chaperonin-containing TCP-1 beta subunit homolog
                   [Homo sapiens]
                   229056
Seq. No.
Seq. ID
                   LIB3196-022-P1-M1-F8
                   BLASTX
Method
```



```
113
Match length
                  74
% identity
                  (U89512) b-keto acyl reductase [Arabidopsis thaliana]
NCBI Description
                  229057
Seq. No.
                  LIB3196-022-P1-M1-F9
Seq. ID
                  BLASTX
Method
                  q1346349
NCBI GI
                  316
BLAST score
                  9.0e-30
E value
                  72
Match length
                  89
% identity
                  KERATIN, TYPE II CYTOSKELETAL 6F (CYTOKERATIN 6F) (CK 6F)
NCBI Description
                  (K6F KERATIN) >gi_2119219_pir__I61771 keratin type II -
                  human >gi 908805 (L42612) keratin type II [Homo sapiens]
                  229058
Seq. No.
                  LIB3196-022-P1-M1-G1
Seq. ID
                  BLASTX
Method
                  g3879146
NCBI GI
                  175
BLAST score
                  1.0e-12
E value
                  100
Match length
                  43
% identity
                  (Z93386) Similarity to Yeast hypothetical 52.9 KD protein
NCBI Description
                   (SW:P43616); cDNA EST EMBL:M89432 comes from this gene;
                  cDNA EST EMBL:D71008 comes from this gene; cDNA EST
                  EMBL:D73578 comes from this gene; cDNA EST EMBL:D69025
                  comes
                  229059
Seq. No.
                  LIB3196-022-P1-M1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                  481
E value
                   1.0e-48
Match length
                  93
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                   229060
Seq. No.
                   LIB3196-022-P1-M1-G7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4249382
BLAST score
                   329
                   7.0e-31
E value
Match length
                   105
% identity
                   (AC005966) Strong similarity to gi 3337350 F13P17.3
NCBI Description
                   putative permease from Arabidopsis thaliana BAC
                   gb AC004481. [Arabidopsis thaliana]
```

229061 Seq. No.

LIB3196-022-P1-M1-G9 Seq. ID

BLASTX Method g137578 NCBI GI 527 BLAST score



```
5.0e-54
E value
Match length
                     121
                     88
% identity
NCBI Description
                     VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
                     >gi_81545_pir__S06398 alpha-globulin type A precursor -
upland cotton >gi_167371 (M19378) vicilin precursor
[Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                      [Artificial gene] >gi_226119_prf__1410330A vicilin gene A
                      [Saguinus oedipus]
Seq. No.
                     229062
                     LIB3196-022-P1-M1-H11
Seq. ID
Method
                     BLASTX
NCBI GI
                     q585165
BLAST score
                     333
E value
                     3.0e - 31
Match length
                     119
                     62
% identity
                     GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM
NCBI Description
                     (G6PD) >gi_2129985_pir__S60287 glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - potato
                     >gi_471345_emb_CAA52442_ (X74421) glucose-6-phosphate
                     1-dehydrogenase [Solanum tuberosum]
Seq. No.
                     229063
                     LIB3196-022-P1-M1-H2
Seq. ID
Method
                     BLASTX
NCBI GI
                     a2388575
                     220
BLAST score
                      5.0e-18
E value
Match length
                     110
% identity
NCBI Description (AC000098) YUP8H12.18 [Arabidopsis thaliana]
                     229064
Seq. No.
Seq. ID
                     LIB3196-022-P1-M1-H5
Method
                     BLASTX
NCBI GI
                      q280816
BLAST score
                      413
E value
                      1.0e-40
Match length
                      82
% identity
                      98
                     keratin 13, type I, cytoskeletal, short form - human
NCBI Description
                     >gi_30377_emb_CAA36673_ (X52426) cytokeratin 13 [Homo sapiens] >gi_3603253 (AF049259) keratin 13 [Homo sapiens]
                      >gi 4504911 ref NP 002265.1 pKRT13 keratin
Seq. No.
                      229065
                     LIB3196-022-P1-M1-H7
Seq. ID
Method
                     BLASTX
NCBI GI
                      q124427
BLAST score
                      605
```

E value 4.0e-63 Match length 116 100 % identity

INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 2 (IMP DEHYDROGENASE NCBI Description



```
dehydrogenase (EC 1.1.1.205) - mouse >gi_309413 (M33934)
IMP dehydrogenase (EC 1.2.1.14) [Mus musculus]

229066
LIB3196-023-P1-M1-A4
BLASTX
g2119228
196
3.0e-15
67
```

Seq. No. 229067 Seq. ID LIB3196-023-P1-M1-A6

Seq. No.

Seq. ID Method

NCBI GI BLAST score

E value

Match length

Method BLASTX
NCBI GI g1223922
BLAST score 441
E value 6.0e-44
Match length 100
% identity 76

NCBI Description (U49445) Vigna radiata vicilin peptidohydrolase [Vigna

radiata]

Seq. No. 229068

Seq. ID LIB3196-023-P1-M1-B3

Method BLASTX
NCBI GI g549090
BLAST score 392
E value 4.0e-38
Match length 76
% identity 95

NCBI Description LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR

RECEPTOR 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR) >gi\_2136332\_pir\_\_I54182 tumor necrosis factor receptor 2-related protein - human >gi\_339762 (L04270) tumor necrosis factor receptor 2 related protein [Homo sapiens] >gi\_4505039\_ref\_NP\_002333.1\_pLTBR\_ lymphotoxin B

receptor

Seq. No. 229069

Seq. ID LIB3196-023-P1-M1-B5

Method BLASTX
NCBI GI g3478700
BLAST score 322
E value 4.0e-30
Match length 96
% identity 62

NCBI Description (AF034387) AFT protein [Arabidopsis thaliana]

Seq. No. 229070

Seq. ID LIB3196-023-P1-M1-C1

Method BLASTX
NCBI GI g125080
BLAST score 599
E value 2.0e-62

32807 -



Match length % identity 98

KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK NCBI Description

14) >gi\_2144816\_pir\_\_KRHUE keratin, 50K type I cytoskeletal - human >gi\_386848 (J00124) keratin [Homo sapiens] >gi\_4504913\_ref\_NP\_000517.1\_pKRT14\_ keratin 14

(epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No. 229071

Seq. ID LIB3196-023-P1-M1-C10

Method BLASTX NCBI GI q167311 BLAST score 465 9.0e-47E value Match length 103 84 % identity

NCBI Description (M83301) 2S albumin storage protein [Gossypium hirsutum]

229072 Seq. No.

Seq. ID LIB3196-023-P1-M1-C12

Method BLASTX NCBI GI q729985 BLAST score 261 E value 7.0e-23 106 Match length % identity 50

PROCESSING ALPHA-1,2-MANNOSIDASE (ALPHA-1,2-MANNOSIDASE 1B) NCBI Description

>gi\_474278 (U03458) alpha-mannosidase [Mus musculus] >gi 3335696 (AF078095) alpha 1,2-mannosidase IB [Mus

musculus]

Seq. No. 229073

LIB3196-023-P1-M1-C2 Seq. ID

Method BLASTX NCBI GI g266691 BLAST score 368 E value 3.0e - 35Match length 113 70 % identity

NCBI Description OLEOSIN 16.4 KD >gi 167361 (L00934) 16.4 kDa oleosin

[Gossypium hirsutum]

229074 Seq. No.

Seq. ID LIB3196-023-P1-M1-C4

Method BLASTX NCBI GI g2498323 BLAST score 590 E value 2.0e-61 107 Match length 62 % identity

EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY NCBI Description

COMPONENT P85) >gi 1488324 (U65932) extracellular matrix protein 1 [Homo sapiens] >gi 1488332 (U65938) extracellular

matrix protein 1 [Homo sapiens] >gi 2654433 (U68186)

extracellular matrix protein 1 [Homo sapiens]

Seq. No. 229075

NCBI Description



```
LIB3196-023-P1-M1-C7
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q1619602
 BLAST score
                    391
 E value
                    5.0e-38
 Match length
                    122
 % identity
                    63
 NCBI Description (Y08726) MtN3 [Medicago truncatula]
                    229076
 Seq. No.
 Seq. ID
                    LIB3196-023-P1-M1-C8
 Method
                    BLASTX
 NCBI GI
                    q1654244
 BLAST score
                    564
 E value
                    2.0e-58
 Match length
                    114
 % identity
                    96
                    (U55339) Gossypium barbadense NADH dehydrogenase [Gossypium
 NCBI Description
                    barbadense]
                    229077
 Seq. No.
 Seq. ID
                    LIB3196-023-P1-M1-D1
 Method
                    BLASTX
 NCBI GI
                    q549063
 BLAST score
                    408
 E value
                    5.0e-40
 Match length
                    92
 % identity
                    84
                    TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
 NCBI Description
                    >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                    21kd polypeptide [Oryza sativa]
 Seq. No.
                    229078
 Seq. ID
                    LIB3196-023-P1-M1-D10
 Method
                    BLASTX
 NCBI GI
                    q4176446
 BLAST score
                    599
 E value
                    2.0e-62
 Match length
                    125
                    97
 % identity
                    (AL022238) dJ1042K10.2.1 (novel protein with probable
 NCBI Description
                    rabGAP domains and Src homology domain 3) (isoform 1) [Homo
                    sapiens]
 Seq. No.
                    229079
                    LIB3196-023-P1-M1-D3
· Seq. ID
                    BLASTX
 Method
                    q3176668
 NCBI GI
 BLAST score
                    544
                     6.0e-56
 E value
                    117
 Match length
 % identity
```

(AC004393) Similar to ribosomal protein L17 gb\_X62724 from

Hordeum vulgare. ESTs gb\_Z34728, gb\_F19974, gb\_T75677 and gb\_Z33937 come from this gene. [Arabidopsis thaliana]



```
229080
Seq. No.
                  LIB3196-023-P1-M1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1363944
BLAST score
                  653
E value
                  1.0e-68
Match length
                  131
                  99
% identity
                  type I keratin 16 - human >gi_1195531_bbs_172338 (S79867)
NCBI Description
                  type I keratin 16, K16 [human, epidermal keratinocytes,
                  Peptide, 473 aa] [Homo sapiens]
                  229081
Seq. No.
                  LIB3196-023-P1-M1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4006893
BLAST score
                  148
                   1.0e-09
E value
Match length
                  55
% identity
                   85
NCBI Description (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]
                   229082
Seq. No.
                   LIB3196-023-P1-M1-E1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3915742
BLAST score
                   559
                   1.0e-57
E value
Match length
                   118
                   91
% identity
NCBI Description LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi 167319
                   (M69188) legumin A [Gossypium hirsutum]
                   >gi 444320 prf 1906369A legumin A:ISOTYPE=D alloallele
                   [Gossypium hirsutum]
Seq. No.
                   229083
                   LIB3196-023-P1-M1-E12
Seq. ID
                   BLASTX
Method
                   g2065531
NCBI GI
BLAST score
                   552
                   7.0e-57
E value
                   126
Match length
                   77
% identity
NCBI Description (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
Seq. No.
                   229084
                   LIB3196-023-P1-M1-E2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g115492
BLAST score
                   505
                   2.0e-51
E value
                   98
Match length
                   50
% identity
NCBI Description CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)
```

Seq. No. 229085

calmodulin-related protein [Petunia hybrida]

Method

NCBI GI

BLASTX

q88044



```
LIB3196-023-P1-M1-E3
Seq. ID
                   BLASTX
Method
                   a3901014
NCBI GI
BLAST score
                   235
                   1.0e-19
E value
                   55
Match length
                   76
% identity
                   (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                   sylvatica]
                   229086
Seq. No.
                   LIB3196-023-P1-M1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q266344
BLAST score
                   640
                   4.0e-67
E value
                   132
Match length
                   95
% identity
                   LEUKOCYTE ELASTASE INHIBITOR (LEI) (MONOCYTE/NEUTROPHIL
NCBI Description
                   ELASTASE INHIBITOR) (EI) >gi 284073_pir S27383 elastase inhibitor - human >gi 2997692 (AF053630)
                   monocyte/neutrophil elastase inhibitor [Homo sapiens]
                   229087
Seq. No.
Seq. ID
                   LIB3196-023-P1-M1-E6
Method
                   BLASTX
                   q2098581
NCBI GI
                   285
BLAST score
                   1.0e-25
E value
Match length
                   79
% identity
                   70
NCBI Description (U53830) interferon regulatory factor 7A [Homo sapiens]
                   229088
Seq. No.
Seq. ID
                   LIB3196-023-P1-M1-F11
Method
                   BLASTX
                   q4240261
NCBI GI
                   157
BLAST score
                   1.0e-10
E value
                   30
Match length
% identity
                   100
NCBI Description (AB020693) KIAA0886 protein [Homo sapiens]
                   229089
Seq. No.
                   LIB3196-023-P1-M1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g35053
                   590
BLAST score
E value
                    3.0e-61
                   115
Match length
                    97
% identity
NCBI Description (X53778) uracil DNA glycosylase [Homo sapiens]
                    229090
Seq. No.
Seq. ID
                   LIB3196-023-P1-M1-F3
```

Method

NCBI GI

BLAST score



```
623
BLAST score
                  3.0e-65
E value
                  130
Match length
                  96
% identity
                  keratin 4, type II, cytoskeletal - human (fragment)
NCBI Description
                  >gi_34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA)
                  [Homo sapiens]
                  229091
Seq. No.
                  LIB3196-023-P1-M1-F4
Seq. ID
                  BLASTX
Method
                  g1350548
NCBI GI
                  241
BLAST score
                  2.0e-20
E value
Match length
                  71
                   59
% identity
                  (L47609) heat shock-like protein [Picea glauca]
NCBI Description
                   229092
Seq. No.
                  LIB3196-023-P1-M1-F7
Seq. ID
                   BLASTX
Method
                   g547752
NCBI GI
                   150
BLAST score
                   1.0e-09
E value
                   30
Match length
                   97
% identity
                  KERATIN, TYPE II CYTOSKELETAL 2 ORAL (CYTOKERATIN 2P) (K2P)
NCBI Description
                   (CK 2P) >gi_2119218_pir__I53169 cytokeratin 2 - human
                   >gi_181390 (M99063) cytokeratin 2 [Homo sapiens]
                   229093
Seq. No.
                   LIB3196-023-P1-M1-F9
Seq. ID
                   BLASTX
Method
                   g2462077
NCBI GI
                   157
BLAST score
                   1.0e-10
E value
                   41
Match length
                   66
% identity
NCBI Description (Y11871) Oxal protein [Arabidopsis thaliana]
                   229094
Seq. No.
                   LIB3196-023-P1-M1-G1
Seq. ID
                   BLASTX
Method
                   g2146926
NCBI GI
                   161
BLAST score
                   1.0e-23
E value
                   82
Match length
                   68
% identity
                   [phosphorylase] phosphatase (EC 3.1.3.17) 55K chain -
NCBI Description
                   African clawed frog (fragment) >gi_963087_emb_CAA56714_
                   (X80697) phosphorylase phosphatase [Xenopus laevis]
                   229095
 Seq. No.
                   LIB3196-023-P1-M1-G10
 Seq. ID
                   BLASTX
```

32812

g1346347



```
8.0e-62
E value
Match length
                  122
                  98
% identity
                  KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D)
NCBI Description
                  (K6D KERATIN) >gi_2119225_pir_161769 keratin type II -
                  human (fragment) >gi_914833 (L42610) keratin type II [Homo
                  sapiens]
                  229096
Seq. No.
                  LIB3196-023-P1-M1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3790610
BLAST score
                  501
                  7.0e-51
E value
                  98
Match length
                  89
% identity
                 (AF093673) layilin [Cricetulus griseus]
NCBI Description
                  229097
Seq. No.
                  LIB3196-023-P1-M1-G2
Seq. ID
Method
                  BLASTX
                  g66179
NCBI GI
BLAST score
                  361
                  2.0e-34
E value
Match length
                  93
                  77
% identity
                  NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 -
NCBI Description
                  common tobacco chloroplast >gi_225255_prf__1211235CP NADH
                  dehydrogenase 4-like ORF 509B [Nicotiana tabacum]
                   229098
Seq. No.
                  LIB3196-023-P1-M1-G4
Seq. ID
Method
                  BLASTX
                  q189049
NCBI GI
                   661
BLAST score
E value
                   1.0e-69
Match length
                  133
% identity
                   92
NCBI Description (L04490) NADH dehydrogenase (ubiquinone) [Homo sapiens]
                   229099
Seq. No.
Seq. ID
                  LIB3196-023-P1-M1-G5
Method
                  BLASTX
NCBI GI
                   g908917
BLAST score
                   577
E value
                   9.0e-60
Match length
                   119
% identity
                   98
NCBI Description (L24544) DNA helicase [Homo sapiens]
Seq. No.
                   229100
                  LIB3196-023-P1-M1-G6
Seq. ID
```

Method BLASTX

NCBI GI g2833388
BLAST score 496
E value 3.0e-50
Match length 123



% identity GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR NCBI Description >gi 629660 pir S43341 ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - cassava >gi\_437042\_emb\_CAA52273\_ (X74160) starch (bacterial glycogen) synthase [Manihot esculenta] 229101 Seq. No. Seq. ID LIB3196-023-P1-M1-G7 BLASTX Method NCBI GI q485514 397 BLAST score 9.0e-39 E value 82 Match length % identity ADR11-2 protein - soybean (fragment) NCBI Description >gi 296443 emb\_CAA49341 (X69640) auxin down regulated [Glycine max] 229102 Seq. No. LIB3196-023-P1-M1-G9 Seq. ID Method BLASTX NCBI GI q2144118 BLAST score 191 1.0e-15 E value Match length 100 44 % identity NCBI Description alpha-macroglobulin - guinea pig >gi\_1304084\_dbj\_BAA12316\_ (D84338) alpha-macroglobulin [Cavia porcellus] Seq. No. 229103 LIB3196-023-P1-M1-H1 Seq. ID Method BLASTX NCBI GI g2950478 BLAST score 180 E value 2.0e-15 98 Match length % identity 48 NCBI Description (AL022070) hypothetical protein [Schizosaccharomyces pombe] Seq. No. 229104 LIB3196-023-P1-M1-H11 Seq. ID Method BLASTX q137578 NCBI GI 449 BLAST score E value 6.0e-45 Match length 110 % identity 84 NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi 81545 pir S06398 alpha-globulin type A precursor upland cotton >gi 167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi\_207906 (M18027) alpha globulin A [Artificial gene] >gi\_226119\_prf\_\_1410330A vicilin gene A [Saguinus oedipus]

Seq. No. 229105

Seq. ID LIB3196-023-P1-M1-H2



```
Method
                  BLASTX
                  q4263646
NCBI GI
                  198
BLAST score
                  1.0e-15
E value
Match length
                  97
% identity
                  43
                  (AC006136) putative TA1-like reverse transcriptase
NCBI Description
                  [Arabidopsis thaliana]
                  229106
Seq. No.
                  LIB3196-023-P1-M1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q126156
BLAST score
                  400
                  4.0e-39
E value
Match length
                  103
                  77
% identity
                  LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
NCBI Description
                  >gi 72288 pir FWCNBB beta-globulin B precursor (clone 134)
                   - upland cotton >gi_167373 (M16936) vicilin precursor
                   [Gossypium hirsutum] >gi_1171335 (U43727) legumin B
                   [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                  protein C134 [Saguinus oedipus]
Seq. No.
                  229107
Seq. ID
                  LIB3196-024-P1-M1-A1
Method
                  BLASTX
NCBI GI
                  q1171978
BLAST score
                   457
                   9.0e-46
E value
Match length
                  124
                   23
% identity
NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
                   (PABP 2) >gi_304109 (L19418) poly(A)-binding protein
                   [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961)
                  poly(A)-binding protein [Arabidopsis thaliana]
                   229108
Seq. No.
                   LIB3196-024-P1-M1-A12
Seq. ID
                   BLASTX
Method
                   g950111
NCBI GI
BLAST score
                   460
                   4.0e-46
E value
Match length
                   116
                   78
% identity
NCBI Description (U22230) ribosomal protein S17 [Felis catus]
Seq. No.
                   229109
                   LIB3196-024-P1-M1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4510339
BLAST score
                   272
                   3.0e-24
E value
                   58
Match length
                   83
% identity
                  (AC006921) putative ABC transporter protein [Arabidopsis
NCBI Description
```

thaliana]



Seq. No.

```
LIB3196-024-P1-M1-A4
Seq. ID
Method
                  BLASTX
                  g125077
NCBI GI
                  646
BLAST score
                  6.0e-68
E value
                  132
Match length
                  98
% identity
                  KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK
NCBI Description
                  13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal,
                  long form - human >gi_34033_emb_CAA32786_ (X14640) keratin
                  13 [Homo sapiens]
                  229111
Seq. No.
                  LIB3196-024-P1-M1-A6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4455367
                  392
BLAST score
                  4.0e-38
E value
                  126
Match length
% identity
                   62
                  (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                  229112
Seq. No.
                  LIB3196-024-P1-M1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3068713
                   240
BLAST score
                   2.0e-20
E value
                  78
Match length
                   71
% identity
                  (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
                   229113
Seq. No.
                   LIB3196-024-P1-M1-B10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3935151
                   438
BLAST score
E value
                   1.0e-43
                   101
Match length
                   74
% identity
NCBI Description (AC005106) T25N20.15 [Arabidopsis thaliana]
                   229114
Seq. No.
                   LIB3196-024-P1-M1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3182976
BLAST score
                   510
                   6.0e-52
E value
                   117
Match length
                   82
% identity
                   C-TERMINAL BINDING PROTEIN 2 >gi 2909777 (AF016507)
NCBI Description
                   C-terminal binding protein 2 [Homo sapiens]
                   >gi_4557499_ref_NP_001320.1_pCTBP2_ C-terminal binding
                   protein
```



```
229115
Seq. No.
                  LIB3196-024-P1-M1-B3
Seq. ID
                  BLASTX
Method
                  q3915742
NCBI GI
                  455
BLAST score
                  1.0e-45
E value
                  95
Match length
                  92
% identity
                  LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319
NCBI Description
                  (M69188) legumin A [Gossypium hirsutum]
                  >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele
                  [Gossypium hirsutum]
                  229116
Seq. No.
                  LIB3196-024-P1-M1-B4
Seq. ID
                  BLASTX
Method
                  g2208944
NCBI GI
                  350
BLAST score
                  3.0e-33
E value
                  118
Match length
                  58
% identity
NCBI Description (Y11120) nodulin-35 homologue [Arabidopsis thaliana]
                  229117
Seq. No.
                  LIB3196-024-P1-M1-B6
Seq. ID
                  BLASTX
Method
                  g1173256
NCBI GI
                  419
BLAST score
                  2.0e-41
E value
                  81
Match length
                   99
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi_629496_pir__S45026 ribosomal
                  protein S4 - upland cotton >gi 488739 emb CAA55882
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
Seq. No.
                   229118
                   LIB3196-024-P1-M1-B9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2497442
BLAST score
                   272
E value
                   5.0e-24
Match length
                   51
% identity
                   INTERFERON REGULATORY FACTOR 3 (IRF-3)
NCBI Description
                   >gi 1107689_emb_CAA91227_ (Z56281) interferon regulatory
                   factor 3 [Homo sapiens] >gi_4504725_ref_NP_001562.1_pIRF3_
                   interferon regulatory factor
Seq. No.
                   229119
                   LIB3196-024-P1-M1-C1
Seq. ID
Method
                   BLASTX
                   g4490741
NCBI GI
                   178
BLAST score
                   5.0e-13
E value
```

94

39

Match length

% identity

% identity

43



```
NCBI Description (AL035708) hypothetical protein [Arabidopsis thaliana]
                  229120
Seq. No.
                  LIB3196-024-P1-M1-C12
Seq. ID
                  BLASTX
Method
                  q4406780
NCBI GI
BLAST score
                  516
                  1.0e-52
E value
                  122
Match length
                  82
% identity
                  (AC006532) putative multispanning membrane protein
NCBI Description
                  [Arabidopsis thaliana]
                  229121
Seq. No.
                  LIB3196-024-P1-M1-C2
Seq. ID
Method
                  BLASTX
                  q1362047
NCBI GI
BLAST score
                  219
                  8.0e-18
E value
                  52
Match length
                  77
% identity
                  cysteine proteinase (EC 3.4.22.-) precursor - soybean
NCBI Description
                  >gi 479060_emb_CAA83673 (Z32795) cysteine proteinase
                  [Glycine max] >gi_1096153 prf _2111244A Cys protease
                   [Glycine max]
                  229122
Seq. No.
                  LIB3196-024-P1-M1-C3
Seq. ID
                  BLASTX
Method
                  q2618686
NCBI GI
                  183
BLAST score
E value
                  1.0e-13
Match length
                  88
                  53
% identity
NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  229123
                  LIB3196-024-P1-M1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  a2146797
                   518
BLAST score
E value
                   7.0e-53
                  128
Match length
                   59
% identity
                  protein disulfide-isomerase (EC 5.3.4.1) - Castor bean
NCBI Description
                   >gi_1134968 (U41385) protein disulphide isomerase PDI
                   [Ricinus communis] >gi 1587210_prf 2206331A protein
                   disulfide isomerase [Ricinus communis]
                   229124
Seq. No.
                   LIB3196-024-P1-M1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1552169
BLAST score
                   198
E value
                   2.0e-15
Match length
                   103
```

E value

Match length

8.0e-54



```
NCBI Description
                 (D42138) PIG-B [Homo sapiens]
                  229125
Seq. No.
                  LIB3196-024-P1-M1-C6
Seq. ID
                  BLASTX
Method
                  g137580
NCBI GI
                  554
BLAST score
                  4.0e-57
E value
                  107
Match length
                  100
% identity
                  VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72)
NCBI Description
                  >gi_72286_pir__FWCNAB alpha-globulin B precursor (clone
                  C72) - upland cotton >gi 167375 (M16891) vicilin precursor
                  [Gossypium hirsutum]
Seq. No.
                  229126
                  LIB3196-024-P1-M1-C9
Seq. ID
Method
                  BLASTX
                  q125077
NCBI GI
                  620
BLAST score
                  7.0e-65
E value
                  129
Match length
                  96
% identity
                  KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK
NCBI Description
                  13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal,
                   long form - human >gi 34033 emb_CAA32786_ (X14640) keratin
                   13 [Homo sapiens]
                   229127
Seq. No.
                  LIB3196-024-P1-M1-D1
Seq. ID
                  BLASTX
Method
                   g4056502
NCBI GI
                   415
BLAST score
                   8.0e-41
E value
                   89
Match length
                   89
% identity
NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
                   229128
Seq. No.
                   LIB3196-024-P1-M1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2135074
BLAST score
                   141
                   5.0e-09
E value
                   31
Match length
% identity
NCBI Description epidermal growth factor receptor-related protein - human
                   (fragment) >gi_178252 (M99624) epidermal growth factor
                   receptor-related protein [Homo sapiens]
                   229129
Seq. No.
                   LIB3196-024-P1-M1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g82426
BLAST score
                   525
```



% identity ubiquitin precursor - barley (fragment) NCBI Description >gi\_755763\_emb\_CAA27751\_ (X04133) ubiquitin polyprecursor (171 aa) [Hordeum vulgare] 229130 Seq. No. LIB3196-024-P1-M1-D4 Seq. ID BLASTX Method q4091879 NCBI GI 157 BLAST score 1.0e-10 E value 53 Match length 64 % identity (AF061812) keratin 16 [Homo sapiens] NCBI Description >gi\_4321795\_gb\_AAD15829\_ (AF061809) keratin 16 [Homo sapiens] 229131 Seq. No. Seq. ID LIB3196-024-P1-M1-D6 BLASTX Method q1397319 NCBI GI 195 BLAST score 5.0e-15 E value 90 Match length 44 % identity (U61953) No definition line found [Caenorhabditis elegans] NCBI Description 229132 Seq. No. Seq. ID LIB3196-024-P1-M1-D8 Method BLASTX g1053047 NCBI GI BLAST score 487 2.0e-49 E value 100 Match length % identity 97 (U38425) histone H3 [Glycine max] >gi\_1053049 (U38426) NCBI Description histone H3 [Glycine max] >gi\_1053051 (U38427) histone H3 [Glycine max] 229133 Seq. No. LIB3196-024-P1-M1-D9 Seq. ID BLASTX Method g4539408 NCBI GI 186 BLAST score 5.0e-14E value 44 Match length 82 % identity NCBI Description (AL049524) putative alpha NAC [Arabidopsis thaliana] 229134 Seq. No. LIB3196-024-P1-M1-E1 Seq. ID BLASTX Method g72287 NCBI GI 663 BLAST score

32820

6.0e-70

124

100

E value

Match length

% identity



```
beta-globulin A precursor (clone 94) - upland cotton
NCBI Description
                  (fragment) >gi 167377 (M16905) legumin precursor [Gossypium
                  hirsutum]
Seq. No.
                  229135
                  LIB3196-024-P1-M1-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g207905
                  277
BLAST score
                  1.0e-24
E value
                  83
Match length
                  64
% identity
                  (M18027) alpha globulin B [Artificial gene]
NCBI Description
Seq. No.
                  229136
                  LIB3196-024-P1-M1-E12
Seq. ID
Method
                  BLASTX
                  q113271
NCBI GI
BLAST score
                  305
                  2.0e-53
E value
                  131
Match length
                  85
% identity
                  ACTIN, CYTOPLASMIC 1 (BETA ACTIN) >gi_85691_pir__S01077
NCBI Description
                  actin beta, cytoskeletal - Kenyan clawed frog
                  >gi 1334642_emb_CAA30390_ (X07507) actin [Xenopus borealis]
                  229137
Seq. No.
                  LIB3196-024-P1-M1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q72287
BLAST score
                   566
                   2.0e-58
E value
Match length
                   126
                   90
% identity
                  beta-globulin A precursor (clone 94) - upland cotton
NCBI Description
                   (fragment) >gi 167377 (M16905) legumin precursor [Gossypium
                   hirsutum]
Seq. No.
                   229138
                   LIB3196-024-P1-M1-E5
Seq. ID
Method
                   BLASTX
                   g1479983
NCBI GI
                   557
BLAST score
                   2.0e-57
E value
Match length
                   121
 % identity
                   84
NCBI Description (L78465) alpha-N-acetylglucosaminidase [Homo sapiens]
                   229139
Seq. No.
                   LIB3196-024-P1-M1-F1
Seq. ID
                   BLASTX
Method
                   g1710401
NCBI GI
                   599
BLAST score
                   2.0e-62
E value
                   123
Match length
                   89
 % identity
```

NCBI Description RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN

Method NCBI GI

E value Match length

BLAST score

% identity



```
>gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase
                  R2 [Nicotiana tabacum]
                  229140
Seq. No.
                  LIB3196-024-P1-M1-F10
Seq. ID
                  BLASTX
Method
                  g2293575
NCBI GI
                  694
BLAST score
                  2.0e-73
E value
                  131
Match length
                  100
% identity
                  (AF013213) elongation factor 1 alpha [Bos taurus]
NCBI Description
                  229141
Seq. No.
                  LIB3196-024-P1-M1-F11
Seq. ID
                  BLASTX
Method
                  q586000
NCBI GI
                   476
BLAST score
                   6.0e-48
E value
                   90
Match length
                   100
% identity
                  SM22-ALPHA HOMOLOG (HA1756) (KIAA0120)
NCBI Description
                   >gi_434763_dbj_BAA04802_ (D21261) similar to human 22kDa,
                   SM22 mRNA (HUM22SM). [Homo sapiens]
                   >gi_4507357_ref_NP_003555.1_pTAGLN2_ transgelin
Seq. No.
                   229142
                  LIB3196-024-P1-M1-F2
Seq. ID
                   BLASTX
Method
                   g629693
NCBI GI
BLAST score
                   155
                   4.0e-11
E value
                   72
Match length
                   53
% identity
                   probable integrase - common tobacco (fragment)
NCBI Description
                   >gi_530742_emb_CAA56791_ (X80830) integrase [Nicotiana
                   tabacum]
                   229143
Seq. No.
                   LIB3196-024-P1-M1-F3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q179212
                   523
BLAST score
                   1.0e-53
E value
                   104
Match length
                   99
% identity
NCBI Description (J03007) Na+ K+ ATPase alpha subunit [Homo sapiens]
                   229144
Seq. No.
                   LIB3196-024-P1-M1-F4
Seq. ID
```

(RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)

32822

BLASTX

g88044 566

1.0e-58



```
keratin 4, type II, cytoskeletal - human (fragment)
NCBI Description
                  >gi 34073_emb_CAA30534_ (X07695) cytokeratin 4 (408 AA)
                  [Homo sapiens]
                  229145
Seq. No.
                  LIB3196-024-P1-M1-F6
Seq. ID
Method
                  BLASTX
                  g1082798
NCBI GI
                  258
BLAST score
                  2.0e-22
E value
                  126
Match length
                  45
% identity
                  spliceosome-associated protein SAP 61 - human >gi_508723
NCBI Description
                  (U08815) SAP 61 [Homo sapiens]
                  229146
Seq. No.
                  LIB3196-024-P1-M1-G12
Seq. ID
                  BLASTX
Method
                  g1170567
NCBI GI
                  573
BLAST score
                  2.0e-59
E value
                  121
Match length
                  90
% identity
                  MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)
NCBI Description
                  >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi
                  >gi 602565_emb CAA83565_ (Z32632) INO1 [Citrus x paradisi]
Seq. No.
                  229147
                  LIB3196-024-P1-M1-G2
Seq. ID
                  BLASTX
Method
                  q231723
NCBI GI
                   478
BLAST score
                  3.0e-48
E value
                  90
Match length
                   100
% identity
NCBI Description CD9 ANTIGEN (27 KD DIPHTHERIA TOXIN RECEPTOR-ASSOCIATED
                   PROTEIN) (DRAP27) >gi_104994_pir__A42929 CD9 antigen -
                   green monkey >gi 218566_dbj BAA01569 (D10726) diphtheria
                   toxin receptor associated protein [Chlorocebus aethiops]
                   229148
Seq. No.
                   LIB3196-024-P1-M1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1351173
                   587
BLAST score
                   6.0e-61
E value
Match length
                   118
% identity
                   97
                   SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)
NCBI Description
                   >qi 1050527 emb CAA62635 (X91257) seryl-tRNA synthetase
                   [Homo sapiens]
```

Seq. No. 229149

LIB3196-024-P1-M1-G6 Seq. ID

Method BLASTX g2117159 NCBI GI BLAST score 146



```
3.0e-09
E value
Match length
                  98
                  28
% identity
                  (Y13247) FB19 protein [Homo sapiens]
NCBI Description
                  >gi 4506009_ref_NP_002705.1_pPPP1R10_ protein phosphatase
                  1, regulatory subunit
                  229150
Seq. No.
                  LIB3196-024-P1-M1-H1
Seq. ID
                  BLASTX
Method
                  g1350680
NCBI GI
                  454
BLAST score
                  2.0e-45
E value
                  123
Match length
% identity
                  74
NCBI Description 60S RIBOSOMAL PROTEIN L1
Seq. No.
                  229151
                  LIB3196-024-P1-M1-H3
Seq. ID
                  BLASTX
Method
                  g386850
NCBI GI
                  655
BLAST score
E value
                  5.0e-69
Match length
                  130
                  100
% identity
NCBI Description (M19723) keratin K5 [Homo sapiens]
Seq. No.
                  229152
                  LIB3196-024-P1-M1-H8
Seq. ID
                  BLASTX
Method
                  q118607
NCBI GI
                   461
BLAST score
                   3.0e-46
E value
                   98
Match length
                   94
% identity
NCBI Description NAD(P)H DEHYDROGENASE (QUINONE) 1 (QUINONE REDUCTASE)
                   (DT-DIAPHORASE) (AZOREDUCTASE) (PHYLLOQUINONE REDUCTASE)
                   (MENADIONE REDUCTASE) >gi_88226_pir__A30879 NAD(P)H
                   dehydrogenase (quinone) (EC 1.6.99.2) 1 - human >gi_189246
                   (J03934) NAD(P)H:menadione oxidoreductase [Homo sapiens]
                   >gi 189292 (M81600) NAD(P)H:quinone oxireductase [Homo
                   sapiens] >gi 4505415 ref NP 000894.1_pNMOR1_ NAD(P)H
                   menadione oxidoreductase 1, dioxin-inducible
                   229153
Seq. No.
                   LIB3196-024-P1-M1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4128133
BLAST score
                   195
```

5.0e-15 E value 81 Match length % identity

NCBI Description (AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]

229154 Seq. No.

LIB3196-025-P1-M1-A3 Seq. ID

Method BLASTX

Method

NCBI GI



```
g2813965
NCBI GI
                  423
BLAST score
                  7.0e-42
E value
                  85
Match length
                  96
% identity
                  (Z97053) adenosine deaminase (ADA) [Homo sapiens]
NCBI Description
                  229155
Seq. No.
                  LIB3196-025-P1-M1-A4
Seq. ID
                  BLASTX
Method
                  g440945
NCBI GI
                  419
BLAST score
                  2.0e-41
E value
                  92
Match length
% identity
                  86
                  (S66773) adenosine deaminase, ADA (exon 10, exon 11)
NCBI Description
                   [human, ADA deficient patient AlNe, peripheral blood T
                   cells, Peptide PartialMutant, 143 aa] [Homo sapiens]
                   229156
Seq. No.
                  LIB3196-025-P1-M1-A5
Seq. ID
                  BLASTX
Method
                   g2459421
NCBI GI
                   434
BLAST score
                   5.0e-43
E value
                   116
Match length
                   68
% identity
                   (AC002332) putative calcium-binding EF-hand protein
NCBI Description
                   [Arabidopsis thaliana]
                   229157
Seq. No.
                   LIB3196-025-P1-M1-A6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g72287
                   582
BLAST score
                   2.0e-60
E value
Match length
                   126
% identity
                   88
                   beta-globulin A precursor (clone 94) - upland cotton
NCBI Description
                   (fragment) >gi_167377 (M16905) legumin precursor [Gossypium
                   hirsutum]
                   229158
Seq. No.
                   LIB3196-025-P1-M1-A8
Seq. ID
Method
                   BLASTX
                   g633890
NCBI GI
BLAST score
                   434
E value
                   4.0e-43
Match length
                   115
% identity
                   (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
NCBI Description
                   vulgare]
Seq. No.
                   229159
                   LIB3196-025-P1-M1-B3
Seq. ID
```

g2578033

BLASTX

Seq. ID

Method



```
BLAST score
                   429
                   2.0e-42
E value
                  83
Match length
                   96
% identity
                  (X97016) omega-6 desaturase [Gossypium hirsutum]
NCBI Description
                   229160
Seq. No.
                  LIB3196-025-P1-M1-B9
Seq. ID
                   BLASTX
Method
                   g120669
NCBI GI
                   435
BLAST score
                   4.0e-43
E value
                   87
Match length
                   92
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi 19566 emb_CAA42905_ (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
                   229161
Seq. No.
                   LIB3196-025-P1-M1-C5
Seq. ID
                   BLASTX
Method
                   g478021
NCBI GI
                   402
BLAST score
                   3.0e-39
E value
                   76
Match length
                   99
% identity
                   tumor surface antigen OA3-305 - human
NCBI Description
                   >gi_396705_emb_CAA80977_ (Z25521) integrin associated
                   protein [Homo sapiens]
                   229162
Seq. No.
                   LIB3196-025-P1-M1-C8
Seq. ID
                   BLASTX
Method
                   g1531539
NCBI GI
                   339
BLAST score
                   7.0e - 32
E value
                   89
Match length
 % identity
                   66
 NCBI Description (D79989) KIAA0167 protein [Homo sapiens]
                   229163
 Seq. No.
                   LIB3196-025-P1-M1-D1
 Seq. ID
                   BLASTX
 Method
                   q4091879
 NCBI GI
                   183
 BLAST score
                   7.0e-14
 E value
                    42
 Match length
                    93
 % identity
                   (AF061812) keratin 16 [Homo sapiens]
 NCBI Description
                    >gi_4321795_gb_AAD15829_ (AF061809) keratin 16 [Homo
                    sapiens]
                    229164
 Seq. No.
```

32826

LIB3196-025-P1-M1-E3

BLASTX



```
g3413167
NCBI GI
                    161
BLAST score
                    4.0e-11
E value
                    34
Match length
                    94
% identity
                    (AJ010225) elongation factor 1-alpha [Cicer arietinum]
NCBI Description
                    229165
Seq. No.
                    LIB3196-025-P1-M1-E6
Seq. ID
                    BLASTX
Method
                    g3152583
NCBI GI
BLAST score
                    315
                    5.0e-29
E value
                    122
Match length
                    55
% identity
                    (ACO02986) Contains similarity to inhibitor of apoptosis
NCBI Description
                    protein gb_U45881 from D. melanogaster. [Arabidopsis
                    thaliana]
                    229166
Seq. No.
                    LIB3196-025-P1-M1-E8
Seq. ID
                    BLASTX
Method
                    g3821055
NCBI GI
                    583
BLAST score
                    2.0e-60
E value
                    127
Match length
                    87
% identity
                    (AJ223603) hypothetical protein [Homo sapiens]
NCBI Description
                    229167
Seq. No.
                    LIB3196-025-P1-M1-E9
Seq. ID
                    BLASTX
Method
                    g137578
NCBI GI
                    394
BLAST score
                    2.0e-38
E value
                    109
Match length
                     68
% identity
                    VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                    >gi_81545_pir__S06398 alpha-globulin type A precursor -
upland cotton >gi_167371 (M19378) vicilin precursor
[Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                     [Artificial gene] >gi_226119_prf _1410330A vicilin gene A
                     [Saguinus oedipus]
                     229168
Seq. No.
                    LIB3196-025-P1-M1-F3
Seq. ID
                    BLASTX
Method
                     g3122659
NCBI GI
                     460
BLAST score
E value
                     4.0e-46
                     106
Match length
                     75
% identity
NCBI Description PEROXIREDOXIN (REHYDRIN HOMOLOG) >gi 1926269 emb CAA72804
                     (Y12089) peroxiredoxin [Arabidopsis thaliana]
```

Seq. No. 229169

Seq. ID LIB3196-025-P1-M1-F4



```
BLASTX
Method
                  g4097583
NCBI GI
                  188
BLAST score
                  3.0e-14
E valu<del>e</del>
                  54
Match length
                  72
% identity
                  (U64924) NTGP3 [Nicotiana tabacum]
NCBI Description
                  229170
Seq. No.
                  LIB3196-025-P1-M1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g113271
                  478
BLAST score
                  4.0e-49
E value
                  104
Match length
                  100
% identity
                  ACTIN, CYTOPLASMIC 1 (BETA ACTIN) >gi_85691_pir__S01077
NCBI Description
                  actin beta, cytoskeletal - Kenyan clawed frog
                   >gi 1334642 emb_CAA30390_ (X07507) actin [Xenopus borealis]
                   229171
Seq. No.
                  LIB3196-025-P1-M1-G1
Seq. ID
Method
                  BLASTX
                  g4455235
NCBI GI
                   255
BLAST score
                   4.0e-22
E value
                   68
Match length
                   75
% identity
                  (AL035523) PROTEIN TRANSPORT PROTEIN SEC61 GAMMA
NCBI Description
                   SUBUNIT-like [Arabidopsis thaliana]
                   229172
Seq. No.
                   LIB3196-025-P1-M1-G3
Seq. ID
                   BLASTX
Method
                   g1480220
NCBI GI
                   503
BLAST score
                   4.0e-51
E value
Match length
                   118
% identity
                   78
NCBI Description (D31816) HLA-B4007 [Homo sapiens]
                   229173
Seq. No.
                   LIB3196-025-P1-M1-G8
Seq. ID
                   BLASTX
Method
                   g730565
NCBI GI
                   692
BLAST score
                   3.0e-73
E value
Match length
                   130
                   100
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_423069 pir S34195 ribosomal
                   protein L3 - human >gi 313659 emb CAA51839_ (X73460)
                   ribosomal protein L3 [Homo sapiens]
                   >gi_3850177_emb_CAA18450_ (AL022326) dJ333H23.1.1 (60S
                   Ribosomal Protein L3) [Homo sapiens]
                   >gi_4506649_ref_NP_000958.1_pRPL3_ ribosomal protein L3
```

229174

Seq. No.



```
LIB3196-025-P1-M1-G9
Seq. ID
Method
                  BLASTX
                  a135655
NCBI GI
BLAST score
                   524
E value
                  8.0e-54
Match length
                  105
                   99
% identity
NCBI Description
                  TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER
                  BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3)
                   (TRANSCRIPTION FACTOR ITF-1) >gi_105865_pir__A34734
                   transcription factor 3 - human >gi_339478 (M31523)
                   transcription factor E2A [Homo sapiens]
                   229175
Seq. No.
                  LIB3196-025-P1-M1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q266945
BLAST score
                   502
E value
                   5.0e-51
Match length
                   116
                   86
% identity
                  60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
NCBI Description
                   >gi_100065_pir__S19978 ribosomal protein L9 - garden pea
                   >gi_20727_emb_CAA46273_ (X65155) GA [Pisum sativum]
                   >gi_12796\overline{4}5emb_CAA659\overline{8}7 (X97322) ribosomal protein L9
                   [Pisum sativum]
Seq. No.
                   229176
                   LIB3196-025-P1-M1-H2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1944193
                   496
BLAST score
E value
                   3.0e-50
                   127
Match length
                   75
% identity
NCBI Description (AB002810) nodulin 35 [Glycine max]
                   229177
Seq. No.
                   LIB3196-025-P1-M1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3182898
BLAST score
                   421
E value
                   1.0e-41
                   99
Match length
% identity
                   85
NCBI Description ACTIN 2 >gi 2653414 emb CAA74016 (Y13665) actin
                   [Saccoglossus kowalevskii]
                   229178
Seq. No.
                   LIB3196-025-P1-M1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1703129
BLAST score
                   568
E value
                   1.0e-58
                   105
Match length
                   99
% identity
```

NCBI Description ACTIN 11 >gi 2129522 pir S68109 actin 11 - Arabidopsis



thaliana >gi\_1002533 (U27981) actin-11 [Arabidopsis thaliana]

229179 Seq. No. LIB3196-025-P1-M1-H8 Seq. ID BLASTX Method g120222 NCBI GI 470 BLAST score 2.0e-47 E value 88 Match length 100 % identity FK506-BINDING PROTEIN (FKBP-12) (PEPTIDYL-PROLYL CIS-TRANS NCBI Description

ISOMERASE) (PPIASE) (ROTAMASE) (IMMUNOPHILIN FKBP12)

>gi\_107276\_pir\_\_A35780 peptidylprolyl isomerase (EC

5.2.1.8) FKBP1 - human >gi\_539777\_pir\_\_A42657 FK506-binding

protein - rabbit >gi\_165023 (M89928) binding protein

[Oryctolagus cuniculus] >gi\_182628 (M34539) FK506-binding

protein (FKBP) [Homo sapiens] >gi\_182633 (M80199) FKBP-12

protein [Homo sapiens] >gi\_182649 (M93060) FK506-binding

protein 12 [Homo sapiens] >gi\_288196\_emb\_CAA39272\_ (X55741)

FKBP [Homo sapiens] >gi\_665650\_emb\_CAA36462\_ (X52220)

FK-506 binding protein [Homo sapiens]

>gi\_227077\_prf 1613455A FK506 binding protein FKBP [Homo sapiens] >gi\_4503725\_ref\_NP\_000792.1\_pFKBP1A\_ FK506-binding

protein 1 (12kD)

Seq. No. 229180

Seq. ID LIB3196-025-P1-M1-H9

Method BLASTX
NCBI GI g2497538
BLAST score 517
E value 7.0e-53
Match length 107

% identity 93

NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi\_466350 (L08632)

pyruvate kinase [Glycine max]

Seq. No. 229181

Seq. ID LIB3196-027-P1-M1-A11

Method BLASTX
NCBI GI g549732
BLAST score 215
E value 2.0e-17
Match length 67
% identity 55

NCBI Description HYPOTHETICAL 16.2 KD PROTEIN IN PIR3-APE2 INTERGENIC REGION >gi\_481110\_pir\_\_S37791 hypothetical protein YKL160w - yeast

(Saccharomyces cerevisiae) >gi\_407488 emb CAA81494\_

(Z26877) unknown [Saccharomyces cerevisiae] >gi\_486279\_emb\_CAA82002\_ (Z28160) ORF YKL160w

[Saccharomyces cerevisiae] >gi\_1582545\_prf\_\_2118404F ORF

[Saccharomyces cerevisiae]

Seq. No. 229182

Seq. ID LIB3196-027-P1-M1-A12

Method BLASTX NCBI GI g49868

BLAST score

Match length

E value

9.0e-32

64



```
BLAST score
                  572
                   3.0e-59
E value
Match length
                  109
                   100
% identity
                   (X03765) put. beta-actin (aa 27-375) [Mus musculus]
NCBI Description
                  >gi_387083 (M12481) cytoplasmic beta-actin [Mus musculus]
                   229183
Seq. No.
                  LIB3196-027-P1-M1-A4
Seq. ID
                   BLASTX
Method
                   g547299
NCBI GI
BLAST score
                   550
                   1.0e-56
E value
                   99
Match length
                   100
% identity
                   beta 2-microglobulin, beta 2-M [Papio hamadryas=baboons,
NCBI Description
                   26CB-1, Peptide, 99 aa]
Seq. No.
                   229184
                   LIB3196-027-P1-M1-A9
Seq. ID
                   BLASTX
Method
                   g2253411
NCBI GI
                   258
BLAST score
                   2.0e-22
E value
                   89
Match length
                   46
% identity
                   (AF007219) PP2A inhibitor [Tetraodon fluviatilis]
NCBI Description
Seq. No.
                   229185
                   LIB3196-027-P1-M1-B11
Seq. ID
                   BLASTX
Method
                   g3334756
NCBI GI
BLAST score
                   442
                   2.0e-50
E value
Match length
                   105
                   87
% identity
                   (Y16672) putative arginine/serine-rich splicing factor
NCBI Description
                   [Medicago sativa]
                   229186
Seq. No.
                   LIB3196-027-P1-M1-B4
Seq. ID
                   BLASTX
Method
                   g4558462
NCBI GI
                   174
 BLAST score
                   4.0e-26
 E value
                   111
 Match length
                   57
 % identity
                   (AF079404) cell cycle switch protein [Medicago sativa
 NCBI Description
                    subsp. X varia]
                    229187
 Seq. No.
                   LIB3196-027-P1-M1-B7
 Seq. ID
                    BLASTX
 Method
                    q1173218
 NCBI GI
                    337
```



```
% identity
                  40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                  229188
Seq. No.
                  LIB3196-027-P1-M1-B9
Seq. ID
                  BLASTX
Method
                  g1743388
NCBI GI
                  146
BLAST score
                  3.0e-09
E value
                  60
Match length
                  55
% identity
                 (Y09874) pSbaNS5 protein [Sorghum bicolor]
NCBI Description
                  229189
Seq. No.
                  LIB3196-027-P1-M1-C10
Seq. ID
                  BLASTX
Method
                  g2117356
NCBI GI
                  624
BLAST score
                  2.0e-65
E value
Match length
                  123
                  96
% identity
NCBI Description core I protein - human >gi_468935_dbj_BAA05495_ (D26485)
                  core I protein [Homo sapiens]
                  229190
Seq. No.
                  LIB3196-027-P1-M1-C11
Seq. ID
                  BLASTX
Method
                   g2828280
NCBI GI
                   584
BLAST score
                   1.0e-60
E value
                   113
Match length
                   95
% identity
                  (AL021687) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi_2832633_emb_CAA16762 (AL021711) putative protein
                   [Arabidopsis thaliana]
                   229191
Seq. No.
                   LIB3196-027-P1-M1-C12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2583108
                   349
BLAST score
                   4.0e-33
E value
                   106
Match length
                   70
% identity
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]
                   229192
Seq. No.
                   LIB3196-027-P1-M1-C2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1346180
                   313
BLAST score
                   7.0e-29
E value
                   79
Match length
                   73
 % identity
NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN GRP1A >gi_496233 (L31374)
```



homology with RNA-binding proteins in meristematic tissue [Sinapis alba]

229193
LIB3196-027-P1-M1-C4
BLASTX
q3687234

Method BLASTX
NCBI GI g3687234
BLAST score 252
E value 1.0e-28
Match length 118
% identity 54

Seq. No.

Seq. ID

NCBI Description (AC005169) putative copia-like transposable element

[Arabidopsis thaliana]

Seq. No. 229194 Seq. ID LIB3196-027-P1-M1-C6

Method BLASTX
NCBI GI g2280476
BLAST score 646
E value 6.0e-68
Match length 125

% identity 100 NCBI Description (AB002313) KIAA0315 [Homo sapiens]

Seq. No. 229195

Seq. ID LIB3196-027-P1-M1-C8

Method BLASTX
NCBI GI g631839
BLAST score 222
E value 3.0e-18
Match length 93
% identity 56

NCBI Description growth factor-responsive protein, vascular smooth muscle -

rat >gi 469478 (U06713) SM-20 [Rattus norvegicus]

Seq. No. 229196

Seq. ID LIB3196-027-P1-M1-C9

Method BLASTX
NCBI GI g3242177
BLAST score 549
E value 2.0e-56
Match length 124
% identity 88

NCBI Description (AL022325) fF27C3.2.1 (unknown protein) (isoform 1) [Homo

sapiens]

Seq. No. 229197

Seq. ID LIB3196-027-P1-M1-D11

Method BLASTX
NCBI GI g2996096
BLAST score 619
E value 8.0e-65
Match length 117
% identity 100

NCBI Description (AF030517) translation elongation factor-1 alpha; EF-1

alpha [Oryza sativa]

Seq. No.

```
229198
Seq. No.
                    LIB3196-027-P1-M1-D12
Seq. ID
                    BLASTX
Method
                    g124219
NCBI GI
                    167
BLAST score
                    9.0e-12
E value
                    100
Match length
                     40
% identity
                    EUKARYOTIC TRANSLATION INITIATION FACTOR 4B (EIF-4B)
NCBI Description
                    >gi_106728_pir__S12566 translation initiation factor eIF-4B
                     - human >gi_288100 emb_CAA39265_ (X55733) initation factor 4B [Homo sapiens] >gi_4503533 ref_NP_001408.1_pEIF4B_
                     eukaryotic translation initiation factor 4B
                    229199
Seq. No.
                    LIB3196-027-P1-M1-D5
Seq. ID
                    BLASTX
Method
                     g1708967
NCBI GI
                     515
BLAST score
```

Method BLASTX
NCBI GI g1708967
BLAST score 515
E value 1.0e-52
Match length 105
% identity 99
NCBI Description MALATE DEHYDROGEN

229200

NCBI Description MALATE DEHYDROGENASE, CYTOPLASMIC >gi\_1255604\_dbj\_BAA09513\_ (D55654) cytosolic malate dehydrogenase [Homo sapiens]

>gi\_3133269 (U20352) malate dehydrogenase [Homo sapiens]

Seq. ID LIB3196-027-P1-M1-D7 Method BLASTX NCBI GI g137578 BLAST score 344 E value 2.0e-32 Match length 120 % identity 62

NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)

>gi\_81545\_pir\_\_S06398 alpha-globulin type A precursor upland cotton >gi\_167371 (M19378) vicilin precursor
[Gossypium hirsutum] >gi\_207906 (M18027) alpha globulin A
[Artificial gene] >gi\_226119\_prf\_\_1410330A vicilin gene A

[Saguinus oedipus]

Seq. No. 229201

Seq. ID LIB3196-027-P1-M1-D8

Method BLASTX
NCBI GI g88044
BLAST score 589
E value 3.0e-61
Match length 125
% identity 97

NCBI Description keratin 4, type II, cytoskeletal - human (fragment)

>gi\_34073\_emb\_CAA30534\_ (X07695) cytokeratin 4 (408 AA)

[Homo sapiens]

Seq. No. 229202

Seq. ID LIB3196-027-P1-M1-D9

Method BLASTX NCBI GI g3913518



```
201
BLAST score
                   3.0e-24
E value
Match length
                   86
% identity
                   76
                   3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE
NCBI Description
                   (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE)
                   (DPNPASE) >gi_1103921 (U40433) 3'(2'),5'-bisphosphate
                   nucleotidase [Arabidopsis thaliana]
                   229203
Seq. No.
                   LIB3196-027-P1-M1-E10
Seq. ID
                   BLASTX
Method
                   q4322822
NCBI GI
BLAST score
                   509
                   8.0e-52
E value
Match length
                   124
                   78
% identity
                   (AF095193) BAG-family molecular chaperone regulator-3;
NCBI Description
                   BAG-3 [Homo sapiens]
                   229204
Seq. No.
                   LIB3196-027-P1-M1-E11
Seq. ID
                   BLASTX
Method
                   g2583108
NCBI GI
                   321
BLAST score
                   8.0e-30
E value
                   88
Match length
                   73
% identity
                  (AC002387) putative surface protein [Arabidopsis thaliana]
NCBI Description
                   229205
Seq. No.
                   LIB3196-027-P1-M1-E7
Seq. ID
                   BLASTX
Method
                   g1170519
NCBI GI
                   345
BLAST score
                    1.0e-32
E value
Match length
                    69
% identity
                    99
NCBI Description INTERFERON GAMMA UP-REGULATED I-5111 PROTEIN PRECURSOR
                   (IGUP I-5111) >gi_627550_pir__A54859 multicatalytic proteinase activator - human >gi_186513 (L07633)
                    interferon-gamma [Homo sapiens] >gi_551491 (U10360)
                    interferon-gamma [Homo sapiens]
                    229206
 Seq. No.
                    LIB3196-027-P1-M1-E9
 Seq. ID
Method
                    BLASTX
NCBI GI
                    q2880033
                    119
 BLAST score
                    1.0e-09
 E value
                    39
Match length
                    100
 % identity
 NCBI Description (U73167) interferon-related putative protein [Homo sapiens]
                    229207
 Seq. No.
                    LIB3196-027-P1-M1-F1
 Seq. ID
```

BLASTX

Method

Seq. ID

Method



```
NCBI GI
                   g2306917
                   469
BLAST score
E value
                   3.0e-47
                   102
Match length
                   89
% identity
                  (AF003728) plasma membrane intrinsic protein [Arabidopsis
NCBI Description
                   thaliana]
                   229208
Seq. No.
                   LIB3196-027-P1-M1-F11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q88044
BLAST score
                   606
                   3.0e-63
E value
Match length
                   125
                   99
% identity
                   keratin 4, type II, cytoskeletal - human (fragment)
NCBI Description
                   >gi 34073 emb CAA30534 (X07695) cytokeratin 4 (408 AA)
                   [Homo sapiens]
                   229209
Seq. No.
                   LIB3196-027-P1-M1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g547753
BLAST score
                   523
                   2.0e-53
E value
Match length
                   121
% identity
                   90
NCBI Description KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)
Seq. No.
                   229210
                   LIB3196-027-P1-M1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1055130
BLAST score
                   183
E value
                   1.0e-13
                 . 103
Match length
                   37
% identity
                  (U39998) coded for by C. elegans cDNA yk92b11.3; coded for
NCBI Description
                   by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA
                   yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by
                   \overline{\text{C.}} elegans cDNA yk66h\overline{\text{8.3}}; coded for by C. elegans cDNA
                   yk78c2.3
                   229211
Seq. No.
Seq. ID
                   LIB3196-027-P1-M1-F5
Method
                   BLASTX
NCBI GI
                   g1857161
BLAST score
                   164
                   2.0e-11
E value
Match length
                   26
                   100
% identity
NCBI Description (U70663) hEZF [Homo sapiens]
Seq. No.
                   229212
```

32836

LIB3196-027-P1-M1-F6

BLASTX



```
NCBI GI
                  q1223922
BLAST score
                  464
                  1.0e-46
E value
Match length
                  108
% identity
                  74
                  (U49445) Vigna radiata vicilin peptidohydrolase [Vigna
NCBI Description
                  radiata]
                  229213
Seq. No.
                  LIB3196-027-P1-M1-F9
Seq. ID
                  BLASTX
Method
                  g2401257
NCBI GI
BLAST score
                  257
                  2.0e-22
E value
                  106
Match length
                   48
% identity
                  (D63951) TBZ17 [Nicotiana tabacum]
NCBI Description
                   229214
Seq. No.
                  LIB3196-027-P1-M1-G12
Seq. ID
                   BLASTX
Method
                   g119339
NCBI GI
                   427
BLAST score
                   3.0e-42
E value
                   86
Match length
                   99
% identity
                   ALPHA ENOLASE (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
NCBI Description
                   (NON-NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE)
                   >gi 87368_pir__A29170 phosphopyruvate hydratase (EC
                   4.2.1.11) alpha - human >gi_182114 (M14328) alpha enolase
                   (EC 4.2.1.11) [Homo sapiens] >gi_1167843_emb_CAA34360_
                   (X16288) alpha-enolase [Homo sapiens]
                   >gi_4503571_ref_NP_001419.1_pEN01_ enolase 1, (alpha)
                   229215
Seq. No.
                   LIB3196-027-P1-M1-G2
Seq. ID
                   BLASTX
Method
                   g3192909
NCBI GI
BLAST score
                   261
                   9.0e-23
E value
                   101
Match length
                   47
% identity
NCBI Description (AF068836) cytohesin binding protein HE [Homo sapiens]
                   229216
Seq. No.
                   LIB3196-027-P1-M1-G4
Seq. ID
                   BLASTX
Method
                   g1644427
NCBI GI
                   264
BLAST score
                   4.0e-23
E value
                   59
Match length
 % identity
NCBI Description (U74610) glyoxalase II [Arabidopsis thaliana]
                   229217
 Seq. No.
                   LIB3196-027-P1-M1-G7
 Seq. ID
```

BLASTX

Method



```
NCBI GI
                  q72287
                  618
BLAST score
                  1.0e-64
E value
                  119
Match length
                  100
% identity
                  beta-globulin A precursor (clone 94) - upland cotton
NCBI Description
                  (fragment) >gi_167377 (M16905) legumin precursor [Gossypium
                  hirsutum]
                  229218
Seq. No.
                  LIB3196-027-P1-M1-G9
Seq. ID
                  BLASTX
Method
                  g2924509
NCBI GI
                  201
BLAST score
                  9.0e-16
E value
                  91
Match length
% identity
                   45
                  (AL022023) subtilisin proteinase - like [Arabidopsis
NCBI Description
                   thaliana]
                   229219
Seq. No.
                   LIB3196-027-P1-M1-H1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g495866
                   326
BLAST score
                   2.0e-30
E value
                   90
Match length
% identity
                  (L23982) collagen type VII [Homo sapiens]
NCBI Description
                   229220
Seq. No.
                   LIB3196-027-P1-M1-H10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g82264
                   140
BLAST score
                   1.0e-08
E value
                   29
Match length
                   90
 % identity
NCBI Description ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
                   c1 precursor (clone pC(1)8I) - potato (fragment)
                   >gi_498789_emb_CAA56109_ (X79597) cytochrome c1 [Solanum
                   tuberosum]
                   229221
 Seq. No.
                   LIB3196-027-P1-M1-H12
 Seq. ID
                   BLASTX
 Method
                   g3859849
 NCBI GI
                   566
 BLAST score
                   2.0e-58
 E value
 Match length
                   97
                   35
 % identity
 NCBI Description (AF063002) LIM protein SLIMMER [Homo sapiens]
                   229222
 Seq. No.
                   LIB3196-027-P1-M1-H3
 Seq. ID
                   BLASTX
 Method
```

g1710151

NCBI GI

Match length

122



```
574
BLAST score
                  2.0e-59
E value
                  120
Match length
                  88
% identity
                  (U72711) proline iminopeptidase [Arabidopsis thaliana]
NCBI Description
                  229223
Seq. No.
                  LIB3196-027-P1-M1-H4
Seq. ID
                  BLASTX
Method
                  g832876
NCBI GI
                  535
BLAST score
                  6.0e-55
E value
                  114
Match length
                  92
% identity
                  (L41345) ascorbate free radical reductase [Solanum
NCBI Description
                  lycopersicum] >gi_1097368_prf__2113407A ascorbate free
                  radical reductase [Lycopersicon esculentum]
                  229224
Seq. No.
                  LIB3196-027-P1-M1-H6
Seq. ID
                  BLASTX
Method
                  g730583
NCBI GI
                  245
BLAST score
                   6.0e-21
E value
                   62
Match length
                   79
% identity
                  60S ACIDIC RIBOSOMAL PROTEIN P2 >gi 551267 emb CAA55047
NCBI Description
                   (X78213) 60s acidic ribosomal protein P2 [Parthenium
                   argentatum]
                   229225
Seq. No.
                   LIB3196-027-P1-M1-H7
Seq. ID
                   BLASTX
Method
                   g4388731
NCBI GI
                   142
BLAST score
                   5.0e-09
E value
Match length
                   55
% identity
                   62
NCBI Description (AC006413) hypothetical protein [Arabidopsis thaliana]
                   229226
Seq. No.
                   LIB3196-027-P1-M1-H8
Seq. ID
Method
                   BLASTX
                   g2996650
NCBI GI
BLAST score
                   634
                   2.0e-66
E value
Match length
                   124
% identity
NCBI Description (AC004493) KIAA0324 [Homo sapiens]
Seq. No.
                   229227
                   LIB3196-027-P1-M1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g126366
BLAST score
                   643
                   1.0e-67
E value
```



```
% identity
                  LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN)
NCBI Description
                  >gi_71422_pir__MMHUB1 laminin chain B1 precursor - human
                  >gi_186837 (M61916) laminin B1 [Homo sapiens] >gi_186876
                  (M5\overline{5}370) laminin B1 [Homo sapiens] >gi_186913 (M6\overline{1}951)
                  laminin B1 [Homo sapiens]
                  >gi 4504951_ref_NP_002282.1_pLAMB1_ laminin, beta
                  229228
Seq. No.
                  LIB3196-028-P1-M1-A10
Seq. ID
                  BLASTX
Method
                  q4159888
NCBI GI
                  267
BLAST score
                   2.0e-23
E value
Match length
                  113
                   6
% identity
                  (AC004908) zinc finger protein from gene of uncertain exon
NCBI Description
                   structure; similar to Q99676 (PID:g3025333) [Homo sapiens]
                   229229
Seq. No.
                  LIB3196-028-P1-M1-A11
Seq. ID
                   BLASTX
Method
                   g3063392
NCBI GI
                   276
BLAST score
                   1.0e-24
E value
Match length
                   113
                   57
% identity
                  (AB012932) Ca2+/H+ exchanger [Vigna radiata]
NCBI Description
                   229230
Seq. No.
                   LIB3196-028-P1-M1-A12
Seq. ID
                   BLASTX
Method
                   g726034
NCBI GI
                   427
BLAST score
                   2.0e-42
E value
                   102
Match length
                   83
% identity
NCBI Description (U19177) Hin-2 [Homo sapiens]
                  -229231
Seq. No.
                   LIB3196-028-P1-M1-A5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3063392
                   292
BLAST score
                   2.0e-26
E value
                   114
Match length
                  . 57
 % identity
NCBI Description (AB012932) Ca2+/H+ exchanger [Vigna radiata]
                   229232
Seq. No.
                   LIB3196-028-P1-M1-A8
Seq. ID
                   BLASTX
Method
 NCBI GI
                   q3023897
                   150
 BLAST score
                    3.0e-10
E value
```

57

Match length

% identity

BLAST score

E value

328

1.0e-30



NCBI Description GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS (RALGEF) >gi\_2135317\_pir\_\_I38853 guanine nucleotide dissociation stimulator ralGDS - human (fragment) >gi 538200 (U14417) Ral quanine nucleotide dissociation stimulator [Homo sapiens] Seq. No. 229233 LIB3196-028-P1-M1-A9 Seq. ID Method BLASTX NCBI GI g1619602 BLAST score 360 E value 2.0e-34 Match length 86 80 % identity NCBI Description (Y08726) MtN3 [Medicago truncatula] Seq. No. 229234 LIB3196-028-P1-M1-B1 Seq. ID Method BLASTX NCBI GI g126156 BLAST score 444 E value 3.0e-44Match length 94 95 % identity NCBI Description LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) >gi\_72288\_pir\_\_FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi\_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi\_1171335 (U43727) legumin B [Gossypium hirsutum] >gi\_225582\_prf\_\_1306412C storage protein C134 [Saguinus oedipus] 229235 Seq. No. Seq. ID LIB3196-028-P1-M1-B10 BLASTX Method NCBI GI g3894189 BLAST score 149 E value 6.0e-10 Match length 50 % identity NCBI Description (AC005662) hypothetical protein [Arabidopsis thaliana] Seq. No. 229236 Seq. ID LIB3196-028-P1-M1-B12 Method BLASTX NCBI GI q225581 BLAST score 393 E value 3.0e-38 Match length 111 % identity 71 NCBI Description storage protein C94 [Saguinus oedipus] Seq. No. 229237 LIB3196-028-P1-M1-B5 Seq. ID Method BLASTX NCBI GI q1381179



Match length 81 % identity 79

NCBI Description (U58766) FX [Homo sapiens]

>gi 4507709 ref\_NP\_003304.1\_pTSTA3\_ tissue specific

transplantation antigen P35B

Seq. No. 229238

Seq. ID LIB3196-028-P1-M1-B7

Method BLASTX
NCBI GI g3080420
BLAST score 359
E value 2.0e-34
Match length 82
% identity 83

NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis

thaliana]

Seq. No. 229239

Seq. ID LIB3196-028-P1-M1-C10

Method BLASTX
NCBI GI g2605714
BLAST score 261
E value 8.0e-23
Match length 67
% identity 81

NCBI Description (AF026275) beta-tonoplast intrinsic protein [Arabidopsis

thaliana]

Seq. No. 229240

Seq. ID LIB3196-028-P1-M1-C12

Method BLASTX
NCBI GI g3879684
BLAST score 278
E value 6.0e-25
Match length 97
% identity 55

NCBI Description (Z74042) predicted using Genefinder; Similarity to

Haemophilus 3-oxoacyl-(acyl-carrier protein) reductase (SW:FABG\_HAEIN); cDNA EST yk470b2.3 comes from this gene; cDNA EST yk470b2.5 comes from this gene [Caenorhabditis

elegans]

Seq. No. 229241

Seq. ID LIB3196-028-P1-M1-C3

Method BLASTX
NCBI GI g3243079
BLAST score 628
E value 9.0e-66
Match length 129
% identity 37

NCBI Description (AF071771) SPH-binding factor [Homo sapiens]

Seq. No. 229242

Seq. ID LIB3196-028-P1-M1-C9

Method BLASTX NCBI GI g1220196 BLAST score 500

Seq. ID

Method



```
8.0e-51
E value
                  97
Match length
                  98
% identity
                  (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
NCBI Description
                  229243
Seq. No.
                  LIB3196-028-P1-M1-D2
Seq. ID
                  BLASTX
Method
                  g730832
NCBI GI
                  174
BLAST score
                  1.0e-12
E value
Match length
                  53
                  58
% identity
                  8.4 KD SULFUR-RICH PROTEIN PRECURSOR (SE60 PROTEIN)
NCBI Description
                   (PROBABLE PROTEINASE INHIBITOR P322) >gi_99949_pir__S24965
                  probable proteinase inhibitor (Bowman-Birk) p322 - soybean
                   >gi_18748_emb_CAA78359_ (Z13956) a protein similar to
                   potato tuber protein p322 homolgous to Bowman-Birk
                   Proteinase Inhibitor [Glycine max]
                   229244
Seq. No.
                   LIB3196-028-P1-M1-D3
Seq. ID
                   BLASTX
Method
                   g1944407
NCBI GI
                   205
BLAST score
                   3.0e-16
E value
                   45
Match length
                   82
% identity
                  (D86988) KIAA0221 [Homo sapiens]
NCBI Description
                   229245
Seq. No.
                   LIB3196-028-P1-M1-D5
Seq. ID
                   BLASTX
Method
                   g3122072
NCBI GI
                   559
BLAST score
                   1.0e-57
E value
                   106
Match length
                   100
% identity
                 ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION
NCBI Description
                   FACTOR TU) (EF-TU) >gi_2119922_pir__I50226 elongation
                   factor 1 alpha - chicken >gi_488468 (L00677) elongation
                   factor 1 alpha [Gallus gallus]
                   229246
Seq. No.
                   LIB3196-028-P1-M1-D6
Seq. ID
                   BLASTX
Method
                   q683553
NCBI GI
                   202
BLAST score
                   7.0e-16
E value
Match length
                   102
                   47
 % identity
                   (Z48450) oleosin-like protein [Citrus sinensis]
NCBI Description
                   >gi 1582679_prf__2119230A oleosin homolog [Citrus sinensis]
                   229247
Seq. No.
```

32843

LIB3196-028-P1-M1-D7

BLASTX



```
NCBI GI
                  q3355468
BLAST score
                  452
                  3.0e-45
E value
Match length
                  109
                  87
% identity
                  (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                  thaliana]
                  229248
Seq. No.
                  LIB3196-028-P1-M1-D8
Seq. ID
                  BLASTX
Method
                  g1703470
NCBI GI
BLAST score
                  656
                  4.0e-69
E value
Match length
                  126
                  97
% identity
                  SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN
NCBI Description
                   (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) >gi 1256802
                   (U51478) sodium/potassium-transporting ATPase beta-3
                   subunit [Homo sapiens] >gi_2224939 (AF005896) Na K-ATPase
                  beta-3 subunit [Homo sapiens]
                   >gi_4502281_ref_NP_001670.1_pATP1B3_ ATPase, Na+/K+
                   transporting, beta 3 polypeptide
Seq. No.
                   229249
                   LIB3196-028-P1-M1-D9
Seq. ID
                   BLASTX
Method
                   q88052
NCBI GI
BLAST score
                   171
                   3.0e-12
E value
Match length
                   67
                   58
% identity
                  keratin K5, 58K type II, epidermal (version 2) - human
NCBI Description
                   (fragment)
                   229250
Seq. No.
                   LIB3196-028-P1-M1-E1
Seq. ID
                   BLASTX
Method
                   g4539292
NCBI GI
                   389
BLAST score
                   8.0e-38
E value
Match length
                   80
                   88
 % identity
                  (AL049480) putative ribosomal protein S10 [Arabidopsis
 NCBI Description
                   thaliana]
                   229251
 Seq. No.
                   LIB3196-028-P1-M1-E10
 Seq. ID
                   BLASTX
 Method
                   g2501572
 NCBI GI
                   375
 BLAST score
                   4.0e-36
 E value
                   113
 Match length
                   65
 % identity
 NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN EMB8 >gi_1350545
```

(L47118) EMB8 gene product [Picea glauca]



```
229252
Seq. No.
                  LIB3196-028-P1-M1-E12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q683553
BLAST score
                  230
                  4.0e-19
E value
                  109
Match length
                  49
% identity
                  (Z48450) oleosin-like protein [Citrus sinensis]
NCBI Description
                  >gi 1582679 prf _2119230A oleosin homolog [Citrus sinensis]
                  229253
Seq. No.
                  LIB3196-028-P1-M1-E2
Seq. ID
                  BLASTX
Method
                  g4249403
NCBI GI
BLAST score
                   498
                   1.0e-50
E value
                  118
Match length
                   78
% identity
                  (AC006072) unknown protein [Arabidopsis thaliana]
NCBI Description
                   229254
Seq. No.
                   LIB3196-028-P1-M1-E5
Seq. ID
                   BLASTX
Method
                   q1841870
NCBI GI
                   265
BLAST score
                   3.0e-23
E value
                   93
Match length
                   60
% identity
                  (U87222) elongation factor 1-beta [Pimpinella brachycarpa]
NCBI Description
                   229255
Seq. No.
                   LIB3196-028-P1-M1-E7
Seq. ID
                   BLASTX
Method
                   g1906828
NCBI GI
                   529
BLAST score
                   3.0e-54
E value
                   105
Match length
                   97
% identity
NCBI Description (Y11828) heat shock protein [Arabidopsis thaliana]
                   229256
Seq. No.
                   LIB3196-028-P1-M1-E9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2924601
                   461
 BLAST score
                   2.0e-46
 E value
                   85
Match length
                   51
 % identity
                   (AB000095) hepatocyte growth factor activator inhibitor
 NCBI Description
                    [Homo sapiens] >gi_4504329_ref_NP_003701.1_pHAI_ hepatocyte
                    growth factor activator inhibitor
                    229257
 Seq. No.
                   LIB3196-028-P1-M1-F1
 Seq. ID
```

BLASTX

g113621

Method

NCBI GI



```
470
BLAST score
                   3.0e-47
E value
                   106
Match length
                   88
% identity
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
NCBI Description
                   >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
                   4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
                   [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A
                   cytoplasmic aldolase [Zea mays]
                   229258
Seq. No.
                   LIB3196-028-P1-M1-F11
Seq. ID
                   BLASTX
Method
                   q2274859
NCBI GI
                    311
BLAST score
                    1.0e-28
E value
Match length
                    71
                    79
% identity
                    (AJ000016) Cksl protein [Arabidopsis thaliana]
NCBI Description
                    >gi 4510420_gb_AAD21506.1_ (AC006929) putative
                    cyclin-dependent kinase regulatory subunit [Arabidopsis
                    thaliana]
                    229259
Seq. No.
                    LIB3196-028-P1-M1-F6
Seq. ID
                    BLASTX
Method
                    q3894183
NCBI GI
BLAST score
                    146
                    3.0e-09
E value
                    104
Match length
                    40
% identity
                   (AC005662) calmodulin-like protein [Arabidopsis thaliana]
NCBI Description
                    229260
Seq. No.
                    LIB3196-028-P1-M1-F9
Seq. ID
                    BLASTX
Method
                    q81546
NCBI GI
                    341
 BLAST score
                    2.0e-32
 E value
                    76
Match length
                    87
 % identity
                    alpha-globulin type B precursor (tandem 1) - upland cotton
 NCBI Description
                    (fragment)
                    229261
 Seq. No.
                    LIB3196-028-P1-M1-G10
 Seq. ID
                    BLASTX
 Method
                    g2961542
 NCBI GI
                    387
 BLAST score
                    9.0e-38
 E value
 Match length
                    86
```

Seq. No. 229262

% identity

NCBI Description

76

thaliana]

(AF050463) zinc finger transcription factor [Arabidopsis



```
LIB3196-028-P1-M1-G11
Seq. ID
Method
                  BLASTX
                  g3892059
NCBI GI
BLAST score
                  182
                  2.0e-13
E value
Match length
                  113
                  43
% identity
                   (AC002330) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                  229263
Seq. No.
                  LIB3196-028-P1-M1-G12
Seq. ID
Method
                  BLASTX
                  q3776005
NCBI GI
BLAST score
                   339
                   6.0e-32
E value
Match length
                   93
                   75
% identity
                  (AJ010466) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   229264
Seq. No.
                   LIB3196-028-P1-M1-G2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1053047
                   565
BLAST score
                   2.0e-58
E value
                   113
Match length
                   100
% identity
                   (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)
NCBI Description
                   histone H3 [Glycine max] >gi_1053051 (U38427) histone H3
                   [Glycine max]
                   229265
Seq. No.
                   LIB3196-028-P1-M1-G3
Seq. ID
                   BLASTX
Method
                   g1731151
NCBI GI
                   564
BLAST score
                   3.0e-58
E value
Match length
                   106
                   98
% identity
                   HYPOTHETICAL PROTEIN S171 >gi 887362 (L40393) ORF; putative
NCBI Description
                   [Homo sapiens] >gi_4505479_ref_NP_003735.1_pNUMB_ homolog
                   of Drosophila numb
                   229266
Seq. No.
                   LIB3196-028-P1-M1-G4
 Seq. ID
                   BLASTX
Method
                   g1706551
NCBI GI
                   226
 BLAST score
                   1.0e-18
 E value
                   87
Match length
                   48
 % identity
 NCBI Description GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR
                   ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
```

1,3-glucanase [Triticum aestivum]

(BETA-1,3-ENDOGLUCANASE) >gi\_924953 (U30323) beta



```
Seq. No.
                  229267
                  LIB3196-028-P1-M1-G5
Seq. ID
                  BLASTX
Method
                  g3327142
NCBI GI
BLAST score
                  531
                  2.0e-54
E value
Match length
                  129
% identity
                  85
NCBI Description (AB014564) KIAA0664 protein [Homo sapiens]
                  229268
Seq. No.
                  LIB3196-028-P1-M1-G6
Seq. ID
Method
                  BLASTX
                  g3327142
NCBI GI
                  185
BLAST score
                  5.0e-14
E value
Match length
                  96
                   52
% identity
                  (AB014564) KIAA0664 protein [Homo sapiens]
NCBI Description
                  229269
Seq. No.
                  LIB3196-028-P1-M1-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                   g547753
                   240
BLAST score
                   2.0e-42
E value
                   106
Match length
                   92
% identity
NCBI Description KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)
                   229270
Seq. No.
                   LIB3196-028-P1-M1-G9
Seq. ID
                   BLASTX
Method
                   g4406775
NCBI GI
                   239
BLAST score
                   3.0e-20
E value
                   116
Match length
                   41
% identity
                  (AC006836) unknown protein [Arabidopsis thaliana]
NCBI Description
                   229271
Seq. No.
                   LIB3196-028-P1-M1-H1
Seq. ID
                   BLASTX
Method
                   g3450889
NCBI GI
                   315
BLAST score
                   4.0e-29
E value
                   92
Match length
                   73
% identity
NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
                   229272
Seq. No.
                   LIB3196-028-P1-M1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4512671
                   211
BLAST score
```

5.0e-17

59

E value

Match length



```
% identity
                  66
                  (AC006931) unknown protein [Arabidopsis thaliana]
NCBI Description
                  229273
Seq. No.
                  LIB3196-028-P1-M1-H2
Seq. ID
                  BLASTX
Method
                  q4062934
NCBI GI
                  457
BLAST score
                  8.0e-46
E value
                  110
Match length
                  79
% identity
                  (D88272) formate dehydrogenase [Hordeum vulgare]
NCBI Description
                  229274
Seq. No.
                  LIB3196-028-P1-M1-H6
Seq. ID
Method
                  BLASTX
                  q3252792
NCBI GI
BLAST score
                  501
                  6.0e-51
E value
                  122
Match length
                  80
% identity
                  (AB015609) S-adenosylmethionine decarboxylase [Nicotiana
NCBI Description
                  sylvestris]
                  229275
Seq. No.
                  LIB3196-028-P1-M1-H9
Seq. ID
                  BLASTX
Method
NCBI GI
                   g72287
                   540
BLAST score
                   1.0e-55
E value
                   103
Match length
                   100
% identity
                  beta-globulin A precursor (clone 94) - upland cotton
NCBI Description
                   (fragment) >gi_167377 (M16905) legumin precursor [Gossypium
                   hirsutum]
                   229276
Seq. No.
                   LIB3196-029-P1-M1-A1
Seq. ID
                   BLASTX
Method
NCBI GI
                   a4467804
BLAST score
                   461
                   3.0e-46
E value
                   114
Match length
% identity
                   (AL031678) TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3
NCBI Description
                   PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3).)
                   [Homo sapiens]
                   229277
Seq. No.
                   LIB3196-029-P1-M1-A10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2217972
BLAST score
                   401
                   4.0e-39
E value
Match length
                   126
                   66
% identity
```

NCBI Description (Y12338) unnamed protein product [Homo sapiens]

NCBI Description



```
229278
Seq. No.
                  LIB3196-029-P1-M1-A12
Seq. ID
Method
                  BLASTX
                  g2970051
NCBI GI
BLAST score
                  177
                   4.0e-13
E value
Match length
                   52
                   63
% identity
                   (AB012110) ARG10 [Vigna radiata]
NCBI Description
                   229279
Seq. No.
                  LIB3196-029-P1-M1-A2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1053047
                   506
BLAST score
                   1.0e-51
E value
Match length
                   104
% identity
                   97
                   (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)
NCBI Description
                   histone H3 [Glycine max] >gi_1053051 (U38427) histone H3
                   [Glycine max]
                   229280
Seq. No.
                   LIB3196-029-P1-M1-A4
Seq. ID
                   BLASTX
Method
                   q2338292
NCBI GI
BLAST score
                   184
E value
                   1.0e-13
                   97
Match length
                   41
% identity
                   (AF009243) proline-rich Gla protein 2 [Homo sapiens]
NCBI Description
                   >gi 4506137_ref_NP_000942.1_pPRRG2_ proline-rich Gla
                   (G-carboxglutamic acid) polypeptide
                   229281
Seq. No.
                   LIB3196-029-P1-M1-A5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g87645
                   306
BLAST score
                   5.0e-28
E value
Match length
                   61
                   97
% identity
                   heparin-binding growth factor-binding protein precursor -
NCBI Description
                   human >gi_183951 (M60047) heparin binding protein [Homo
                   sapiens]
                   229282
Seq. No.
                   LIB3196-029-P1-M1-A7
Seq. ID
                   BLASTX
Method
                   q4467804
NCBI GI
                   495
BLAST score
                   3.0e-50
E value
Match length
                   114
                   85
 % identity
```

(AL031678) TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3

PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3).)



## [Homo sapiens]

```
Seq. No.
                   229283
                   LIB3196-029-P1-M1-A8
Seq. ID
                   BLASTX
Method
                   q1346342
NCBI GI
                   298
BLAST score
                   3.0e-27
E value
                   58
Match length
                   100
% identity
                   KERATIN, TYPE I CYTOSKELETAL 17 (CYTOKERATIN 17) (K17) (CK
NCBI Description
                   17) (VERSION 2) >gi_186685 (M28439) keratin type 16 [Homo
                   sapiens]
                   229284
Seq. No.
                   LIB3196-029-P1-M1-B1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1346347
BLAST score
                   636
                   8.0e-67
E value
                   128
Match length
                   99
% identity
                   KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D)
NCBI Description
                   (K6D KERATIN) >gi_2119225_pir__161769 keratin type II -
                   human (fragment) \overline{>}gi_9148\overline{3}3 (\overline{L4}2610) keratin type II [Homo
                   sapiens]
Seq. No.
                   229285
                   LIB3196-029-P1-M1-B10
Seq. ID
                   BLASTX
Method
                   q3845409
NCBI GI
                   667
BLAST score
                   2.0e-70
E value
                   125
Match length
                   98
% identity
                  (ACO04976) glycyl tRNA synthetase [Homo sapiens]
NCBI Description
                   229286
Seq. No.
                   LIB3196-029-P1-M1-B11
Seq. ID
                   BLASTX
Method
                   q71611
NCBI GI
                   634
BLAST score
                   1.0e-66
E value
                   118
Match length
                   100
% identity
NCBI Description actin, skeletal muscle - rabbit
                   229287
Seq. No.
                   LIB3196-029-P1-M1-B2
Seq. ID
Method
                   BLASTX
                   q72287
NCBI GI
                   174
BLAST score
                   8.0e-13
E value
                   74
Match length
% identity
                   55
NCBI Description beta-globulin A precursor (clone 94) - upland cotton
```

(fragment) >gi\_167377 (M16905) legumin precursor [Gossypium

Seq. ID



## hirsutum]

```
229288
Seq. No.
                  LIB3196-029-P1-M1-B3
Seq. ID
                  BLASTX
Method ·
                  q1890182
NCBI GI
                  426
BLAST score
                  4.0e-42
E value
                  86
Match length
                  90
% identity
                  (Y11731) DNA glycosylase/AP lyase [Homo sapiens]
NCBI Description
                  >gi 1903206_emb_CAA72536_ (Y11838) 8-oxoguanine DNA
                  qlycosylase homolog 1 [Homo sapiens]
                  >gi 1906757_dbj_BAA19103_ (AB000410) hOGG1 [Homo sapiens]
                  >qi 2197083 (AF003595) 8-oxoguanine DNA glycosylase 1 [Homo
                  sapiens] >gi_2351704 (U88527) 8-hydroxyguanine
                  glycosylase/lyase [Homo sapiens]
                  >gi 4505495_ref_NP_002533.1_pOGG1_ 8-oxoguanine DNA
                  glycosylase
                  229289
Seq. No.
                  LIB3196-029-P1-M1-B4
Seq. ID
Method
                  BLASTX
                  g2894378
NCBI GI
                  140
BLAST score
                  4.0e-09
E value
                  67
Match length
% identity
                  38
                  (Y14573) putative ribophorin I homologue [Hordeum vulgare]
NCBI Description
                  229290
Seq. No.
                  LIB3196-029-P1-M1-B7
Seq. ID
                  BLASTX
Method
                  q4539660
NCBI GI
                  186
BLAST score
                   5.0e-14
E value
Match length
                  77
% identity
                   47
NCBI Description (AF061282) polyprotein [Sorghum bicolor]
                   229291
Seq. No.
                  LIB3196-029-P1-M1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g121567
                   654
BLAST score
                   8.0e-69
E value
Match length
                   127
% identity
                   100
                  78 KD GLUCOSE REGULATED PROTEIN PRECURSOR (GRP 78)
NCBI Description
                   (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN) (BIP)
                   >gi_87528_pir__A29821 Ig heavy chain-binding protein
                   precursor - human >gi_386758 (M19645) GRP78 precursor [Homo
                   sapiens] >gi_1143492 emb CAA61201 (X87949) BiP [Homo
                   sapiens]
                   229292
Seq. No.
```

LIB3196-029-P1-M1-C1



```
Method
                   BLASTX
NCBI GI
                   g683553
BLAST score
                   229
                   5.0e-19
E value
Match length
                   104
                   50
% identity
                   (Z48450) oleosin-like protein [Citrus sinensis]
NCBI Description
                   >gi 1582679_prf__2119230A oleosin homolog [Citrus sinensis]
Seq. No.
                   229293
                   LIB3196-029-P1-M1-C10
Seq. ID
Method
                   BLASTX
                   q167367
NCBI GI
BLAST score
                   556
                   2.0e-57
E value
Match length
                   119
                    90
% identity
                   (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                    229294
Seq. No.
                   LIB3196-029-P1-M1-C12
Seq. ID
Method
                    BLASTX
NCBI GI
                    q416662
BLAST score
                    326
                    2.0e-30
E value
Match length
                    116
                    54
% identity
                    21 KD SEED PROTEIN PRECURSOR >gi_99954_pir__S16252 trypsin inhibitor homolog - soybean >gi_21909_emb_CAA39860_
NCBI Description
                    (X56509) 21 kDa seed protein [Theobroma cacao]
                    229295
Seq. No.
                    LIB3196-029-P1-M1-C6
Seq. ID
Method
                    BLASTX
                    g3513294
NCBI GI
                    307
BLAST score
                    3.0e-28
E value
Match length
                    118
                    50
% identity
                   (AC005591) PkB-like [Homo sapiens]
NCBI Description
                    229296
Seq. No.
                    LIB3196-029-P1-M1-C8
Seq. ID
                    BLASTX
Method
NCBI GI
                    g1173027
BLAST score
                    380
                    1.0e-36
E value
Match length
                    103
                    75
% identity
                    60S RIBOSOMAL PROTEIN L31 >gi 915313 (U23784) ribosomal
NCBI Description
                    protein L31 [Nicotiana glutinosa]
                    229297
Seq. No.
                    LIB3196-029-P1-M1-C9
Seq. ID
```

BLASTX

663

g2266994

Method NCBI GI

BLAST score



```
7.0e-70
E value
                  127
Match length
% identity
                  98
                  (U77413) O-linked GlcNAc transferase [Homo sapiens]
NCBI Description
                  >qi 4505499 ref NP 003596.1_pOGT_ O-GlcNAc transferase
                  (uridine diphospho-N-acetylglucosamine:polypeptide
                  beta-N-acetylglucosaminyl transferase)
                  229298
Seq. No.
                  LIB3196-029-P1-M1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g71625
                  641
BLAST score
                  2.0e-67
E value
Match length
                  125
                  99
% identity
                  actin gamma - bovine (tentative sequence)
NCBI Description
                  229299
Seq. No.
                  LIB3196-029-P1-M1-D5
Seq. ID
                  BLASTX
Method
                  g2500399
NCBI GI
BLAST score
                   428
                   2.0e-42
E value
                   99
Match length
                   89
% identity
                   40S RIBOSOMAL PROTEIN S3 >gi_1836060_bbs_179561 (S83098)
NCBI Description
                   ribosomal protein S3 [Ambystoma mexicanum=Mexican axolotls,
                   embryos, Peptide, 253 aa] [Ambystoma mexicanum]
                   229300
Seq. No.
                   LIB3196-029-P1-M1-D9
Seq. ID
                   BLASTX
Method
                   g266691
NCBI GI
                   179
BLAST score
                   4.0e-13
E value
                   81
Match length
                   48
% identity
                   OLEOSIN 16.4 KD >gi_167361 (L00934) 16.4 kDa oleosin
NCBI Description
                   [Gossypium hirsutum]
                   229301
Seq. No.
                   LIB3196-029-P1-M1-E1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3901014
                   234
BLAST score
                   1.0e-19
E value
Match length
                   55
                   76
% identity
                   (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                   sylvatica]
```

Seq. No. 229302

Seq. ID LIB3196-029-P1-M1-E3 Method BLASTX

Method BLASTX NCBI GI g1905998 BLAST score 526



```
8.0e-54
E value
                   119
Match length
% identity
                   87
                   (U90426) nuclear RNA helicase [Homo sapiens]
NCBI Description
                   229303
Seq. No.
                   LIB3196-029-P1-M1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g120669
BLAST score
                   391
                   5.0e-38
E value
Match length
                   77
                   92
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
                   229304
Seq. No.
                   LIB3196-029-P1-M1-E6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3688177
BLAST score
                   318
                   2.0e-29
E value
Match length
                   93
                   65
% identity
                   (AL031804) putative protein [Arabidopsis thaliana]
NCBI Description
                   229305
Seq. No.
                   LIB3196-029-P1-M1-E8
Seq. ID
                   BLASTX
Method
                   g1304668
NCBI GI
                   395
BLAST score
                   2.0e-38
E value
                   77
Match length
                   96
% identity
                   (U42376) RIG-E precursor [Homo sapiens] >gi_1465747
NCBI Description
                    (U56145) thymic shared antigen-1/stem cell antigen-2 [Homo
                   sapiens] >gi_1519440 (U66711) 9804 [Homo sapiens]
                   >gi_4454267_emb_CAA92321_ (Z68179) retinoic acid induced
gene E [Homo sapiens] >gi_4505049_ref_NP_002337.1_pLY6E_
                    lymphocyte antigen 6 complex, locus E
                    229306
Seq. No.
                   LIB3196-029-P1-M1-F1
Seq. ID
                   BLASTX
Method
                    g4107099
NCBI GI
                    178
BLAST score
                    5.0e-13
E value
                    116
```

Match length 29 % identity

(AB015141) AHP1 [Arabidopsis thaliana] NCBI Description

>gi 4156245 dbj\_BAA37112 (AB012570) ATHP3 [Arabidopsis

thaliana]

229307 Seq. No.



% identity

```
LIB3196-029-P1-M1-F11
Seq. ID
Method
                  BLASTX
                  g2961178
NCBI GI
BLAST score
                   171
                   3.0e-12
E value
                   41
Match length
                   76
% identity
                   (AF050675) GTP-binding protein [Oryza sativa]
NCBI Description
                   229308
Seq. No.
                  LIB3196-029-P1-M1-F12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g137578
BLAST score
                   514
                   2.0e-52
E value
                   119
Match length
% identity
                   87
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                   >gi 81545_pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                   [Artificial gene] >gi 226119_prf__1410330A vicilin gene A
                   [Saguinus oedipus]
                   229309
Seq. No.
                   LIB3196-029-P1-M1-F5
Seq. ID
                   BLASTX
Method
                   g2558501
NCBI GI
BLAST score
                   167
                   7.0e-12
E value
Match length
                   104
                   38
% identity
                  (D63850) hepatoma-derived growth factor [Mus musculus]
NCBI Description
                   229310
Seq. No.
                   LIB3196-029-P1-M1-F7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1710401
BLAST score
                   442
                   4.0e-44
E value
                   99
Match length
                   82
% identity
                   RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN
NCBI Description
                   (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)
                   >gi 1044912 emb CAA63194_ (X92443) ribonucleotide reductase
                   R2 [Nicotiana tabacum]
                   229311
Seq. No.
                   LIB3196-029-P1-M1-F9
Seq. ID
                   BLASTX
Method
                   q3860255
NCBI GI
BLAST score
                   283
                   2.0e-25
E value
Match length
                   112
```

NCBI Description (AC005824) hypothetical protein [Arabidopsis thaliana]



```
Seq. No.
                  229312
                  LIB3196-029-P1-M1-G2
Seq. ID
Method
                  BLASTX
                  g137578
NCBI GI
                   455
BLAST score
                   2.0e-45
E value
                  119
Match length
                   47
% identity
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                   >gi_81545_pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi 207906 (M18027) alpha globulin A
                   [Artificial gene] >gi 226119 prf 1410330A vicilin gene A
                   [Saguinus oedipus]
Seq. No.
                   229313
                  LIB3196-029-P1-M1-G3
Seq. ID
Method
                   BLASTX
                   q4417309
NCBI GI
BLAST score
                   168
                   6.0e-12
E value
Match length
                   108
                   35
% identity
                  (AC006446) putative pol polyprotein with a reverse
NCBI Description
                   transcriptase domain [Arabidopsis thaliana]
                   229314
Seq. No.
Seq. ID
                   LIB3196-029-P1-M1-G4
Method
                   BLASTX
                   g2921447
NCBI GI
BLAST score
                   395
                   2.0e-38
E value
                   100
Match length
                   78
% identity
                   (AF037260) non-receptor protein tyrosine kinase Ack [Mus
NCBI Description
                   musculus]
Seq. No.
                   229315
                   LIB3196-029-P1-M1-G5
Seq: ID
Method
                   BLASTX
                   q1708624
NCBI GI
                   98
BLAST score
E value
                   1.0e-08
                   41
Match length
                   78
% identity
                  DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE)
NCBI Description
                   (DGK-DELTA) (DAG KINASE DELTA) (80 KD DIACYLGLYCEROL
                   KINASE) >gi_606757 (L38707) diacylglycerol kinase [Homo
                   sapiens] >gi_1589110_prf__2210300A diacylglycerol kinase 4
                   [Homo sapiens] >gi_4557519_ref NP_001338.1 pDGKQ
                   diacylglycerol kinase, the \overline{t}a (110\overline{k}D)
```

Seq. No. 229316

Seq. ID LIB3196-029-P1-M1-G6

Method BLASTX
NCBI GI g1703018
BLAST score 577



7.0e-60 E value Match length 120 95 % identity 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING NCBI Description >gi 984325 (U30255) phosphogluconate dehydrogenase [Homo sapiens] >gi 4505759 ref NP 002622.1\_pPGD\_ phosphogluconate dehydrogenase 229317 Seq. No. LIB3196-029-P1-M1-H3 Seq. ID BLASTX Method g4140326

NCBI GI 240 BLAST score 3.0e-20 E value 52 Match length 83 % identity

(AL031282) dJ283E3.6.1 (PUTATIVE novel protein similar to NCBI Description

many (archae) bacterial, worm and yeast hypothetical

proteins) [Homo sapiens]

229318 Seq. No.

LIB3196-029-P1-M1-H5 Seq. ID

Method BLASTX NCBI GI g729022 399 BLAST score 4.0e-39 E value Match length 94 % identity 84

MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G) NCBI Description

>gi\_346234\_pir\_\_A43358 macrophage capping protein - human

>gi 187456 (M94345) macrophage capping protein [Homo

sapiens] >gi 4502561 ref\_NP\_001738.1\_pCAPG\_ capping protein

(actin filament), gelsolin-like

Seq. No. 229319

Seq. ID LIB3196-029-P1-M1-H7

Method BLASTX NCBI GI q3023512 308 BLAST score 3.0e-28 E value Match length 119 53 % identity

PUTATIVE ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT NCBI Description

PRECURSOR (ENDOPEPTIDASE CLP) >gi\_2134793\_pir\_\_\$68421 ATP-dependent Clp proteinase (EC 3.4.21.92) chain P homolog

- human >gi\_963048\_emb\_CAA90705\_ (Z50853) CLPP [Homo

sapiens]

Seq. No. 229320

LIB3196-030-P1-M1-A11 Seq. ID

BLASTX Method NCBI GI q2344889 BLAST score 172 E value 2.0e-12 Match length 114 % identity

NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

BLAST score

E value

286

7.0e-26



```
229321
Seq. No.
                    LIB3196-030-P1-M1-A2
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2764583
BLAST score
                     495
                     3.0e-50
E value
                     112
Match length
                     79
% identity
                     (AJ001043) metastasis-associated GPI-anchored protein
NCBI Description
                     [Rattus norvegicus]
                     229322
Seq. No.
                    LIB3196-030-P1-M1-A3
Seq. ID
Method
                    BLASTX
NCBI GI
                     g72287
BLAST score
                     647
                     5.0e-68
E value
                     121
Match length
                     100
% identity
                    beta-globulin A precursor (clone 94) - upland cotton
NCBI Description
                     (fragment) >gi 167377 (M16905) legumin precursor [Gossypium
                     hirsutum]
Seq. No.
                     229323
                     LIB3196-030-P1-M1-A5
Seq. ID
Method
                     BLASTX
NCBI GI
                     g126156
BLAST score
                     298
E value
                     4.0e-27
Match length
                     101
% identity
                     61
                     LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
NCBI Description
                     >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134)
                     - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                     protein C134 [Saguinus oedipus]
                     229324
Seq. No.
Seq. ID
                     LIB3196-030-P1-M1-B1
Method
                     BLASTX
NCBI GI
                     g665584
BLAST score
                     531
E value
                     2.0e-54
Match length
                     107
% identity
                     99
                     (D16561) ATP synthase gamma-subunit [Homo sapiens]
NCBI Description
                     >gi_665585_dbj_BAA03997_ (D16563) ATP synthase gamma-subunit [Homo sapiens]
Seq. No.
                     229325
Seq. ID
                     LIB3196-030-P1-M1-B10
                     BLASTX
Method
NCBI GI
                     g4467804
```



```
82
Match length
                  71
% identity
                  (AL031678) TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3
NCBI Description
                  PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3).)
                  [Homo sapiens]
                  229326
Seq. No.
                  LIB3196-030-P1-M1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2132930
BLAST score
                  180
                  3.0e-13
E value
                  48
Match length
                  67
% identity
                  probable membrane protein YOR262w - yeast (Saccharomyces
NCBI Description
                  cerevisiae) >gi 1420591 emb CAA99484_ (Z75170) ORF YOR262w
                  [Saccharomyces cerevisiae]
                  229327
Seq. No.
                  LIB3196-030-P1-M1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g81546
                  267
BLAST score
                  8.0e-24
E value
                  70
Match length
                  70
% identity
                  alpha-globulin type B precursor (tandem 1) - upland cotton
NCBI Description
                  (fragment)
                  229328
Seq. No.
                  LIB3196-030-P1-M1-B4
Seq. ID
Method
                  BLASTX
                  g386849
NCBI GI
                   621
BLAST score
E value
                   6.0e-65
                  126
Match length
% identity
                   99
NCBI Description (L00205) keratin type II [Homo sapiens]
                   229329
Seq. No.
                  LIB3196-030-P1-M1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q137578
                   437
BLAST score
E value
                   2.0e-43
Match length
                   117
% identity
                   45
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                   >gi_81545_pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi 167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi 207906 (M18027) alpha globulin A
                   [Artificial gene] >qi 226119 prf 1410330A vicilin gene A
                   [Saguinus oedipus]
```

Seq. No. 229330

Seq. ID LIB3196-030-P1-M1-B9

Method BLASTX



```
g2388689
NCBI GI
                  356
BLAST score
                   6.0e-34
E value
Match length
                   91
                   79
% identity
                  (AF016633) GH1 protein [Glycine max]
NCBI Description
                  229331
Seq. No.
                  LIB3196-030-P1-M1-C1
Seq. ID
                  BLASTX
Method
                   g125887
NCBI GI
BLAST score
                   160
                   6.0e-11
E value
Match length
                   83
                   47
% identity
                  ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
NCBI Description
                   >gi_82092_pir__S04765 LAT52 protein precursor - tomato
                   >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon
                   esculentum]
                   229332
Seq. No.
                   LIB3196-030-P1-M1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4539944
BLAST score
                   356
                   6.0e - 34
E value
Match length
                   97
                   65
% identity
                  (AF133841) aldose reductase ALDRXV4 [Xerophyta viscosa]
NCBI Description
                   229333
Seq. No.
                   LIB3196-030-P1-M1-C11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g113463
                   369
BLAST score
                   2.0e-35
E value
                   76
Match length
                   99
% identity
                   ADP, ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP
NCBI Description
                   TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
                   >gi_86757_pir__S03894 ADP,ATP carrier protein T2 - human
                   229334
Seq. No.
                   LIB3196-030-P1-M1-C12
Seq. ID
                   BLASTX
Method
                   g3915742
NCBI GI
                   596
BLAST score
                   4.0e-62
E value
                   114
Match length
                   99
% identity
                  LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319
NCBI Description
                   (M69188) legumin A [Gossypium hirsutum]
                   >gi 444320 prf 1906369A legumin A:ISOTYPE=D alloallele
                   [Gossypium hirsutum]
```

32861

229335

LIB3196-030-P1-M1-C2

Seq. No.

Seq. ID



```
Method
                  BLASTX
NCBI GI
                  g2501719
BLAST score
                  233
                  2.0e-19
E value
Match length
                  44
                  100
% identity
                  ZINC FINGER PROTEIN 177 >gi 1049301 (U37263) KRAB zinc
NCBI Description
                  finger protein; Method: conceptual translation supplied by
                  author [Homo sapiens] >gi 4508009 ref NP 003442.1_pZNF177_
                  zinc finger protein
                  229336
Seq. No.
                  LIB3196-030-P1-M1-C4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2842486
BLAST score
                  209
E value
                  1.0e-16
                  71
Match length
% identity
                   61
                  (AL021749) putative protein [Arabidopsis thaliana]
NCBI Description
                   229337
Seq. No.
                  LIB3196-030-P1-M1-C6
Seq. ID
Method
                  BLASTX
                   g267072
NCBI GI
BLAST score
                   615
                   3.0e-64
E value
                   119
Match length
% identity
                   97
                  TUBULIN BETA-1 CHAIN >qi 100072 pir S20868 tubulin beta-1
NCBI Description
                   chain - garden pea >gi_20758_emb_CAA38613_ (X54844)
                   beta-tubulin 1 [Pisum sativum]
Seq. No.
                   229338
                   LIB3196-030-P1-M1-C8
Seq. ID
                   BLASTX
Method
                   g2213558
NCBI GI
                   217
BLAST score
E value
                   1.0e-17
Match length
                   118
                   42
% identity
                  (Z97052) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                   229339
Seq. No.
                   LIB3196-030-P1-M1-C9
Seq. ID
                   BLASTX
Method
                   g3834321
NCBI GI
                   554
BLAST score
                   3.0e-57
E value
                   117
Match length
                   93
% identity
                  (AC005679) Strong similarity to F13P17.9 gi 3337356
NCBI Description
```

transport protein SEC61 alpha subunit homolog from Arabidopsis thaliana BAC gb\_AC004481. [Arabidopsis

thaliana]

Seq. No. 229340



```
LIB3196-030-P1-M1-D10
Seq. ID
Method
                    BLASTX
                    q1399329
NCBI GI
BLAST score
                    629
E value
                    6.0e-66
Match length
                    122
                    92
% identity
                    (U41834) MHC class I antigen Mamu A*06 [Macaca mulatta]
NCBI Description
Seq. No.
                    229341
                    LIB3196-030-P1-M1-D11
Seq. ID
Method
                    BLASTX
NCBI GI
                    q481821
BLAST score
                    358
E value
                    3.0e - 34
Match length
                    113
                    64
% identity
                    probable glutathione transferase (EC 2.5.1.18) (clone
NCBI Description
                    ERD11) - Arabidopsis thaliana >gi_497788_dbj_BAA04553
                    (D17672) glutathione S-transferase [Arabidopsis thaliana]
                    229342
Seq. No.
                    LIB3196-030-P1-M1-D2
Seq. ID
Method
                    BLASTX
NCBI GI
                    a167367
BLAST score
                    646
E value
                    6.0e-68
                    122
Match length
                    100
% identity
                    (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                    229343
Seq. No.
                    LIB3196-030-P1-M1-D3
Seq. ID
Method
                    BLASTX
NCBI GI
                    q1706518
BLAST score
                    631
E value
                    4.0e-66
Match length
                    127
                    99
% identity
                    DEVELOPMENTALLY REGULATED GTP-BINDING PROTEIN DRG
NCBI Description
                    >gi_1082424_pir__A55014 GTP-binding protein - human
>gi_577779_emb_CAA56730_ (X80754) GTP-binding protein [Homo sapiens] >gi_4557537_ref_NP_001379.1_pDRG2_ developmentally
                    regulated GTP-binding protein
Seq. No.
                    229344
                    LIB3196-030-P1-M1-D4
Seq. ID
Method
                    BLASTX
NCBI GI
                    q121116
BLAST score
                    646
E value
                    6.0e-68
Match length
                    123
                    53
% identity
                   GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR)
NCBI Description
                    (ADF) (BREVIN) (AGEL) >gi 71649 pir FAHUP gelsolin
```

precursor, plasma - human >gi\_736249\_emb\_CAA28000\_ (X04412) plasma gelsolin [Homo sapiens] >gi\_225304\_prf\_\_1211330A



gelsolin [Homo sapiens] >gi\_4504165\_ref\_NP\_000168.1\_pGSN\_ gelsolin (amyloidosis, Finnish type)

Seq. No. 229345

Seq. ID LIB3196-030-P1-M1-D5

Method BLASTX
NCBI GI g120672
BLAST score 552
E value 6.0e-57
Match length 114
% identity 94

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_66016\_pir\_\_DEPZG glyceraldehyde-3-phosphate

dehydrogenase (EC 1.2.1.12) - parsley

>gi\_20549\_emb\_CAA42902\_ (X60344) glyceraldehyde 3-phosphate

dehydrogenase [Petroselinum crispum]

Seq. No. 229346

Seq. ID LIB3196-030-P1-M1-D7

Method BLASTX
NCBI GI g4206785
BLAST score 662
E value 8.0e-70
Match length 125
% identity 98

NCBI Description (AF107848) guanine nucleotide-binding protein [Mus

musculus]

Seq. No. 229347

Seq. ID LIB3196-030-P1-M1-E10

Method BLASTX
NCBI GI g88044
BLAST score 563
E value 3.0e-58
Match length 123
% identity 97

NCBI Description keratin 4, type II, cytoskeletal - human (fragment)

>gi\_34073\_emb\_CAA30534\_ (X07695) cytokeratin 4 (408 AA)

[Homo sapiens]

Seq. No. 229348

Seq. ID LIB3196-030-P1-M1-E5

Method BLASTX
NCBI GI g3152595
BLAST score 482
E value 1.0e-48
Match length 118
% identity 75

NCBI Description (AC002986) Similar to D. melanogaster sno gene gb\_U95760.

EST gb N97148 and gb Z26221 come from this gene.

[Arabidopsis thaliana]

Seq. No. 229349

Seq. ID LIB3196-030-P1-M1-E6

Method BLASTX NCBI GI g4454467 BLAST score 280



```
5.0e-25
E value
                  116
Match length
                  46
% identity
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                  229350
Seq. No.
                  LIB3196-030-P1-M1-E7
Seq. ID
                  BLASTX
Method
                  g421960
NCBI GI
BLAST score
                  381
                  7.0e-37
E value
                  100
Match length
                  73
% identity
                  small nuclear ribonucleoprotein U2B'' - potato >gi_169589
NCBI Description
                   (M72892) spliceosomal protein [Solanum tuberosum]
                  229351
Seq. No.
                  LIB3196-030-P1-M1-E8
Seq. ID
Method
                  BLASTX
                  g4539660
NCBI GI
BLAST score
                  324
                  3.0e - 30
E value
                  116
Match length
                  53
% identity
NCBI Description (AF061282) polyprotein [Sorghum bicolor]
Seq. No.
                  229352
                  LIB3196-030-P1-M1-F2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4008159
BLAST score
                   557
E value
                   2.0e-57
                  115
Match length
% identity
NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]
Seq. No.
                   229353
                   LIB3196-030-P1-M1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2245069
BLAST score
                   435
E value
                   3.0e-43
Match length
                   117
% identity
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   229354
Seq. ID
                   LIB3196-030-P1-M1-F8
Method
                   BLASTX
NCBI GI
                   q4204684
BLAST score
                   284
E value
                   1.0e-25
Match length
                   58
                   90
% identity
                  (AF102542) beta-1,6-N-acetylglucosaminyltransferase [Homo
NCBI Description
```

sapiens] >gi\_4511881\_gb\_AAD21525.1\_ (AF038650) core 2/core
4 beta-1,6-N-acetylglucosaminyltransferase; core 2/4-GnT



## [Homo sapiens]

 Seq. No.
 229355

 Seq. ID
 LIB3196-030-P1-M1-F9

 Method
 BLASTX

 NCBI GI
 g4336205

 BLAST score
 530

BLAST score 530 E value 2.0e-54 Match length 113 % identity 84

NCBI Description (AF077372) cytochrome b5 reductase [Zea mays]

Seq. No. 229356

Seq. ID LIB3196-030-P1-M1-G10

Method BLASTX
NCBI GI g1076291
BLAST score 175
E value 1.0e-12
Match length 117
% identity 36

NCBI Description amino acid transporter AAT1 - Arabidopsis thaliana

>gi\_2911069\_emb\_CAA17531\_ (AL021960) amino acid transport

protein AATI [Arabidopsis thaliana]

Seq. No. 229357

Seq. ID LIB3196-030-P1-M1-G12

Method BLASTX
NCBI GI g3122072
BLAST score 530
E value 2.0e-54
Match length 105
% identity 98

NCBI Description ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION

FACTOR TU) (EF-TU) >gi\_2119922\_pir\_\_\_I50226 elongation factor 1 alpha - chicken >gi\_488468 (L00677) elongation

factor 1 alpha [Gallus gallus]

Seq. No. 229358

Seq. ID LIB3196-030-P1-M1-G2

Method BLASTX
NCBI GI g3915742
BLAST score 488
E value 2.0e-49
Match length 116
% identity 84

NCBI Description LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi\_167319

(M69188) legumin A [Gossypium hirsutum]

>gi 444320 prf 1906369A legumin A:ISOTYPE=D alloallele

[Gossypium hirsutum]

Seq. No. 229359

Seq. ID LIB3196-030-P1-M1-G5

Method BLASTX
NCBI GI g136479
BLAST·score 461
E value 3.0e-46
Match length 90

NCBI Description

Seq. No.

229364



```
% identity
                  100
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN (TCTP) (P23)
NCBI Description
                  >gi_88948_pir__S06590 IgE-dependent histamine-releasing
                  factor - human >gi_37496_emb_CAA34200_ (X16064) tumor
                  protein (AA 1 - 172) [Homo sapiens]
                  >gi 4507669 ref NP 003286.1 pTPT1 tumor protein,
                  translationally-controlled
                  229360
Seq. No.
                  LIB3196-030-P1-M1-G6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2811001
BLAST score
                  508
                  1.0e-51
E value
                  99
Match length
                  100
% identity
                  NUCLEOLAR PROTEIN NOP56 >gi_2230878_emb_CAA72789_ (Y12065)
NCBI Description
                  hNop56 [Homo sapiens]
                  229361
Seq. No.
                  LIB3196-030-P1-M1-G9
Seq. ID
                  BLASTX
Method
                  g117501
NCBI GI
                  513
BLAST score
                  2.0e-52
E value
                  95
Match length
                  100
% identity
                  CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60)
NCBI Description
                   (52 KD RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A)
                  >gi 87015_pir__A37047 calreticulin precursor - human
                  >gi_179882 (M84739) calreticulin [Homo sapiens] >gi_337487
                   (M32294) Ro ribonucleoprotein autoantigen (Ro/SS-A)
                  precursor [Homo sapiens] >gi_1905911 (AD000092)
                   calreticulin [Homo sapiens]
                  229362
Seq. No.
                  LIB3196-030-P1-M1-H11
Seq. ID
                  BLASTX
Method
                   g2306917
NCBI GI
                   371
BLAST score
                   1.0e-35
E value
Match length
                   83
                   89
% identity
                  (AF003728) plasma membrane intrinsic protein [Arabidopsis
NCBI Description
                   thaliana]
                   229363
Seq. No.
                   LIB3196-030-P1-M1-H5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2995405
BLAST score
                   472
                   1.0e-47
E value
Match length
                   117
% identity
                   74
                  (Y12432) polyprotein [Ananas comosus]
```



```
LIB3196-030-P1-M1-H6
Seq. ID
                    BLASTX
Method
                    g1346344
NCBI GI
BLAST score
                    636
                    1.0e-66
E value
Match length
                    126
                    100
% identity
                    KERATIN, TYPE II CYTOSKELETAL 6A (CYTOKERATIN 6A) (CK 6A)
NCBI Description
                    (K6A KERATIN) >gi 2119221 pir A57398 keratin type II -
                    human >gi 908779 (L42583) keratin type II [Homo sapiens]
                    229365
Seq. No.
                    LIB3196-030-P1-M1-H8
Seq. ID
                    BLASTX
Method
                    g284691
NCBI GI
                    204
BLAST score
                    4.0e-16
E value
                    51
Match length
                    80
% identity
                    transcription factor ATF-4 - mouse >gi 50050 emb CAA43723
NCBI Description
                    (X61507) activating transcriptionn factor 4 [Mus musculus]
                    229366
Seq. No.
                    LIB3196-031-P1-M1-A4
Seq. ID
                    BLASTX
Method
NCBI GI
                    g432977
                    584
BLAST score
E value
                    1.0e-60
                    124
Match length
                    93
% identity
                    (M75884) sterol carrier protein-2 [Homo sapiens]
NCBI Description
                    >gi 4506823 ref NP 002970.1 pSCP2 sterol carrier protein
                    229367
Seq. No.
                    LIB3196-031-P1-M1-A5
Seq. ID
                    BLASTX
Method
NCBI GI
                    g2605714
BLAST score
                    448
E value
                    1.0e-44
Match length
                    124
% identity
                    47
NCBI Description
                    (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
                    thaliana]
                    229368
Seq. No.
                    LIB3196-031-P1-M1-B11
Seq. ID
Method
                    BLASTX
NCBI GI
                    g122085
BLAST score
                    527
                    6.0e-54
E value
Match length
                    124
                    85
% identity
                   HÏSTONE H3 >qi 81641 pir S06250 histone H3 - Arabidopsis
NCBI Description
                    thaliana >gi 8\overline{2}482 pir \overline{50}4099 histone H3 (variant H3R-21) - rice >gi \underline{13}62194 \underline{pir} \underline{557}626 histone H3 - maize
```

>gi\_20251\_emb\_CAA31969\_ (X13678) histone H3 (AA 1-136)
[Oryza sativa] >gi 20253 emb CAA31970 (X13680) histone H3



(AA 1-136) [Oryza sativa] >gi\_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi 168495 (M13378) histone H3 [Zea mays] >qi 168497 (M13379) histone H3 [Zea mays] >qi 168506  $(M3\overline{5}388)$  histone H3 [Zea mays] >gi\_169655 (M77493) histone H3 [Petroselinum crispum]  $>gi_1696\overline{57}$  (M77494) histone H3 [Petroselinum crispum] >gi\_169659 (M77495) histone H3 [Petroselinum crispum] >gi\_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi\_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi 886738 emb CAA59111 (X84377) histone 3 [Zea mays]  $>gi_1\overline{040764}$  (M35 $\overline{387}$ ) histone H3 [Arabidopsis thaliana] >gi\_1314779 (U54827) histone H3  $\label{local_condition} \mbox{homolog [Brassica napus] } > \mbox{$\overline{g}i$\_1531754 $emb\_CAA57811} \mbox{$(X82414)$}$ Histone H3 [Asparagus officinalis] >gi 1667592 (U77296) histone 3 [Oryza sativa] >gi\_3249101 (AC003114) Match to histone H3 gene gb M17131 and gb M35387 from A. thaliana. ESTs gb\_H76511 gb\_ $\overline{\text{H}}$ 76255, gb\_AA7 $\overline{\text{1}}$ 2452, gb N65260 and gb T42306 come from this gene. [Arabidopsis thaliana] >gi 225459\_prf\_\_1303352A histone H3 [Helicoverpa zea] >qi 225839 prf 1314298B histone H3 [Arabidopsis thaliana]

```
Seq. No.
                   229369
                   LIB3196-031-P1-M1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2497539
BLAST score
                   604
                   5.0e-63
E value
Match length
                   122
                   98
% identity
```

NCBI Description PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi\_169703 (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]

229370 Seq. No. LIB3196-031-P1-M1-B4 Seq. ID Method BLASTX g125077 NCBI GI 158 BLAST score 1.0e-10 E value Match length 31 % identity 100

NCBI Description KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK 13) >gi\_71526\_pir\_\_KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi\_34033\_emb\_CAA32786\_ (X14640) keratin

13 [Homo sapiens]

Seq. No. 229371

Seq. ID LIB3196-031-P1-M1-B6

Method BLASTX
NCBI GI g167311
BLAST score 492
E value 7.0e-50
Match length 93
% identity 100

NCBI Description (M83301) 2S albumin storage protein [Gossypium hirsutum]

Seq. No. 229372

Seq. ID LIB3196-031-P1-M1-B8

Method BLASTX

Seq. ID

Method



```
q4200327
NCBI GI
                    485
BLAST score
                    4.0e-49
E value
Match length
                    94
                    97
% identity
NCBI Description
                   (AL022313) thioredoxin [Homo sapiens]
                    229373
Seq. No.
                    LIB3196-031-P1-M1-C1
Seq. ID
Method
                    BLASTX
                    g2652938
NCBI GI
BLAST score
                    248
E value
                    3.0e-21
                    62
Match length
                    45
% identity
NCBI Description
                   (Z47554) orf [Zea mays]
                    229374
Seq. No.
                    LIB3196-031-P1-M1-C10
Seq. ID
                    BLASTX
Method
NCBI GI
                    g87333
                    383
BLAST score
                    4.0e-37
E value
                    115
Match length
                    70
% identity
NCBI Description
                    DNA-binding protein B - human (fragment) >gi_181486
                    (M24070) DNA-binding protein B [Homo sapiens]
                    229375
Seq. No.
                    LIB3196-031-P1-M1-C12
Seq. ID
Method
                    BLASTX
NCBI GI
                    g125080
                    353
BLAST score
                    1.0e-33
E value
Match length
                    69
                    100
% identity
                    KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK
NCBI Description
                    14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14
                     (epidermolysis bullosa simplex, Dowling-Meara, Koebner)
                    229376
Seq. No.
                    LIB3196-031-P1-M1-C5
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1363944
BLAST score
                    669
E value
                    1.0e-70
Match length
                    133
                    99
% identity
                    type I keratin 16 - human >gi_1195531_bbs_172338 (S79867)
NCBI Description
                    type I keratin 16, K16 [human, epidermal keratinocytes,
                    Peptide, 473 aa] [Homo sapiens]
                    229377
Seq. No.
```

32870

LIB3196-031-P1-M1-C7

BLASTX .



```
NCBI GI
                  q4432821
BLAST score
                  161
                  3.0e-11
E value
Match length
                  80
                  50
% identity
                   (AC006593) putative transmembrane protein [Arabidopsis
NCBI Description
                  thaliana]
                  229378
Seq. No.
                  LIB3196-031-P1-M1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q137580
                   407
BLAST score
                   6.0e-40
E value
Match length
                  78
% identity
                  100
                  VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72)
NCBI Description
                  >gi 72286_pir__FWCNAB alpha-globulin B precursor (clone
                   C72) - upland cotton >gi 167375 (M16891) vicilin precursor
                   [Gossypium hirsutum]
                   229379
Seq. No.
Seq. ID
                  LIB3196-031-P1-M1-D12
Method
                   BLASTX
                   q2492517
NCBI GI
BLAST score
                   352
                   1.0e-60
E value
Match length
                   127
% identity
                   98
                  26S PROTEASE REGULATORY SUBUNIT 6B (TAT-BINDING PROTEIN-7)
NCBI Description
                   (TBP-7) >gi 1395186 dbj BAA09340 (D50695) proteasomal
                   ATPase (Tat-binding protein7) [Rattus norvegicus]
                   229380
Seq. No.
                   LIB3196-031-P1-M1-D3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q125077
BLAST score
                   154
                   3.0e-10
E value
                   30
Match length
                   100
% identity
                  KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK
NCBI Description
                   13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal,
                   long form - human >gi 34033 emb CAA32786 (X14640) keratin
                   13 [Homo sapiens]
                   229381
Seq. No.
Seq. ID
                   LIB3196-031-P1-M1-D4
Method
                   BLASTX
NCBI GI
                   q4539005
BLAST score
                   592
                   1.0e-61
E value
Match length
                   125
% identity
                  (AL049481) putative oxidoreductase [Arabidopsis thaliana]
NCBI Description
```

229382

Seq. No.

NCBI Description

arietinum]



```
LIB3196-031-P1-M1-D6
Seq. ID
                  BLASTX
Method
                  g3334147
NCBI GI
                  228
BLAST score
                  1.0e-35
E value
                  117
Match length
                  60
% identity
                  ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I
NCBI Description
                  chitinase [Gossypium hirsutum]
                  229383
Seq. No.
                  LIB3196-031-P1-M1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3549652
BLAST score
                  246
                  5.0e-21
E value
Match length
                  88
% identity
                  66
                  (AJ224982) MAP3K epsilon protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  229384
Seq. No.
Seq. ID
                  LIB3196-031-P1-M1-D9
Method
                  BLASTX
NCBI GI
                  g3738288
BLAST score
                  163
                  3.0e-11
E value
Match length
                  105
% identity
                  43
                  (AC005309) auxin-responsive GH3-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  229385
Seq. No.
                  LIB3196-031-P1-M1-E10
Seq. ID
Method
                  BLASTX
                  g137473
NCBI GI
BLAST score
                  264
E value
                  4.0e-23
                  100
Match length
                   61
% identity
                  VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
NCBI Description
                   (V-ATPASE 31 KD SUBUNIT) (P31) >gi_89601_pir__A31335
                  H+-transporting ATPase (EC 3.6.1.35) 31K chain, vacuolar -
                  bovine >gi 163132 (J03244) H+ ATPase 31kDa subunit (EC
                   3.6.1.3) [Bos taurus]
Seq. No.
                   229386
Seq. ID
                  LIB3196-031-P1-M1-E12
Method
                  BLASTX
NCBI GI
                  q3319882
                   383
BLAST score
                   5.0e-37
E value
Match length
                   77
                   95
% identity
```

(AJ004960) elongation factor 1-alpha (EF1-a) [Cicer



```
Seq. No.
                  229387
                  LIB3196-031-P1-M1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q992706
BLAST score
                  174
                  1.0e-12
E value
Match length
                  36
                  86
% identity
                  (U33758) UBC13 [Arabidopsis thaliana]
NCBI Description
                  229388
Seq. No.
Seq. ID
                  LIB3196-031-P1-M1-E3
Method
                  BLASTX
                  g28595
NCBI GI
BLAST score
                  552
                  7.0e-57
E value
                  107
Match length
% identity
                  100
                  (X06352) aldolase A protein [Homo sapiens]
NCBI Description
                  229389
Seq. No.
                  LIB3196-031-P1-M1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220532
                  262
BLAST score
                  7.0e-23
E value
Match length
                  123
% identity
                  50
                  (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
                  229390
Seq. No.
                  LIB3196-031-P1-M1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g129916
                   601
BLAST score
                  1.0e-62
E value
Match length
                  124
% identity
                   95
                 PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY
NCBI Description
                   phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                   >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                   (AA 1 - 401) [Triticum aestivum]
                   229391
Seq. No.
                  LIB3196-031-P1-M1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g683553
BLAST score
                   220
                   5.0e-18
E value
Match length
                   102
% identity
                   49
                  (Z48450) oleosin-like protein [Citrus sinensis]
NCBI Description
                   >gi 1582679 prf 2119230A oleosin homolog [Citrus sinensis]
```

Seq. No. 229392

Seq. ID LIB3196-031-P1-M1-F10

Method BLASTX



```
g2500813
NCBI GI
BLAST score
                  606
                  3.0e-63
E value
Match length
                  131
                  93
% identity
                  NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) >gi 1236986 (U51432)
NCBI Description
                  nuclear protein Skip [Homo sapiens] >gi 3417599 (AF045184)
                  nuclear receptor coactivator NCoA-62 [Homo sapiens]
                  229393
Seq. No.
                  LIB3196-031-P1-M1-F2
Seq. ID
Method
                  BLASTX
                  g112925
NCBI GI
BLAST score
                  146
                  3.0e-09
E value
Match length
                  93
                  39
% identity
                 41-2 PROTEIN ANTIGEN PRECURSOR >qi 320938 pir A45503 41-2
NCBI Description
                  protein antigen precursor - Plasmodium falciparum
                  >gi 160039 (J04656) 41-2 protein antigen [Plasmodium
                  falciparum]
                  229394
Seq. No.
                  LIB3196-031-P1-M1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g167367
BLAST score
                  435
                  4.0e-43
E value
                  95
Match length
                  87
% identity
                 (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                  229395
Seq. No.
                  LIB3196-031-P1-M1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g137578
BLAST score
                  610
E value
                  1.0e-63
Match length
                  129
% identity
                  89
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                  >gi_81545_pir__S06398 alpha-globulin type A precursor -
                  upland cotton >gi 167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                   [Artificial gene] >gi 226119 prf 1410330A vicilin gene A
                   [Saguinus oedipus]
Seq. No.
                  229396
Seq. ID
                  LIB3196-031-P1-M1-F7
Method
                  BLASTX
NCBI GI
                  q1351722
BLAST score
                  220
```

Method BLASTX
NCBI GI g1351722
BLAST score 220
E value 6.0e-18
Match length 121
% identity 39

NCBI Description HYPOTHETICAL 29.7 KD PROTEIN C18G6.06 IN CHROMOSOME I >gi\_1122371\_emb\_CAA92386\_ (Z68198) hypothetical protein

% identity

66



## [Schizosaccharomyces pombe]

```
Seq. No.
                  229397
                  LIB3196-031-P1-M1-G4
Seq. ID
Method
                  BLASTX
                  q1518540
NCBI GI
                  591
BLAST score
                  2.0e-61
E value
Match length
                  127
% identity
                  89
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                  229398
Seq. No.
                  LIB3196-031-P1-M1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4567303
BLAST score
                  382
                  6.0e-37
E value
Match length
                  77
% identity
                  86
                  (AC005956) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  229399
                  LIB3196-031-P1-M1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1336807
BLAST score
                  268
E value
                  1.0e-23
Match length
                  96
                   60
% identity
                  (S81193) CEN=GTP-binding protein homolog
NCBI Description
                   [Antirrhinum=snapdragons, Peptide, 181 aa] [Antirrhinum]
                  >gi 1587482 prf 2206476A CEN gene [Antirrhinum sp.]
                   229400
Seq. No.
                  LIB3196-031-P1-M1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g137578
BLAST score
                   643
E value
                  1.0e-67
Match length
                  124
                   99
% identity
NCBI Description
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
                   >gi_81545_pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                   [Artificial gene] >gi_226119_prf__1410330A vicilin gene A
                   [Saguinus oedipus]
Seq. No.
                   229401
                  LIB3196-031-P1-M1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539660
BLAST score
                  449
                  8.0e-45
E value
Match length
                  124
```



```
(AF061282) polyprotein [Sorghum bicolor]
NCBI Description
                  229402
Seq. No.
                  LIB3196-031-P1-M1-H11
Seq. ID
                  BLASTX
Method
                  g137578
NCBI GI
                  503
BLAST score
                  4.0e-51
E value
                  129
Match length
                  78
% identity
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                  >gi_81545_pir__S06398 alpha-globulin type A precursor -
                  upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                   [Artificial gene] >gi 226119 prf 1410330A vicilin gene A
                   [Saguinus oedipus]
                  229403
Seq. No.
                  LIB3196-031-P1-M1-H5
Seq. ID
                  BLASTX
Method
                  g3386610
NCBI GI
                  160
BLAST score
                  1.0e-20
E value
                  85
Match length
                  58
% identity
                  (AC004665) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  229404
                  LIB3196-031-P1-M1-H7
Seq. ID
                  BLASTX
Method
                  g386850
NCBI GI
                   250
BLAST score
                   9.0e-22
E value
                   74
Match length
                   72
% identity
NCBI Description (M19723) keratin K5 [Homo sapiens]
Seq. No.
                   229405
                  LIB3196-032-P1-M1-A10
Seq. ID
Method
                  BLASTX
                   g2072972
NCBI GI
BLAST score
                   483
                   2.0e-58
E value
                   122
Match length
% identity
NCBI Description (U93572) putative p150 [Homo sapiens]
Seq. No.
                   229406
                   LIB3196-032-P1-M1-A11
Seq. ID
                   BLASTX
Method
                   q3192969
NCBI GI
BLAST score
                   570
E value
                   4.0e-59
Match length
                   109
                   99
% identity
                   (AF043106) sarco/endoplasmic reticulum Ca2+-ATPase [Rattus
NCBI Description
```

32876

norvegicus]



```
229407
Seq. No.
                  LIB3196-032-P1-M1-A2
Seq. ID
                  BLASTX
Method
                  g126156
NCBI GI
BLAST score
                  520
                  4.0e-53
E value
                  100
Match length
                  100
% identity
                  LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
NCBI Description
                  >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134)
                  - upland cotton >gi_167373 (M16936) vicilin precursor
                  [Gossypium hirsutum] >gi_1171335 (U43727) legumin B
                  [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                  protein C134 [Saguinus oedipus]
                  229408
Seq. No.
                  LIB3196-032-P1-M1-A3
Seq. ID
                  BLASTX
Method
                  g129034
NCBI GI
                  523
BLAST score
E value
                  2.0e-53
                  102
Match length
                  96
% identity
                  2-OXOISOVALERATE DEHYDROGENASE BETA SUBUNIT PRECURSOR
NCBI Description
                   (BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPONENT
                  BETA CHAIN (E1)) (BCKDH E1-BETA) >gi_105120_pir__A37157
                  3-methyl-2-oxobutanoate dehydrogenase (lipoamide) (EC
                  1.2.4.4) E1-beta chain precursor - human >gi_179362
                   (M55575) branched chain alpha-keto acid dehydrogenase
                  E1-beta subunit [Homo sapiens] >gi_219493_dbj_BAA14389_
                   (D90391) E-1-beta subunit [Homo sapiens] >gi_1480477
                   (U50708) branched chain alpha-ketoacid dehydrogenase E1
                  beta subunit [Homo sapiens]
                  >gi_4557353_ref_NP_000047.1_pBCKDHB_ branched chain keto
                  acid dehydrogenase El, beta polypeptide precursor
Seq. No.
                  229409
                  LIB3196-032-P1-M1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  a399365
BLAST score
                  459
E value
                  3.0e-46
                  89
Match length
% identity
                  100
                  ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (CLASS 3)
NCBI Description
                  >gi 178402 (M74542) aldehyde dehydrogenase type III [Homo
                  sapiens] >gi_4502035_ref_NP_000682.1_pALDH3_ aldehyde
                  dehydrogenase
```

Seq. No. 229410 Seq. ID LIB3196-032-P1-M1-A9

Method BLASTX
NCBI GI g683553
BLAST score 203
E value 6.0e-16
Match length 98

Match length



```
% identity
                   48
                   (Z48450) oleosin-like protein [Citrus sinensis]
NCBI Description
                   >gi 1582679 prf 2119230A oleosin homolog [Citrus sinensis]
                   229411
Seq. No.
                   LIB3196-032-P1-M1-B11
Seq. ID
                   BLASTX
Method
                   g3914977
NCBI GI
                   265
BLAST score
                   3.0e-23
E value
Match length
                   52
                   96
% identity
                   SERINE/THREONINE-PROTEIN KINASE SGK
NCBI Description
                   (SERUM/GLUCOCORTICOID-REGULATED KINASE)
                   >gi_1834511_emb_CAA71138_ (Y10032) serine/threonine protein kinase [Homo sapiens] >gi_2463201_emb_CAA04146_ (AJ000512)
                   serine/threonine protein kinase [Homo sapiens]
                   229412
Seq. No.
                   LIB3196-032-P1-M1-B3
Seq. ID
                   BLASTX
Method
                   g4406801
NCBI GI
BLAST score
                   192
                   1.0e-14
E value
                   57
Match length
% identity
                   63
NCBI Description
                  (AC006304) unknown protein [Arabidopsis thaliana]
                   229413
Seq. No.
                   LIB3196-032-P1-M1-B4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g266691
BLAST score
                   168
                   4.0e-12
E value
                   68
Match length
                   53
% identity
NCBI Description OLEOSIN 16.4 KD >gi_167361 (L00934) 16.4 kDa oleosin
                   [Gossypium hirsutum]
                   229414
Seq. No.
                   LIB3196-032-P1-M1-C2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1703375
                   490
BLAST score
                   1.0e-49
E value
Match length
                   96
% identity
                   99
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 965483 dbj BAA08259 (D45420)
                   DcARF1 [Daucus carota]
                   229415
Seq. No.
                   LIB3196-032-P1-M1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g685073
BLAST score
                   174
E value
                   8.0e-13
```



```
% identity
                  11
                  SPRC=small proline-rich protein [human, odontogenic
NCBI Description
                  keratocysts, Peptide Partial, 161 aa]
                  229416
Seq. No.
                  LIB3196-032-P1-M1-D10
Seq. ID
                  BLASTX
Method
                  g730922
NCBI GI
BLAST score
                  573
                  2.0e-59
E value
Match length
                  113
                  97
% identity
                  T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA)
NCBI Description
                  (TCP20) (HTR3) >gi_627402_pir__S48087 chaperonin TCP20 -
                  human >gi_517065 (L27706) chaperonin-like protein [Homo
                  sapiens] >gi_4502643_ref_NP_001753.1_pCCT6_ chaperonin
                  containing T-complex subunit
                  229417
Seq. No.
                  LIB3196-032-P1-M1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g730922
BLAST score
                  321
                  3.0e-49
E value
                  130
Match length
                  81
% identity
NCBI Description
                  T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA)
                  (TCP20) (HTR3) >gi_627402_pir__S48087 chaperonin TCP20 -
                  human >gi 517065 (L27706) chaperonin-like protein [Homo
                  sapiens] >gi 4502643 ref NP 001753.1 pCCT6 chaperonin
                  containing T-complex subunit
                  229418
Seq. No.
                  LIB3196-032-P1-M1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4185819
BLAST score
                  192
E value
                  1.0e-14
Match length
                  47
% identity
                  68
NCBI Description
                  (AF116845) metallothionein-like type 1 protein [Ipomoea
                  batatas]
                  229419
Seq. No.
                  LIB3196-032-P1-M1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4220474
BLAST score
                  451
E value
                  4.0e-45
Match length
                  102
% identity
NCBI Description
                  (AC006069) putative myosin heavy chain [Arabidopsis
```

Seq. No. 229420

Seq. ID LIB3196-032-P1-M1-D8

thaliana]

Method BLASTX

BLAST score

E value

489

1.0e-49



```
NCBI GI
                  g1336807
BLAST score
                  293
                  1.0e-26
E value
Match length
                  106
                  58
% identity
                  (S81193) CEN=GTP-binding protein homolog
NCBI Description
                   [Antirrhinum=snapdragons, Peptide, 181 aa] [Antirrhinum]
                  >gi 1587482 prf 2206476A CEN gene [Antirrhinum sp.]
                  229421
Seq. No.
                  LIB3196-032-P1-M1-D9
Seq. ID
                  BLASTX
Method
                  g2137308
NCBI GI
BLAST score
                  272
                  9.0e-45
E value
Match length
                  99
                  95
% identity
                  G protein beta subuit like - mouse >gi 475012 dbj BAA06185
NCBI Description
                   (D29802) G protein beta subuit like [Mus musculus]
                  229422
Seq. No.
                  LIB3196-032-P1-M1-E1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3062801
BLAST score
                  347
                  4.0e-33
E value
Match length
                  93
% identity
                  68
                  (AB012873) arginine decarboxylase [Nicotiana sylvestris]
NCBI Description
                  229423
Seq. No.
                  LIB3196-032-P1-M1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1263291
BLAST score
                  412
E value
                  1.0e-40
Match length
                  85
% identity
NCBI Description
                  (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]
Seq. No.
                  229424
Seq. ID
                  LIB3196-032-P1-M1-E5
Method
                  BLASTX
NCBI GI
                  g1256259
BLAST score
                  427
E value
                   3.0e-42
Match length
                  96
% identity
NCBI Description
                  (U50900) voltage-dependent anion channel protein [Spinacia
                  oleracea]
Seq. No.
                  229425
Seq. ID
                  LIB3196-032-P1-M1-E7
Method
                  BLASTX
NCBI GI
                  g2662341
```

Seq. No.

Seq. ID

Method

NCBI GI

229430

BLASTX

g106323

LIB3196-032-P1-M1-F6



```
Match length
                  93
                  100
% identity
                  (D63580) EF-1 alpha [Oryza sativa]
NCBI Description
                  >gi 2662345 dbj_BAA23659 (D63582) EF-1 alpha [Oryza
                  satīva] >gi 2662347 dbj BAA23660 (D63583) EF-1 alpha
                  [Oryza sativa]
                  229426
Seq. No.
                  LIB3196-032-P1-M1-E9
Seq. ID
                  BLASTX
Method
                  g2833280
NCBI GI
BLAST score
                  542
                  8.0e-56
E value
Match length
                  110
% identity
                  94
                  NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR
NCBI Description
                  (COMPLEX I-39KD) (CI-39KD)
                  229427
Seq. No.
                  LIB3196-032-P1-M1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g119354
BLAST score
                  215
                  9.0e-18
E value
Match length
                  49
                  90
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_82082_pir__JQ1185
                  phosphopyruvate hydratase (EC 4.2.1.11) - tomato
                  >gi 19281 emb CAA41115 (X58108) enolase [Lycopersicon
                  esculentum]
Seq. No.
                  229428
                  LIB3196-032-P1-M1-F10
Seq. ID
                  BLASTX
Method
                  g2879811
NCBI GI
BLAST score
                   481
E value
                  2.0e-48
                  94
Match length
                   95
% identity
                  (AJ223316) ribosomal protein L30 [Lupinus luteus]
NCBI Description
                  229429
Seq. No.
                  LIB3196-032-P1-M1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g291888
BLAST score
                   283
E value
                   1.0e-39
Match length
                   84
% identity
                   88
                  (L16510) cathepsin B [Homo sapiens]
NCBI Description
                   >gi 4503139 ref NP 001899.1 pCTSB cathepsin B
```

Seq. ID Method



```
BLAST score
                  477
                  4.0e-48
E value
                  129
Match length
                  65
% identity
                  hypothetical protein (L1H 5' region) - human
NCBI Description
                  229431
Seq. No.
                  LIB3196-032-P1-M1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3915742
                  372
BLAST score
                  4.0e-53
E value
                  119
Match length
                  91
% identity
                  LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi 167319
NCBI Description
                   (M69188) legumin A [Gossypium hirsutum]
                  >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele
                   [Gossypium hirsutum]
                  229432
Seq. No.
                  LIB3196-032-P1-M1-G11
Seq. ID
                  BLASTX
Method
                  g137578
NCBI GI
                  455
BLAST score
                  1.0e-45
E value
                  110
Match length
                  85
% identity
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                  >gi_81545_pir__S06398 alpha-globulin type A precursor -
                  upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                   [Artificial gene] >gi_226119_prf__1410330A vicilin gene A
                   [Saguinus oedipus]
                   229433
Seq. No.
                  LIB3196-032-P1-M1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4432846
BLAST score
                   454
                   2.0e-45
E value
                   124
Match length
                   68
% identity
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                   229434
Seq. No.
                   LIB3196-032-P1-M1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3212869
BLAST score
                   201
                   3.0e-16
E value
                   41
Match length
% identity
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                   229435
Seq. No.
```

32882

LIB3196-032-P1-M1-G4

BLASTX



```
NCBI GI
                  g2623304
BLAST score
                  148
E value
                  8.0e-10
Match length
                  66
% identity
                  48
NCBI Description
                  (AC002409) similar to Medicago nodulin N21 [Arabidopsis
                  thaliana]
                  229436
Seq. No.
Seq. ID
                  LIB3196-032-P1-M1-G7
Method
                  BLASTX
NCBI GI
                  g1171035
BLAST score
                  171
E value
                  2.0e-12
Match length
                  43
                  72
% identity
                  METALLOTHIONEIN-LIKE PROTEIN TYPE 2 PKIWI504
NCBI Description
                  >gi 1086021 pir S48038 metallothionein-like protein - kiwi
                  fruit >gi 450245 (L27813) metallothionein-like protein
                   [Actinidia deliciosa]
Seq. No.
                  229437
Seq. ID
                  LIB3196-032-P1-M1-G9
Method
                  BLASTX
NCBI GI
                  q662366
BLAST score
                  172
                  1.0e-12
E value
Match length
                  60
% identity
                  55
                  (L39786) conglutin gamma [Lupinus angustifolius]
NCBI Description
                  >gi 666056 emb CAA46552 (X65601) conglutin gamma [Lupinus
                  angustifolius]
                  229438
Seq. No.
                  LIB3196-032-P1-M1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2149640
BLAST score
                  648
E value
                  4.0e-68
Match length
                  132
                  92
% identity
                  (U91995) Argonaute protein [Arabidopsis thaliana]
NCBI Description
                  229439
Seq. No.
                  LIB3196-032-P1-M1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1304227
BLAST score
                  544
                  5.0e-56
E value
                  116
Match length
                  84
% identity
```

NCBI Description (D63781) Epoxide hydrolase [Glycine max]

>gi\_2764804\_emb\_CAA55293\_ (X78547) epoxide hydrolase

[Glycine max]

Seq. No. 229440

Seq. ID LIB3196-032-P1-M1-H6

% identity

100



```
Method
                    BLASTX
NCBI GI
                    q3023847
BLAST score
                    402
E value
                    2.0e-39
Match length
                    90
                    45
% identity
NCBI Description
                   GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                    PROTEIN >gi 2385376 emb CAA69934 (Y08678) G protein beta
                    subunit-like [Medicago sativa]
Seq. No.
                    229441
Seq. ID
                    LIB3196-033-P1-M1-A11
Method
                    BLASTX
NCBI GI
                    g3334115
BLAST score
                    381
E value
                    7.0e-37
Match length
                    78
% identity
                    95
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                    (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664
                    (AF006489) adenine nucleotide translocator 1 [Gossypium
                    hirsutum]
Seq. No.
                    229442
                    LIB3196-033-P1-M1-A12
Seq. ID
Method
                    BLASTX
NCBI GI
                    q2980784
BLAST score
                    224
E value
                    1.0e-18
Match length
                    91
% identity
                    53
NCBI Description (AL022198) puative protein [Arabidopsis thaliana]
                    229443
Seq. No.
Seq. ID
                    LIB3196-033-P1-M1-A3
Method
                    BLASTX
NCBI GI
                    q126156
BLAST score
                    488
E value
                    2.0e-49
Match length
                    97
% identity
                    100
NCBI Description
                   LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
                    >gi_72288_pir FWCNBB beta-globulin B precursor (clone 134)
                    - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                    protein C134 [Saguinus oedipus]
Seq. No.
                    229444
Seq. ID
                    LIB3196-033-P1-M1-A4
Method
                    BLASTX
NCBI GI
                    g126156
BLAST score
                    488
E value
                    2.0e-49
Match length
                    97
```

32884

NCBI Description LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)



229445

>gi 72288 pir FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi\_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi\_1171335 (U43727) legumin B [Gossypium hirsutum] >gi 225582 prf 1306412C storage protein C134 [Saguinus oedipus]

LIB3196-033-P1-M1-A5 Seq. ID Method BLASTX NCBI GI g106322 BLAST score 205 2.0e-16 E value 104 Match length 45 % identity

Seq. No.

NCBI Description hypothetical protein (L1H 3' region) - human

Seq. No. 229446

LIB3196-033-P1-M1-A7 Seq. ID

Method BLASTX NCBI GI q4539335 BLAST score 430 E value 1.0e-42 Match length 116 69 % identity

(AL035539) putative protein [Arabidopsis thaliana] NCBI Description

229447 Seq. No.

Seq. ID LIB3196-033-P1-M1-B10

Method BLASTX NCBI GI g3868758 BLAST score 347 E value 7.0e-33 Match length 87

% identity 75

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 229448

LIB3196-033-P1-M1-B2 Seq. ID

Method BLASTX NCBI GI q4097712 BLAST score 719 E value 2.0e-76 Match length 125 % identity

NCBI Description (U67322) HBV associated factor [Homo sapiens]

Seq. No. 229449

Seq. ID LIB3196-033-P1-M1-B3

Method BLASTX NCBI GI q1469930 BLAST score 286 E value 1.0e-25 Match length 92 % identity

(U48777) fiber-specific acyl carrier protein [Gossypium NCBI Description

hirsutum]

Match length

% identity

109



```
Seq. No.
                  229450
                  LIB3196-033-P1-M1-B6
Seq. ID
Method
                  BLASTX
                  q137580
NCBI GI
BLAST score
                  561
                  5.0e-58
E value
Match length
                  120
% identity
                  91
                  VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72)
NCBI Description
                  >gi 72286 pir FWCNAB alpha-globulin B precursor (clone
                  C72) - upland cotton >gi_167375 (M16891) vicilin precursor
                   [Gossypium hirsutum]
                  229451
Seq. No.
                  LIB3196-033-P1-M1-B8
Seq. ID
Method
                  BLASTX
                   q2736288
NCBI GI
BLAST score
                   574
                   2.0e-59
E value
Match length
                   118
                   87
% identity
                  (AF031080) isopentenyl diphosphate isomerase II
NCBI Description
                   [Camptotheca acuminata]
                   229452
Seq. No.
                   LIB3196-033-P1-M1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3914449
BLAST score
                   606
                   3.0e-63
E value
Match length
                   118
                   100
% identity
                   26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
NCBI Description
                   7) >gi 3172331 (AF041258) 26S proteasome subunit 7 [Prunus
                   persica]
                   229453
Seq. No.
Seq. ID
                   LIB3196-033-P1-M1-C1
Method
                   BLASTX
NCBI GI
                   q4566614
BLAST score
                   328
                   1.0e-30
E value
Match length
                   89
                   71
% identity
                  (AF112887) actin depolymerizing factor [Populus alba x
NCBI Description
                   Populus tremula]
Seq. No.
                   229454
                   LIB3196-033-P1-M1-C10
Seq. ID
Method
                   BLASTX
                   g3953471
NCBI GI
BLAST score
                   384
E value
                   3.0e-37
```

NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

NCBI Description



```
229455
Seq. No.
                  LIB3196-033-P1-M1-C11
Seq. ID
Method
                  BLASTX
                  g1709990
NCBI GI
BLAST score
                  239
                  3.0e-20
E value
                  50
Match length
                  88
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L35A
                  229456
Seq. No.
                  LIB3196-033-P1-M1-C3
Seq. ID
Method
                  BLASTX
                  g130582
NCBI GI
                  186
BLAST score
                  5.0e-14
E value
Match length
                  107
                  36
% identity
                  RETROVIRUS-RELATED POL POLYPROTEIN FROM TRANSPOSON TNT 1-94
NCBI Description
                  [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
                  >gi_100342_pir__S04273 hypothetical protein - common
                  tobacco >gi_20045_emb_CAA32025_ (X13777) ORF [Nicotiana
                  tabacum]
                  229457
Seq. No.
                  LIB3196-033-P1-M1-C4
Seq. ID
Method
                  BLASTX
                  g3769300
NCBI GI
                  203
BLAST score
                  5.0e-16
E value
                  58
Match length
% identity
                  66
NCBI Description (AB018552) AtRER1C [Arabidopsis thaliana]
                  229458
Seq. No.
Seq. ID
                  LIB3196-033-P1-M1-C5
Method
                  BLASTX
NCBI GI
                  q1352440
BLAST score
                  262
                   6.0e-23
E value
Match length
                  56
% identity
                   79
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E)
NCBI Description
                   (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT)
                   (EIF-4F P26 SUBUNIT) >gi 1002915 (U34597) p26 [Oryza
                   sativa]
Seq. No.
                   229459
                  LIB3196-033-P1-M1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g137580
BLAST score
                  554
E value
                   4.0e-57
Match length
                  107
% identity
                   100
```

VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72)

>gi 72286 pir FWCNAB alpha-globulin B precursor (clone



C72) - upland cotton >gi\_167375 (M16891) vicilin precursor [Gossypium hirsutum]

Seq. No. 229460 LIB3196-033-P1-M1-C9 Seq. ID Method BLASTX NCBI GI g2119228 BLAST score 188 E value 3.0e-14Match length 67 % identity 60 NCBI Description keratin K4a - human (fragment) >gi\_313159\_emb\_CAA47914\_ (X67683) keratin K4a [Homo sapiens] Seq. No. 229461 LIB3196-033-P1-M1-D10 Seq. ID Method BLASTX NCBI GI g122106 BLAST score 370 E value 1.0e-35 Match length 75 % identity 100 HISTONE H4 >gi\_70771\_pir\_\_HSZM4 histone H4 - maize NCBI Description >gi\_81642\_pir\_\_S06904 histone H4 - Arabidopsis thaliana >gi\_2119028\_pir\_\_S60475 histone H4 - garden pea >gi\_21795\_emb\_CAA24924\_ (X00043) histone H4 [Triticum aestivum] >gi\_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi\_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi\_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi\_168501 (M $\overline{1}$ 3370) histone H4 [Zea mays] >gi\_168503  $(M1\overline{3}377)$  histone H4 [Zea mays] >gi\_498898 ( $\overline{U}1\overline{0}042$ ) histone H4 homolog [Pisum sativum] >gi\_1806285\_emb\_CAB01914\_(Z79638) histone H4 homologue [Sesbania rostrata] >gi\_3927823 (AC005727) histone H4 [Arabidopsis thaliana]

>gi\_392/823 (AC005/27) histone H4 [Arabidopsis thaliana]
>gi\_4580385\_gb\_AAD24364.1\_AC007184\_4 (AC007184) histone H4
[Arabidopsis thaliana] >gi\_225838\_prf\_\_1314298A histone H4
[Arabidopsis thaliana]

Seq. No. 229462

Seq. ID LIB3196-033-P1-M1-D11

Method BLASTX
NCBI GI g1843527
BLAST score 319
E value 1.0e-29
Match length 91
% identity 74

NCBI Description (U73747) annexin [Gossypium hirsutum]

Seq. No. 229463

Seq. ID LIB3196-033-P1-M1-D2

Method BLASTX
NCBI GI g178685
BLAST score 265
E value 3.0e-23
Match length 82
% identity 65

NCBI Description (J03569) lymphocyte activation antigen [Homo sapiens]

% identity

NCBI Description



>gi\_4505141\_ref\_NP\_002385.1\_pMDU1\_ antigen identified by monoclonal antibodies 4F2, TRA1.10, TROP4, and T43

229464 Seq. No. LIB3196-033-P1-M1-D4 Seq. ID Method BLASTX NCBI GI g88044 589 BLAST score 3.0e-61 E value 125 Match length 94 % identity keratin 4, type II, cytoskeletal - human (fragment) NCBI Description >gi 34073\_emb\_CAA30534\_ (X07695) cytokeratin 4 (408 AA) [Homo sapiens] 229465 Seq. No. LIB3196-033-P1-M1-D5 Seq. ID Method BLASTX NCBI GI g3914191 BLAST score 335 2.0e-31 E value Match length 115 58 % identity UDP-N-ACETYLGLUCOSAMINE--PEPTIDE NCBI Description N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (O-GLCNAC TRANSFERASE P110 SUBUNIT) >gi\_1931579 (U76557) O-GlcNAc transferase, p110 subunit [Rattus norvegicus] 229466 Seq. No. LIB3196-033-P1-M1-D6 Seq. ID Method BLASTX NCBI GI g4325338 BLAST score 558 E value 1.0e-57 Match length 119 88 % identity NCBI Description (AF128392) No definition line found [Arabidopsis thaliana] Seq. No. 229467 LIB3196-033-P1-M1-E11 Seq. ID Method BLASTX NCBI GI q3702339 BLAST score 353 1.0e-33 E value 109 Match length 60 % identity NCBI Description (AC005397) unknown protein [Arabidopsis thaliana] Seq. No. 229468 LIB3196-033-P1-M1-E3 Seq. ID Method BLASTX NCBI GI q3510297 BLAST score 171 E value 3.0e-12 Match length 31

32889

(AB006746) hMmTRA1b [Homo sapiens] >gi\_4092081 (AF098642)



phospholipid scramblase; plasma membrane phospholipid scramblase [Homo sapiens]

Seq. No. 229469 LIB3196-033-P1-M1-E4 Séq. ID Method BLASTX NCBI GI g225581 BLAST score 370 E value 1.0e-35 Match length 88 86 % identity NCBI Description storage protein C94 [Saguinus oedipus] 229470 Seq. No. Seq. ID LIB3196-033-P1-M1-F1 Method BLASTX NCBI GI q2739008 BLAST score 389 E value 7.0e-38 Match length 110 % identity 71 NCBI Description (AF022463) CYP78A3p [Glycine max] 229471 Seq. No. LIB3196-033-P1-M1-F11 Seq. ID Method BLASTX NCBI GI q1049086 BLAST score 330 7.0e-31 E value Match length 62 % identity 100 NCBI Description (U30829) SRp55-3 [Homo sapiens] 229472 Seq. No. Seq. ID LIB3196-033-P1-M1-F6 Method BLASTX NCBI GI q3128225 BLAST score 220 E value 5.0e-18 Match length 66 % identity 68 NCBI Description (AC004077) unknown protein [Arabidopsis thaliana] Seq. No. 229473 Seq. ID LIB3196-033-P1-M1-F8 Method BLASTX NCBI GI g120676 BLAST score 351 E value 2.0e-41 Match length 113 77 % identity NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi 82165 pir C24430 glyceraldehyde-3-phosphate

dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) C, cytosolic - common tobacco (fragment) >gi 170241 (M14419)

glyceraldehyde-3-phosphate dehydrogenase [Nicotiana

ťabacum]

E value

2.0e-36

```
229474
Seq. No.
                  LIB3196-033-P1-M1-F9
Seq. ID
                  BLASTX
Method
                   g4097579
NCBI GI
                   290
BLAST score
                   2.0e-26
E value
                   63
Match length
                   87
% identity
                  (U64922) NTGP1 [Nicotiana tabacum]
NCBI Description
                   229475
Seq. No.
                  LIB3196-033-P1-M1-G1
Seq. ID
Method
                  BLASTX
                   g4335731
NCBI GI
                   205
BLAST score
                   3.0e-16
E value
                   90
Match length
                   41
% identity
                  (AC006248) putative polyprotein [Arabidopsis thaliana]
NCBI Description
                   229476
Seq. No.
                   LIB3196-033-P1-M1-G11
Seq. ID
Method
                   BLASTX
                   g4263787
NCBI GI
BLAST score
                   318
E value
                   2.0e-29
Match length
                   112
% identity
                   57
                  (AC006068) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   229477
                   LIB3196-033-P1-M1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4263787
BLAST score
                   218
E value
                   9.0e-18
                   109
Match length
                   48
% identity
NCBI Description
                  (AC006068) unknown protein [Arabidopsis thaliana]
Seq. No.
                   229478
                   LIB3196-033-P1-M1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2961300
BLAST score
                   486
E value
                   3.0e-49
Match length
                   100
% identity
                   92
                  (AJ225027) ribosomal protein L24 [Cicer arietinum]
NCBI Description
Seq. No.
                   229479
                   LIB3196-033-P1-M1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4006829
BLAST score
                   374
```



```
Match length
                  84
% identity
                  86
                  (AC005970) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  229480
Seq. No.
                  LIB3196-033-P1-M1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1710401
                  167
BLAST score
                  3.0e-12
E value
Match length
                  56
                  55
% identity
                  RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN
NCBI Description
                  (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)
                  >gi 1044912_emb_CAA63194_ (X92443) ribonucleotide reductase
                  R2 [Nicotiana tabacum]
                  229481
Seq. No.
                  LIB3196-033-P1-M1-H10
Seq. ID
                  BLASTX
Method
                  g4240315
NCBI GI
BLAST score
                  178
                  3.0e-16
E value
Match length
                  101
                  53
% identity
                  (AB020720) KIAA0913 protein [Homo sapiens]
NCBI Description
Seq. No.
                  229482
                  LIB3196-033-P1-M1-H11
Seq. ID
Method
                  BLASTX
                  g81546
NCBI GI
BLAST score
                   535
                   6.0e-55
E value
                  106
Match length
                   99
% identity
                  alpha-globulin type B precursor (tandem 1) - upland cotton
NCBI Description
                   (fragment)
                   229483
Seq. No.
                   LIB3196-033-P1-M1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1169475
                   332
BLAST score
                   4.0e-31
E value
                   63
Match length
                   100
% identity
NCBI Description
                  ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION
                   FACTOR TU) (EF-TU) >gi_556301 (M22432) elongation factor Tu
                   [Mus musculus]
                   229484
Seq. No.
Seq. ID
                   LIB3196-033-P1-M1-H3
```

Method BLASTX
NCBI GI g4455179
BLAST score 239
E value 3.0e-20
Match length 112

% identity



```
% identity
NCBI Description
                  (AL035521) hypothetical protein [Arabidopsis thaliana]
                   229485
Seq. No.
Seq. ID
                   LIB3196-033-P1-M1-H6
Method
                   BLASTX
NCBI GI
                   g2498434
BLAST score
                   511
E value
                   5.0e-52
Match length
                   110
% identity
                   14
NCBI Description
                  HIGH DENSITY LIPOPROTEIN BINDING PROTEIN (HDL-BINDING
                   PROTEIN) >gi_345882_pir__A44125 high density
                   lipoprotein-binding protein, 110K - human >gi_183892
                   (M64098) high density lipoprotein binding protein [Homo
                   sapiens]
Seq. No.
                   229486
Seq. ID
                   LIB3196-033-P1-M1-H9
Method
                   BLASTX
NCBI GI
                   q1346766
BLAST score
                   195
E value
                   4.0e-15
Match length
                   108
% identity
                   38
NCBI Description
                   26S PROTEASOME REGULATORY SUBUNIT S14 (P31)
                   >gi_1362741_pir__S56108 multicatalytic endopeptidase complex (EC 3.4.99.46) regulatory chain 31 - human
                   >gi 1037164 dbj BAA07237_ (D38047) 26S proteasome subunit
                   p31 [Homo sapiens] >gi_3702282 (AC005789) PP31 HUMAN [Homo
                   sapiens] >gi_4506233_ref_NP_002803.1_pPSMD8_ proteasome
                   (prosome, macropain) 26S subunit, non-ATPase,
Seq. No.
                   229487
Seq. ID
                   LIB3196-034-P1-M1-A1
Method
                   BLASTX
NCBI GI
                   g137578
BLAST score
                   411
E value
                   2.0e-40
Match length
                   100
% identity
                   45
                   VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                   >gi 81545 pir S06398 alpha-globulin type A precursor -
                   upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                   [Artificial gene] >gi 226119 prf 1410330A vicilin gene A
                   [Saguinus oedipus]
Seq. No.
                   229488
Seq. ID
                   LIB3196-034-P1-M1-A11
Method
                   BLASTX
NCBI GI
                   g4467804
BLAST score
                   600
E value
                   2.0e-62
Match length
                   122
```

32893

NCBI Description (AL031678) TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3



Seq. No. Seq. ID

Method

NCBI GI

BLAST score E value

% identity

Seq. No.

Seq. ID Method

NCBI GI

E value

Seq. No.

Seq. ID

Method

NCBI GI

E value

Seq. No.

Seq. ID

Method

NCBI GI

E value

BLAST score

BLAST score

% identity

BLAST score

% identity

```
PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3).)
                  [Homo sapiens]
                  229489
                  LIB3196-034-P1-M1-A2
                  BLASTX
                  g4415908
                  391
                  5.0e - 38
Match length
                  111
                  63
NCBI Description
                 (AC006282) unknown protein [Arabidopsis thaliana]
                  229490
                  LIB3196-034-P1-M1-A6
                  BLASTX
                  g125077
                  142
                  4.0e-09
                  90
Match length
                  43
NCBI Description
                  KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK
                  13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal,
                  long form - human >gi 34033 emb CAA32786 (X14640) keratin
                  13 [Homo sapiens]
                  229491
                  LIB3196-034-P1-M1-A7
                  BLASTX
                  g118458
                  408
                  5.0e-40
Match length
                  119
                  73
NCBI Description DESMOPLAKIN I AND II (DPI AND DPII) >gi 181608 (J05211)
                  desmoplakin [Homo sapiens]
                  229492
                  LIB3196-034-P1-M1-A8
                  BLASTX
                  q730645
                  400
                  4.0e-39
Match length
                  91
                  88
                  40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal
```

% identity NCBI Description

protein S15 - Arabidopsis thaliana >gi\_313152\_emb\_CAA80679\_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi\_313188\_emb\_CAA80681\_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi\_1903366\_gb\_AAB70449\_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb R29788, gb ATTS0365 come from this gene. [Arabidopsis

thaliana]

Seq. No. 229493

Seq. ID LIB3196-034-P1-M1-A9

Method BLASTX

BLAST score

E value

328

1.0e-30



```
NCBI GI
                   g3811383
BLAST score
                   169
E value
                   5.0e-12
Match length
                   115
% identity
                   34
NCBI Description (AF100956) Sacm21 [Mus musculus]
                   229494
Seq. No.
                   LIB3196-034-P1-M1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3549657
BLAST score
                   213
E value
                   3.0e-17
Match length
                   89
                   46
% identity
NCBI Description (AL031394) putative protein [Arabidopsis thaliana]
Seq. No.
                   229495
                   LIB3196-034-P1-M1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4490728
BLAST score
                   286
E value
                   1.0e-25
                   75
Match length
                   71
% identity
NCBI Description (AL035709) putative protein [Arabidopsis thaliana]
                   229496
Seq. No.
                  LIB3196-034-P1-M1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1352450
BLAST score
                   561
E value
                   6.0e-58
Match length
                   112
                   100
% identity
NCBI Description
                   INTERLEUKIN-1 ALPHA PRECURSOR (IL-1 ALPHA)
                   (HEMATOPOIETIN-1) >gi_644806 (U19844) interleukin-1 alpha
                   [Macaca mulatta]
Seq. No.
                   229497
Seq. ID
                   LIB3196-034-P1-M1-B5
Method
                   BLASTX
NCBI GI
                   g1352450
BLAST score
                   561
E value
                   6.0e-58
Match length
                   112
% identity
                   100
                  INTERLEUKIN-1 ALPHA PRECURSOR (IL-1 ALPHA)
NCBI Description
                   (HEMATOPOIETIN-1) >gi_644806 (U19844) interleukin-1 alpha
                   [Macaca mulatta]
Seq. No.
                   229498
Seq. ID
                  LIB3196-034-P1-M1-B6
Method
                  BLASTX
NCBI GI
                   q4240175
```



```
121
Match length
% identity
                   43
                  (AB020650) KIAA0843 protein [Homo sapiens]
NCBI Description
                  229499
Seq. No.
                  LIB3196-034-P1-M1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g231723
BLAST score
                  381
E value
                  8.0e-37
Match length
                  73
                  100
% identity
NCBI Description
                  CD9 ANTIGEN (27 KD DIPHTHERIA TOXIN RECEPTOR-ASSOCIATED
                  PROTEIN) (DRAP27) >gi 104994 pir A42929 CD9 antigen -
                   green monkey >gi 218566 dbj BAA01569 (D10726) diphtheria
                  toxin receptor associated protein [Chlorocebus aethiops]
                  229500
Seq. No.
                  LIB3196-034-P1-M1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g137578
BLAST score
                  437
E value
                  2.0e-43
Match length
                  114
% identity
                  76
NCBI Description
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
                  >gi_81545_pir__S06398 alpha-globulin type A precursor -
                  upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                   [Artificial gene] >gi_226119_prf__1410330A vicilin gene A
                   [Saguinus oedipus]
                  229501
Seq. No.
Seq. ID
                  LIB3196-034-P1-M1-B9
Method
                  BLASTX
NCBI GI
                  q167367
BLAST score
                  274
E value
                   7.0e-36
Match length
                  105
                   79
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                   229502
Seq. ID
                  LIB3196-034-P1-M1-C1
Method
                  BLASTX
NCBI GI
                   g225580
BLAST score
                  521
E value
                   3.0e-53
Match length
                  119
% identity
                  87
NCBI Description storage protein C72 [Saguinus oedipus]
```

Seq. No. 229503

Seq. ID LIB3196-034-P1-M1-C12

Method BLASTX
NCBI GI g3702293
BLAST score 519

Match length

% identity

112



```
4.0e-53
E value
                  104
Match length
                   99
% identity
                  (AC005784) RFX2 HUMAN, [AA 620-723] [Homo sapiens]
NCBI Description
                  229504
Seq. No.
                  LIB3196-034-P1-M1-C4
Seq. ID
                  BLASTX
Method
                  g441457
NCBI GI
                  481
BLAST score
                  1.0e-48
E value
                  90
Match length
                  98
% identity
                   (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                  esculentum]
Seq. No.
                  229505
                  LIB3196-034-P1-M1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q441457
                   481
BLAST score
                   1.0e-48
E value
                   90
Match length
                   98
% identity
                  (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                  esculentum]
                   229506
Seq. No.
                  LIB3196-034-P1-M1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2431769
BLAST score
                   234
                   1.0e-19
E value
                  57
Match length
                   81
% identity
                  (U62752) acidic ribosomal protein Pla [Zea mays]
NCBI Description
                   229507
Seq. No.
                  LIB3196-034-P1-M1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2160158
BLAST score
                   153
E value
                   3.0e-10
Match length
                   35
% identity
                   83
NCBI Description
                   (ACO00132) Similar to elongation factor 1-gamma
                   (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come
                   from this gene. [Arabidopsis thaliana]
                   229508
Seq. No.
Seq. ID
                   LIB3196-034-P1-M1-D3
Method
                   BLASTX
NCBI GI
                   q4220541
BLAST score
                   261
E value
                   8.0e-23
```



```
(AL035356) Rab geranylgeranyl transferase like protein
NCBI Description
                    [Arabidopsis thaliana]
                    229509
Seq. No.
Seq. ID
                    LIB3196-034-P1-M1-D4
Method
                    BLASTX
NCBI GI
                    g3334115
BLAST score
                    288
E value
                    6.0e-26
Match length
                    117
                    59
% identity
                    ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                     (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664
                     (AF006489) adenine nucleotide translocator 1 [Gossypium
                    hirsutum]
                    229510
Seq. No.
                    LIB3196-034-P1-M1-D8
Seq. ID
Method
                    BLASTX
NCBI GI
                    q2687726
BLAST score
                    314
E value
                    5.0e-29
Match length
                    101
                    57
% identity
NCBI Description
                    (AJ003246) 2'-hydroxydihydrodaidzein reductase [Glycine
                    max]
Seq. No.
                    229511
                    LIB3196-034-P1-M1-D9
Seq. ID
Method
                    BLASTX
NCBI GI
                    q126156
                    395
BLAST score
                    2.0e-38
E value
Match length
                    74
                    100
% identity
NCBI Description
                    LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
                    >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134)
                    - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                    protein C134 [Saguinus oedipus]
Seq. No.
                    229512
Seq. ID
                    LIB3196-034-P1-M1-E10
Method
                    BLASTX
NCBI GI
                    g1346772
BLAST score
                    527
E value
                     6.0e-54
Match length
                    106
                    95
% identity
                    PHOSPHATIDYLINOSITOL TRANSFER PROTEIN BETA ISOFORM (PTDINS
NCBI Description
```

TRANSFER PROTEIN BETA) (PTDINSTP) (PI-TP-BETA)

>gi 1060905 dbj BAA06277 (D30037) phosphatidylinositol

transfer protein [Homo sapiens]

229513 Seq. No.

LIB3196-034-P1-M1-E11 Seq. ID



```
Method
                    BLASTX
NCBI GI
                    g2833242
BLAST score
                    240
E value
                    3.0e-20
Match length
                    122
                    49
% identity
NCBI Description G PROTEIN PATHWAY SUPPRESSOR 2 (GPS2 PROTEIN)
                    229514
Seq. No.
Seq. ID
                   LIB3196-034-P1-M1-E2
Method
                   BLASTX
NCBI GI
                    g1346772
BLAST score
                    392
E value
                    5.0e-38
Match length
                    106
% identity
                    74
                  PHOSPHATIDYLINOSITOL TRANSFER PROTEIN BETA ISOFORM (PTDINS
NCBI Description
                    TRANSFER PROTEIN BETA) (PTDINSTP) (PI-TP-BETA)
                    >gi_1060905 dbj_BAA06277 (D30037) phosphatidylinositol
                    transfer protein [Homo sapiens]
                    229515
Seq. No.
Seq. ID
                   LIB3196-034-P1-M1-E4
Method
                   BLASTX
NCBI GI
                    g126156
BLAST score
                    410
E value
                    3.0e-40
Match length
                    117
                    70
% identity
NCBI Description
                  LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
                    >gi 72288 pir FWCNBB beta-globulin B precursor (clone 134)
                    - upland cotton >gi_167373 (M16936) vicilin precursor
                    [Gossypium hirsutum] >gi_1171335 (U43727) legumin B
                    [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                    protein C134 [Saguinus oedipus]
Seq. No.
                    229516
Seq. ID
                   LIB3196-034-P1-M1-E5
Method
                   BLASTX
NCBI GI
                    q126156
BLAST score
                    148
E value
                    8.0e-10
Match length
                    53
% identity
                    60
NCBI Description
                   LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
                    >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134)
                   - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf_1306412C storage
                    protein C134 [Saguinus oedipus]
```

Seq. No. 229517

LIB3196-034-P1-M1-E7 Seq. ID

Method BLASTX NCBI GI g1420936 BLAST score 554 E value 3.0e-57



```
Match length
                  117
                  85
% identity
                  (U61396) Vigna unquiculata aspartic proteinase mRNA,
NCBI Description
                  complete cds. [Vigna unguiculata]
Seq. No.
                  229518
                  LIB3196-034-P1-M1-F1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g136060
                  545
BLAST score
E value
                  2.0e-62
                  123
Match length
                  97
% identity
NCBI Description
                 TRIOSEPHOSPHATE ISOMERASE (TIM) >gi 68420 pir ISCZT1
                  triose-phosphate isomerase (EC 5.3.1.1) 1 - chimpanzee
                  >gi 2144541 pir ISHUT triose-phosphate isomerase (EC
                  5.3.1.1) - human >gi 37247 emb CAA49379 (X69723)
                  triosephosphate isomerase [Homo sapiens] >gi 176960
                  (M57946) triose-phosphate isomerase [Pan troglodytes]
                  >gi 339841 (M10036) triosephosphate isomerase (EC 5.3.1.1)
                  [Homo sapiens] >gi 1200507 (U47924) triosephosphate
                  isomerase [Homo sapiens] >gi 4507645 ref NP 000356.1 pTPI1_
                  triosephosphate isomerase
Seq. No.
                  229519
                  LIB3196-034-P1-M1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2398807
BLAST score
                  222
                  2.0e-18
E value
Match length
                  69
                  62
% identity
NCBI Description
                  (Z99091) succinate dehydrogenase [Schizosaccharomyces
                  pombe]
                  229520
Seq. No.
                  LIB3196-034-P1-M1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q136117
BLAST score
                  433
                  6.0e-43
E value
Match length
                  76
% identity
                  100
                  ORPHAN RECEPTOR TR2 >gi_87334_pir__A31521 DNA-binding
NCBI Description
                  protein TR2 - human >gi 338486 (M21985) steroid receptor
                  TR2 [Homo sapiens]
Seq. No.
                  229521
                  LIB3196-034-P1-M1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q136091
BLAST score
                  232
```

Method BLASTX
NCBI GI g136091
BLAST score 232
E value 2.0e-19
Match length 96
% identity 56

NCBI Description TROPOMYOSIN BETA CHAIN, SKELETAL MUSCLE

>gi\_71600\_pir\_\_TMRBB tropomyosin beta chain, skeletal

Method

NCBI GI

BLAST score E value

BLASTX

g3347848 158

1.0e-10



muscle - rabbit >gi\_91852\_pir\_\_S03838 tropomyosin beta, skeletal muscle - mouse >gi\_92922\_pir\_\_B25073 tropomyosin beta, skeletal muscle - rat >gi\_54857\_emb\_CAA31181\_(X12650) beta-tropomyosin (AA 1-284) [Mus musculus] >gi\_202163 (M81086) beta-tropomyosin [Mus musculus] >gi\_207497 (L00382) skeletal muscle beta-tropomyosin [Rattus norvegicus] >gi\_223122\_prf\_\_0510185A tropomyosin beta [Oryctolagus cuniculus]

```
Seq. No.
                  229522
Seq. ID
                  LIB3196-034-P1-M1-F6
Method
                  BLASTX
NCBI GI
                  g3859675
BLAST score
                  176
E value
                  8.0e-13
Match length
                  86
% identity
                  42
NCBI Description
                  (AL033503) nadh-ubiquinone oxidoreductase [Candida
                  albicans]
Seq. No.
                  229523
                  LIB3196-034-P1-M1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2262100
BLAST score
                  316
E value
                  1.0e-37
Match length
                  114
% identity
                  70
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
Seq. No.
                  229524
Seq. ID
                  LIB3196-034-P1-M1-F9
Method
                  BLASTX
NCBI GI
                  g3790587
BLAST score
                  236
E value
                  7.0e-20
Match length
                  50
% identity
NCBI Description
                  (AF079182) RING-H2 finger protein RHF2a [Arabidopsis
                  thaliana]
                  229525
Seq. No.
Seq. ID
                  LIB3196-034-P1-M1-G1
Method
                  BLASTX
NCBI GI
                  g225581
BLAST score
                  536
E value
                  5.0e-55
Match length
                  117
                  87
% identity
NCBI Description storage protein C94 [Saguinus oedipus]
Seq. No.
                  229526
Seq. ID
                  LIB3196-034-P1-M1-G10
```

E value

Match length % identity

2.0e-20 57

82



```
Match length
                 81
                  46
% identity
NCBI Description (AF055666) kinesin light chain 2 [Mus musculus]
                 229527
Seq. No.
Seq. ID
                 LIB3196-034-P1-M1-G11
Method
                 BLASTX
NCBI GI
                 g267131
BLAST score
                 178
                 4.0e-13
E value
Match length
                 81
% identity
                 14
NCBI Description NUCLEOLYSIN TIAR (TIA-1 RELATED PROTEIN)
                 >gi 423120 pir A46174 RNA-binding protein TIAR - human
                  >gi 189310 (M96954) nucleolysin TIAR [Homo sapiens]
                  >gi 4507499 ref NP 003243.1 pTIAL1 TIA1 cytotoxic
                  granule-associated RNA-binding protein-like
                 229528
Seq. No.
Seq. ID
                 LIB3196-034-P1-M1-G12
Method
                 BLASTX
NCBI GI
                 g1220196
BLAST score
                 447
                 1.0e-44
E value
                 90
Match length
% identity
                 94
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
                 229529
Seq. No.
Seq. ID
                 LIB3196-034-P1-M1-G3
                 BLASTX
Method
NCBI GI
                 g547753
BLAST score
                 420
                 2.0e-41
E value
                 120
Match length
                 72
% identity
NCBI Description KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)
                  229530
Seq. No.
Seq. ID
                 LIB3196-034-P1-M1-G4
Method
                 BLASTX
                 g4378765
NCBI GI
BLAST score
                  517
E value
                  8.0e-53
Match length
                 102
                  97
% identity
NCBI Description (AF115516) orphan G protein-coupled receptor GPR54 [Rattus
                 norvegicus]
                  229531
Seq. No.
Seq. ID
                 LIB3196-034-P1-M1-G5
Method
                 BLASTX
NCBI GI
                 g4378765
BLAST score
                 239
```

NCBI Description



```
(AF115516) orphan G protein-coupled receptor GPR54 [Rattus
NCBI Description
                  norvegicus]
                  229532
Seq. No.
Seq. ID
                  LIB3196-034-P1-M1-G6
                  BLASTX
Method
                  g3211975
NCBI GI
BLAST score
                  190
                  2.0e-14
E value
                  40
Match length
                  97
% identity
                  (AF068195) putative glialblastoma cell
NCBI Description
                  differentiation-related protein [Homo sapiens]
                  229533
Seq. No.
Seq. ID
                  LIB3196-034-P1-M1-G7
                  BLASTX
Method
                  g1842140
NCBI GI
                  209
BLAST score
                  7.0e-17
E value
Match length
                  92
% identity
                  40
                  (AB001024) similar to Saccharomyces cerevisiae ORM1 gene:
NCBI Description
                  EMBL Accession Number Y08687 [Schizosaccharomyces pombe]
                  229534
Seq. No.
                  LIB3196-034-P1-M1-G9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g280816
BLAST score
                  297
E value
                  4.0e-27
Match length
                  66
                  88
% identity
                  keratin 13, type I, cytoskeletal, short form - human
NCBI Description
                  >gi 30377 emb CAA36673 (X52426) cytokeratin 13 [Homo
                  sapiens] >gi_3603253 (AF049259) keratin 13 [Homo sapiens]
                  >gi 4504911 ref NP 002265.1 pKRT13 keratin
                  229535
Seq. No.
Seq. ID
                  LIB3196-034-P1-M1-H12
Method
                  BLASTX
NCBI GI
                  g2765366
                  217
BLAST score
                  1.0e-17
E value
Match length
                  81
                   47
% identity
                  (Y14038) putative Ole e 1 protein [Betula pendula]
NCBI Description
                  229536
Seq. No.
Seq. ID
                  LIB3196-034-P1-M1-H2
Method
                  BLASTX
                  q1399321
NCBI GI
BLAST score
                   478
E value
                  3.0e-48
Match length
                  118
                  78
% identity
```

(U41830) MHC class I antigen Mamu B\*08 [Macaca mulatta]



```
229537
Seq. No.
Seq. ID
                  LIB3196-034-P1-M1-H7
                  BLASTX
Method
                  g464707
NCBI GI
                  246
BLAST score
                  3.0e-21
E value
                  51
Match length
% identity
                  96
                  40S RIBOSOMAL PROTEIN S18 >qi 480908 pir S37496 ribosomal
NCBI Description
                  protein S18.A - Arabidopsis thaliana
                  >qi 405613 emb CAA80684 (Z23165) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi 434343 emb CAA82273 (Z28701)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi 434345 emb CAA82274 (Z28702) S18 ribosomal protein
                  [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi 3287678 (AC003979) Match to
                  ribosomal S18 gene mRNA gb Z28701, DNA gb Z23165 from A.
                  thaliana. ESTs gb T21121, gb Z17755, gb R64776 and
                  gb R30430 come from this gene. [Arabidopsis thaliana]
                  >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal
                  protein [Arabidopsis thaliana]
                  229538
Seq. No.
                  LIB3196-034-P1-M1-H8
Seq. ID
                  BLASTX
Method
                  g4104681
NCBI GI
BLAST score
                  219
E value
                  7.0e-18
Match length
                  45
                  98
% identity
                  (AF038844) MKP-1 like protein tyrosine phosphatase [Homo
NCBI Description
                  sapiens]
                  229539
Seq. No.
Seq. ID
                  LIB3196-035-P1-M1-A1
Method
                  BLASTX
                  q1351901
NCBI GI
BLAST score
                  390
                  6.0e-38
E value
Match length
                  112
% identity
                  [Segment 2 of 2] NEUROBLAST DIFFERENTIATION ASSOCIATED
NCBI Description
                  PROTEIN AHNAK (DESMOYOKIN) >qi 897824 (M80899) AHNAK gene
                  product [Homo sapiens]
                  229540
Seq. No.
Seq. ID
                  LIB3196-035-P1-M1-A2
                  BLASTX
Method
NCBI GI
                  g2497938
BLAST score
                  467
                  5.0e-47
E value
Match length
                  96
% identity
                  95
```

NCBI Description AQUAPORIN 3 >gi 1854374 dbj BAA19237 (AB001325) aquaporin

BLAST score

E value

338

9.0e-32



## 3 [Homo sapiens]

```
Seq. No.
                   229541
Seq. ID
                   LIB3196-035-P1-M1-A3
Method
                   BLASTX
NCBI GI
                   g2072023
                   276
BLAST score
                   2.0e-24
E value
Match length
                   83
                   71
% identity
NCBI Description
                  (U93506) symbiosis-related protein [Laccaria bicolor]
Seq. No. Seq. ID
                   229542
                   LIB3196-035-P1-M1-A4
Method
                   BLASTX
NCBI GI
                   g2497487
BLAST score
                   415
                   9.0e-41
E value
                   89
Match length
% identity
                   90
NCBI Description
                   UMP-CMP KINASE (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE)
                   >gi_1085437_pir__JC4181 cytidylate kinase (EC 2.7.4.14) -
                   pig->gi 893400 dbj BAA06130 (D29655) UMP-CMP kinase [Sus
                   scrofa] >gi 1096714 prf 2112267A UMP-CMP kinase [Sus
                   scrofa domestica]
Seq. No.
                   229543
Seq. ID
                   LIB3196-035-P1-M1-A6
                   BLASTX
Method
NCBI GI
                   g728835
BLAST score
                   157
E value
                   3.0e-14
Match length
                   88
% identity
NCBI Description ALU SUBFAMILY SC WARNING ENTRY !!!!
Seq. No.
                   229544
Seq. ID
                   LIB3196-035-P1-M1-A7
Method
                   BLASTX
NCBI GI
                   g137578
BLAST score
                   342
E value
                   2.0e-32
Match length
                   102
                   72
% identity
                   VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                   >gi_81545_pir__S06398 alpha-globulin type A precursor -
upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi 207906 (M18027) alpha globulin A
                   [Artificial gene] >gi 226119 prf 1410330A vicilin gene A
                   [Saguinus oedipus]
Seq. No.
                   229545
Seq. ID
                   LIB3196-035-P1-M1-C10
                   BLASTX
Method
NCBI GI
                   q1706379
```



```
Match length
                  69
% identity
                  FATTY ALDEHYDE DEHYDROGENASE (ALDEHYDE DEHYDROGENASE,
NCBI Description
                  MICROSOMAL) (CLASS 3) >gi_1082036 (L47162) fatty aldehyde
                  dehydrogenase [Homo sapiens] >gi_1666530 (U75297) fatty
                  aldehyde dehydrogenase [Homo sapiens] >gi_1870244 (U46689)
                  aldehyde dehydrogenase [Homo sapiens]
                  >gi_1586822_prf__2204389A fatty aldehyde dehydrogenase
                  [Homo sapiens] >gi 4557303 ref NP 000373.1_pALDH10
                  aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase)
                  229546
Seq. No.
Seq. ID
                  LIB3196-035-P1-M1-C11
                  BLASTX
Method
                  g1173027
NCBI GI
BLAST score
                  298
                  4.0e-27
E value
                  101
Match length
                  61
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L31 >gi 915313 (U23784) ribosomal
                  protein L31 [Nicotiana glutinosa]
                  229547
Seq. No.
Seq. ID
                  LIB3196-035-P1-M1-C12
                  BLASTX
Method
NCBI GI
                  g3402711
BLAST score
                  376
E value
                  3.0e-36
                  127
Match length
% identity
NCBI Description
                  (AC004261) putative RNA-binding protein [Arabidopsis
                  thaliana]
                  229548
Seq. No.
Seq. ID
                  LIB3196-035-P1-M1-C8
Method
                  BLASTX
                  q2498323
NCBI GI
BLAST score
                  265
                  2.0e-23
E value
Match length
                  61
                  84
% identity
NCBI Description
                  EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY
                  COMPONENT P85) >gi 1488324 (U65932) extracellular matrix
                  protein 1 [Homo sapiens] >qi 1488332 (U65938) extracellular
                  matrix protein 1 [Homo sapiens] >gi 2654433 (U68186)
                  extracellular matrix protein 1 [Homo sapiens]
Seq. No.
                  229549
Seq. ID
                  LIB3196-035-P1-M1-D1
Method
                  BLASTX
NCBI GI
                  g2765097
```

Method BLASTX
NCBI GI g2765097
BLAST score 192
E value 6.0e-15
Match length 81
% identity 48

NCBI Description (Y11207) P54 protein [Pisum sativum]



```
229550
Seq. No.
Seq. ID
                  LIB3196-035-P1-M1-D2
Method
                  BLASTX
NCBI GI
                  g4235430
BLAST score
                  392
E value
                  3.0e-38
Match length
                  92
% identity
                  82
NCBI Description
                 (AF098458) latex-abundant protein [Hevea brasiliensis]
                  229551
Seq. No.
Seq. ID
                  LIB3196-035-P1-M1-D4
                  BLASTX
Method
NCBI GI
                  g1524121
                  534
BLAST score
                  1.0e-54
E value
                  133
Match length
                  76
% identity
                  (X96539) malate dehydrogenase [Mesembryanthemum
NCBI Description
                  crystallinum]
                  229552
Seq. No.
Seq. ID
                  LIB3196-035-P1-M1-D7
Method
                  BLASTX
NCBI GI
                  g3522925
BLAST score
                  260
                  3.0e-23
E value
                  53
Match length
                  96
% identity
NCBI Description
                  (AC005545) AP-3 complex delta subunit, partial CDS [Homo
                  sapiens]
Seq. No.
                  229553
                  LIB3196-035-P1-M1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076669
BLAST score
                  366
                  5.0e-35
E value
Match length
                  100
% identity
                  76
                  NADH dehydrogenase (EC 1.6.99.3) - potato
NCBI Description
                  >gi_668987_emb_CAA59063_ (X84320) NADH dehydrogenase
                  [Solanum tuberosum]
Seq. No.
                  229554
Seq. ID
                  LIB3196-035-P1-M1-E11
Method
                  BLASTX
NCBI GI
                  g3947448
BLAST score
                  212
E value
                  4.0e-17
Match length
                  106
% identity
                  39
NCBI Description
                  (AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA
```

gene; cDNA EST yk499q5.5 comes from this gene

EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this

[Caenorhabdi... >gi 3947543 emb CAA88952 (Z49127) cDNA EST



yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene [Caenorhabditi

229555 Seq. No. LIB3196-035-P1-M1-E12 Seq. ID BLASTX Method g88044 NCBI GI 628 BLAST score 1.0e-65 E value Match length 137 % identity 94 keratin 4, type II, cytoskeletal - human (fragment) NCBI Description >gi 34073 emb CAA30534 (X07695) cytokeratin 4 (408 AA) [Homo sapiens] Seq. No. 229556 LIB3196-035-P1-M1-E2 Seq. ID Method BLASTX g3913018 NCBI GI BLAST score 460 3.0e-46E value Match length 109 83 % identity FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR NCBI Description (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic aldolase [Oryza sativa] 229557 Seq. No. LIB3196-035-P1-M1-E4 Seq. ID BLASTX Method g445613 NCBI GI BLAST score 325 3.0e-30 E value 95 Match length 69 % identity NCBI Description ribosomal protein L7 [Solanum tuberosum] 229558 Seq. No. LIB3196-035-P1-M1-E7 Seq. ID BLASTX Method g2894306 NCBI GI 372 BLAST score 5.0e-36 E value

% identity 74
NCBI Description (AJ223329) ubiquitin extension protein [Nicotiana tabacum]

 Seq. No.
 229559

 Seq. ID
 LIB3196-035-P1-M1-E9

 Method
 BLASTX

 NCBI GI
 g2738520

105

BLAST score 407 E value 5.0e-40 Match length 80 % identity 99

Match length



NCBI Description (AF010187) FGF-1 intracellular binding protein [Homo

sapiens] >gi\_2738522 (AF010188) FGF-1 intracellular binding

protein [Chlorocebus aethiops]

Seq. No. 229560

Seq. ID LIB3196-035-P1-M1-F1

Method BLASTX
NCBI GI g2499819
BLAST score 494
E value 5.0e-50
Match length 131
% identity 68

NCBI Description ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR

>gi\_2130068\_pir\_\_S66516 aspartic proteinase 1 precursor rice >gi\_1030715\_dbj\_BAA06876\_ (D32165) aspartic protease
[Oryza sativa] >gi\_1711289\_dbj\_BAA06875\_ (D32144) aspartic

protease [Oryza sativa]

Seq. No. 229561

Seq. ID LIB3196-035-P1-M1-F2

Method BLASTX
NCBI GI g683553
BLAST score 270
E value 9.0e-24
Match length 121
% identity 50

NCBI Description (Z48450) oleosin-like protein [Citrus sinensis]

>gi 1582679 prf 2119230A oleosin homolog [Citrus sinensis]

Seq. No. 229562

Seq. ID LIB3196-035-P1-M1-F3

Method BLASTX
NCBI GI g124224
BLAST score 578
E value 7.0e-60
Match length 124
% identity 90

NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)

>gi\_100345\_pir\_\_S21060 translation initiation factor eIF-5A

- common tobacco >gi\_19887\_emb\_CAA45105\_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No. 229563

Seq. ID LIB3196-035-P1-M1-F4

Method BLASTX
NCBI GI g124224
BLAST score 206
E value 1.0e-16
Match length 82
% identity 56

NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)

>gi 100345 pir S21060 translation initiation factor eIF-5A

- common tobacco >gi\_19887\_emb\_CAA45105\_ (X63543) eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]

Seq. No. 229564

Seq. ID LIB3196-035-P1-M1-F8



```
Method
                   BLASTX
NCBI GI
                   a4218034
BLAST score
                   169
                   3.0e-12
E value
Match length
                   43
                   81
% identity
                   (U73169) GTP-binding regulatory protein Gi alpha-2 chain
NCBI Description
                   [Homo sapiens]
                   229565
Seq. No.
                   LIB3196-035-P1-M1-F9
Seq. ID
                   BLASTX
Method
                   g3413165
NCBI GI
                   161
BLAST score
                   1.0e-17
E value
Match length
                   103
                   54
% identity
                  (AJ010224) glyceraldehyde 3-phosphate dehydrogenase,
NCBI Description
                   cytosolic [Cicer arietinum]
Seq. No.
                   229566
                   LIB3196-035-P1-M1-G12
Seq. ID
                   BLASTX
Method
                   g416917
NCBI GI
BLAST score
                   227
                   1.0e-18
E value
Match length
                   91
                   54
% identity
                  DESMOGLEIN 1 PRECURSOR (DESMOSOMAL GLYCOPROTEIN 1) (DG1)
NCBI Description
                   >gi_319948_pir__IJHUG1 desmoglein 1 precursor - human
                   >gi_30506_emb_CAA39976_ (X56654) desmoglein type 1 [Homo sapiens] >gi_3983129 (AF097935) desmoglein 1 [Homo sapiens]
                   >gi_4503401_ref_NP_001933.1_pDSG1_ desmoglein
                   229567
Seq. No.
Seq. ID
                   LIB3196-035-P1-M1-G2
Method
                   BLASTX
NCBI GI
                   q137578
BLAST score
                   472
E value
                   1.0e-47
Match length
                   115
% identity
                   VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                   >gi_81545_pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi 167371 (M19378) vicilin precursor
                    [Gossypium hirsutum] >gi 207906 (M18027) alpha globulin A
                    [Artificial gene] >gi_226119_prf__1410330A vicilin gene A
                    [Saguinus oedipus]
                   229568
Seq. No.
Seq. ID
                   LIB3196-035-P1-M1-G4
Method
                   BLASTX
NCBI GI
                   g2286153
BLAST score
                   533
E value
                   1.0e-54
Match length
                   110
```

97

% identity



```
(AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
                   229569
Seq. No.
                   LIB3196-035-P1-M1-G5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g609342
                   471
BLAST score
                   2.0e-47
E value
                   94
Match length
                   98
% identity
                   (U04946) nucleophosmin-anaplastic lymphoma kinase fusion
NCBI Description
                   protein [Homo sapiens]
                   229570
Seq. No.
                   LIB3196-035-P1-M1-G6
Seq. ID
Method
                   BLASTX
                   g4530585
NCBI GI
BLAST score
                   332
                   5.0e-31
E value
Match length
                   80
                   75
% identity
                  (AF130978) B12D protein [Ipomoea batatas]
NCBI Description
                   229571
Seq. No.
                   LIB3196-035-P1-M1-G8
Seq. ID
                   BLASTX
Method
                   g3024812
NCBI GI
BLAST score
                   359
                   3.0e - 34
E value
                   80
Match length
                   95
% identity
NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi 2599050
                   (AF027705) vacuolar ATPase 16kDa subunit c [Ovis aries]
Seq. No.
                   229572
                   LIB3196-035-P1-M1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q207905
                   435
BLAST score
                   3.0e-43
E value
                   101
Match length
                   82
% identity
                  (M18027) alpha globulin B [Artificial gene]
NCBI Description
                   229573
Seq. No.
                   LIB3196-035-P1-M1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g130348
BLAST score
                   227
E value
                   1.0e-18
Match length
                   45
% identity
                   100
NCBI Description
                   PHOSPHOGLYCERATE MUTASE, BRAIN FORM (PGAM-B) (BPG-DEPENDENT
                   PGAM) >gi 68469 pir PMHUYB phosphoglycerate mutase (EC
                   5.4.2.1) B - human >gi_551174 (J04173) phosphoglycerate mutase 2 [Homo sapiens] >gi_4505753_ref_NP_002620.1_pPGAM1_
```

phosphoglycerate mutase 1 (brain)



```
Seq. No.
                  229574
Seq. ID
                  LIB3196-035-P1-M1-H9
Method
                  BLASTX
NCBI GI
                  q2723393
BLAST score
                  172
E value
                  3.0e-12
Match length
                  120
% identity
                  38
                  (AB009284) EXTR2 [Homo sapiens] >gi_2895062 (AF000416)
NCBI Description
                  EXT-like protein 2 [Homo sapiens]
                  229575
Seq. No.
Seq. ID
                  LIB3196-036-P1-M1-A10
Method
                  BLASTX
NCBI GI
                  q2735857
BLAST score
                  317
                  2.0e-29
E value
Match length
                  80
% identity
                  79
NCBI Description
                 (AF012073) cAMP-specific phosphodiesterase PDE4D5 [Homo
                  sapiens]
Seq. No.
                  229576
                  LIB3196-036-P1-M1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  a2435512
BLAST score
                  237
E value
                  2.0e-20
Match length
                  59
% identity
NCBI Description (AF024504) No definition line found [Arabidopsis thaliana]
Seq. No.
                  229577
Seq. ID
                  LIB3196-036-P1-M1-A5
Method
                  BLASTX
NCBI GI
                  g1706326
BLAST score
                  397
E value
                  1.0e-38
Match length
                  84
% identity
                  83
NCBI Description
                  PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC)
                  >gi_2146786_pir__S65470 pyruvate decarboxylase (EC 4.1.1.1)
                   (clone PDC1) - Garden pea >gi_1177603_emb_CAA91444_
                   (Z66543) pyruvate decarboxylase [Pisum sativum]
Seq. No.
                  229578
Seq. ID
                  LIB3196-036-P1-M1-B1
Method
                  BLASTX
NCBI GI
                  g114682
BLAST score
                  289
E value
                  4.0e-26
                  99
Match length
% identity
                  64
NCBI Description ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
```

(OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)

>gi\_100471 pir A35227 H+-transporting ATP synthase (EC



3.6.1.34) gamma chain precursor, mitochondrial - sweet potato >gi\_168270 (J05397) F-1-ATPase delta subunit precursor (EC 3.6.1.3) [Ipomoea batatas]

 Seq. No.
 229579

 Seq. ID
 LIB3196-036-P1-M1-B10

 Method
 BLASTX

 NCRI GI
 24335751

NCBI GI g4335751 BLAST score 207 E value 2.0e-16 Match length 120 % identity 42

NCBI Description (AC006284) putative methyltransferase [Arabidopsis

thaliana]

Seq. No. 229580

Seq. ID LIB3196-036-P1-M1-B11

Method BLASTX
NCBI GI g137580
BLAST score 246
E value 5.0e-21
Match length 118
% identity 47

NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72)

>gi\_72286\_pir\_\_FWCNAB alpha-globulin B precursor (clone
C72) - upland cotton >gi\_167375 (M16891) vicilin precursor

[Gossypium hirsutum]

Seq. No. 229581

Seq. ID LIB3196-036-P1-M1-B12

Method BLASTX
NCBI GI g464981
BLAST score 391
E value 5.0e-38
Match length 74
% identity 96

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi\_388207 (L23762)

ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 229582

Seq. ID LIB3196-036-P1-M1-B3

Method BLASTX
NCBI GI g167311
BLAST score 311
E value 7.0e-29
Match length 79
% identity 78

NCBI Description (M83301) 2S albumin storage protein [Gossypium hirsutum]

Seq. No. 229583

Seq. ID LIB3196-036-P1-M1-B6

Method BLASTX
NCBI GI g126156
BLAST score 372
E value 8.0e-43
Match length 128



```
% identity
                   LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
NCBI Description
                    >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134)
                    - upland cotton >gi_167373 (M16936) vicilin precursor
                    [Gossypium hirsutum] >gi_1171335 (U43727) legumin B
                    [Gossypium hirsutum] >gi 225582_prf__1306412C storage
                    protein C134 [Saguinus oedipus]
                    229584
Seq. No.
                   LIB3196-036-P1-M1-B8
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3212868
                    512
BLAST score
                    3.0e-52
E value
                    107
Match length
                    86
% identity
                   (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                    229585
Seq. No.
                    LIB3196-036-P1-M1-C10
Seq. ID
Method
                    BLASTX
NCBI GI
                    g128378
                    274
BLAST score
                    3.0e-24
E value
                    91
Match length
                    56
% identity
NCBI Description
                   NONSPECIFIC LIPID-TRANSFER PROTEIN A (NS-LTP A)
                    (PHOSPHOLIPID TRANSFER PROTEIN) (PLTP)
                    >gi_82031_pir__S07142 nonspecific lipid transfer protein -
                    castor bean >gi_224909_prf__1204170A protein, nonspecific
                    lipid transfer [Ricinus communis]
                    229586
Seq. No.
                    LIB3196-036-P1-M1-C11
Seq. ID
                    BLASTX
Method
NCBI GI
                    g126156
BLAST score
                    482
E value
                    1.0e-48
                    121
Match length
% identity
                    LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
NCBI Description
                    >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134)
                    - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                    protein C134 [Saguinus oedipus]
Seq. No.
                    229587
Seq. ID
                    LIB3196-036-P1-M1-C12
Method
                    BLASTX
                    q1170505
NCBI GI
BLAST score
                    185
E value
                    5.0e-14
Match length
                    39
% identity
                    92
NCBI Description EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2)
```

>gi 322504 pir JC1453 translation initiation factor



eIF-4A2 - Arabidopsis thaliana >gi\_16556\_emb\_CAA46189\_(X65053) eukaryotic translation initiation factor 4A-2 [Arabidopsis thaliana]

229588 Seq. No. LIB3196-036-P1-M1-C4 Seq. ID BLASTX Method g2407800 NCBI GI 349 BLAST score 4.0e-33 E value 78 Match length 90 % identity (Y12575) histone H2A.F/Z [Arabidopsis thaliana] NCBI Description

Seq. No. 229589

Seq. ID LIB3196-036-P1-M1-C8

Method BLASTX
NCBI GI g3582332
BLAST score 316
E value 2.0e-29
Match length 82
% identity 73

NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No. 229590

Seq. ID LIB3196-036-P1-M1-D12

Method BLASTX
NCBI GI g2765837
BLAST score 256
E value 3.0e-22
Match length 110
% identity 55

NCBI Description (Z96936) NAP16kDa protein [Arabidopsis thaliana]

Seq. No. 229591

Seq. ID LIB3196-036-P1-M1-D3

Method BLASTX
NCBI GI g1771780
BLAST score 435
E value 3.0e-43
Match length 112
% identity 79

NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]

Seq. No. 229592

Seq. ID LIB3196-036-P1-M1-D5

Method BLASTX
NCBI GI g224293
BLAST score 410
E value 3.0e-40
Match length 82
% identity 100

NCBI Description histone H4 [Triticum aestivum]

Seq. No. 229593

Seq. ID LIB3196-036-P1-M1-D7

Method BLASTX

Seq. ID

Method



```
q423053
NCBI GI
                   200
BLAST score
                   1.0e-15
E value
                   40
Match length
                   97
% identity
NCBI Description protransglutaminase E, TGase3 - human
                   229594
Seq. No.
                   LIB3196-036-P1-M1-D8
Seq. ID
Method
                   BLASTX
                   q2497542
NCBI GI
BLAST score
                   467
E value
                   4.0e-47
                   99
Match length
                   92
% identity
                   PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR
NCBI Description
                   >gi 629696 pir__S44287 pyruvate kinase, plastid - common
                   tobacco >gi_482938_emb_CAA82223_ (Z28374) Pyruvate kinase;
                   plastid isozyme [Nicotiana tabacum]
                   229595
Seq. No.
                   LIB3196-036-P1-M1-D9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g125351
BLAST score
                   315
                   1.0e-37
E value
Match length
                   104
                   84
% identity
                   PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FER (P94-FER)
NCBI Description
                   (C-FER) >gi_66833_pir__TVHUFE protein-tyrosine kinase (EC 2.7.1.112) fer - human >gi_339715 (J03358) tyrosine kinase
                    (FER) [Homo sapiens]
                   229596
Seq. No.
Seq. ID
                   LIB3196-036-P1-M1-E10
Method
                   BLASTX
NCBI GI
                   g177207
BLAST score
                    561
E value
                    6.0e-58
Match length
                   130
% identity
                    86
NCBI Description (J02769) 4F2 antigen heavy chain [Homo sapiens]
Seq. No.
                    229597
                   LIB3196-036-P1-M1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                    g266691
BLAST score
                    351
                    3.0e-33
E value
Match length
                    106
                    70
% identity
NCBI Description OLEOSIN 16.4 KD >gi_167361 (L00934) 16.4 kDa oleosin
                    [Gossypium hirsutum]
                    229598
Seq. No.
```

32916

LIB3196-036-P1-M1-E7

BLASTX



```
NCBI GI
                   q416563
BLAST score
                   512
                   4.0e-52
E value
Match length
                   98
                   99
% identity
                   INTESTINAL MEMBRANE A4 PROTEIN (DIFFERENTIATION-DEPENDENT
NCBI Description
                   PROTEIN A4) >gi_422742_pir__S32567 A4 protein - human >gi_177900 (L09604) A4 protein [Homo sapiens] >gi_2707599
                   (U93305) A4 differentiation-dependent protein [Homo
                   sapiens] >gi_4505893_ref_NP_002659.1_pPLP2_ proteolipid
                   protein 2 (colonic epithelium-enriched)
                   229599
Seq. No.
                   LIB3196-036-P1-M1-E9
Seq. ID
Method
                   BLASTX
                   q267069
NCBI GI
BLAST score
                   525
                   1.0e-53
E value
                   97
Match length
                   99
% identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                   229600
                   LIB3196-036-P1-M1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3493660
BLAST score
                   669
E value
                   1.0e-70
Match length
                   132
% identity
                   99
NCBI Description (AF084530) cyclin-D binding Myb-like protein [Homo sapiens]
Seq. No.
                   229601
Seq. ID
                   LIB3196-036-P1-M1-F2
Method
                   BLASTX
NCBI GI
                   g3033391
BLAST score
                   223
E value
                   2.0e-18
Match length
                   95
% identity
                   58
                   (AC004238) putative amino acid transporter [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   229602
Seq. ID
                   LIB3196-036-P1-M1-F3
Method
                   BLASTX
NCBI GI
                   q3915031
BLAST score
                   638
E value
                   6.0e-67
```

95 NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi 1217628 emb CAA65232

126

Match length

% identity

(X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase

Match length

% identity

117

90



## [Gossypium hirsutum]

```
229603
Seq. No.
Seq. ID
                   LIB3196-036-P1-M1-F4
Method
                   BLASTX
NCBI GI
                   g398953
BLAST score
                   659
E value
                   2.0e-69
Match length
                   133
% identity
                   98
NCBI Description
                   14-3-3 PROTEIN SIGMA (STRATIFIN) (EPITHELIAL CELL MARKER
                   PROTEIN 1) >gi_486666_pir__S34753 stratifin - human
                   >gi_23940_emb_CAA40623_ (X57348) 9112 [Homo sapiens] >gi_2702353 (AF029081) 14-3-3 sigma protein [Homo sapiens]
                   >gi_2702355 (AF029082) 14-3-3 sigma protein [Homo sapiens]
                   229604
Seq. No.
                   LIB3196-036-P1-M1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3915742
BLAST score
                   618
                   1.0e-64
E value
Match length
                   127
% identity
                   91
                   LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi 167319
NCBI Description
                   (M69188) legumin A [Gossypium hirsutum]
                   >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele
                   [Gossypium hirsutum]
                   229605
Seq. No.
Seq. ID
                   LIB3196-036-P1-M1-F6
Method
                   BLASTX
NCBI GI
                   q4006867
BLAST score
                   183
E value
                   1.0e-13
Match length
                   126
% identity
                   45
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
Seq. No.
                   229606
Seq. ID
                   LIB3196-036-P1-M1-F7
Method
                   BLASTX
NCBI GI
                   g4567181
BLAST score
                   170
E value
                   4.0e-12
Match length
                   64
% identity
NCBI Description (AC007228) BC37295 3 [Homo sapiens]
                   229607
Seq. No.
Seq. ID
                   LIB3196-036-P1-M1-G10
Method
                   BLASTX
NCBI GI
                   g167367
BLAST score
                   533
E value
                   1.0e-54
```

NCBI Description



```
NCBI Description. (L08199) peroxidase [Gossypium hirsutum]
                   229608
Seq. No.
Seq. ID
                  LIB3196-036-P1-M1-G12
Method
                  BLASTX
NCBI GI
                  q1730288
                   370
BLAST score
                  2.0e-35
E value
Match length
                  89
% identity
                  83
NCBI Description
                  (U61263) acetolactate synthase homolog [Homo sapiens]
Seq. No.
                  229609
                  LIB3196-036-P1-M1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g477138
                  179
BLAST score
                   3.0e-23
E value
                  63
Match length
                   92
% identity
NCBI Description
                  carcinoma-associated antigen GA733-1 precursor - human
                   >gi_31591_emb_CAA31781_ (X13425) GA733-1 protein (AA 1-323)
                   [Homo sapiens]
Seq. No.
                  229610
Seq. ID
                  LIB3196-036-P1-M1-G6
Method
                  BLASTX
                  q631131
NCBI GI
                  424
BLAST score
                   5.0e-42
E value
Match length
                  97
                  89
% identity
                  epithelial cell marker protein 1 - human >gi 187302
NCBI Description
                   (M93010) epithelial cell marker protein 1 [Homo sapiens]
Seq. No.
                  229611
Seq. ID
                  LIB3196-036-P1-M1-G8
Method
                  BLASTX
NCBI GI
                  q479532
BLAST score
                  469
E value
                   4.0e-47
Match length
                  96
% identity
                  99
NCBI Description
                  GTP-binding regulatory protein Gs alpha chain - human
                   >gi_1335091_emb_CAA39484_ (X56009) alpha subunit of GsGTP
                  binding protein [Homo sapiens]
Seq. No.
                   229612
Seq. ID
                  LIB3196-036-P1-M1-G9
Method
                  BLASTX
NCBI GI
                  g1346347
BLAST score
                  431
E value
                  1.0e-42
                  90
Match length
                  98
% identity
```

KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D) (K6D KERATIN) >gi\_2119225\_pir\_\_161769 keratin type II -



Seq. No.

Seq. ID Method

NCBI GI

E value

Seq. No. Seq. ID

Method

NCBI GI

E value

Seq. No. Seq. ID

Method

NCBI GI

E value

Seq. No. Seq. ID

Method NCBI GI

E value

Seq. No. Seq. ID

Method NCBI GI

E value

Match length % identity

135

100

```
sapiens]
                  229613
                  LIB3196-036-P1-M1-H1
                  BLASTX
                  g3915742
BLAST score
                  427
                  8.0e-46
Match length
                  119
% identity
                  80
                  LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >qi 167319
NCBI Description
                  (M69188) legumin A [Gossypium hirsutum]
                  >gi 444320 prf 1906369A legumin A:ISOTYPE=D alloallele
                  [Gossypium hirsutum]
                  229614
                  LIB3196-036-P1-M1-H11
                  BLASTX
                  q3834322
BLAST score
                  169
                  5.0e-12
Match length
                  39
% identity
                  82
NCBI Description
                  (AC005679) EST gb R30300 comes from this gene. [Arabidopsis
                  thaliana]
                  229615
                  LIB3196-036-P1-M1-H3
                  BLASTX
                  g3297823
BLAST score
                  300
                  3.0e-27
Match length
                  82
% identity
                  66
NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
                  229616
                  LIB3196-036-P1-M1-H4
                  BLASTX
                  g2120082
BLAST score
                  355
                  9.0e-34
Match length
                  94
% identity
NCBI Description hypothetical protein II (retroposon LINE-1) - human
                  229617
                  LIB3196-036-P1-M1-H9
                  BLASTX
                  g120649
BLAST score
                  686
                  1.0e-72
```

human (fragment) >gi 914833 (L42610) keratin type II [Homo

>gi\_625203\_pir\_\_DEHUG3 glyceraldehyde-3-phosphate

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER



dehydrogenase (EC 1.2.1.12) - human >gi 182861 (M17851) glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens] >qi 182863 (J02642) qlyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi\_182977 (M33197) glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi 182981 (J04038) glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]
>gi\_224880\_prf\_\_1203217A dehydrogenase, glyceraldehydephosphate [Homo sapiens]

```
229618
Seq. No.
Seq. ID
                  LIB3196-037-P1-M1-A11
Method
                  BLASTX
                  q1916290
NCBI GI
BLAST score
                  147
                   2.0e-09
E value
                  72
Match length
                   49
% identity
                  (U89876) ALY [Mus musculus]
NCBI Description
                   229619
Seq. No.
                  LIB3196-037-P1-M1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1346349
BLAST score
                   217
E value
                   1.0e-17
                   43
Match length
                   100
% identity
                  KERATIN, TYPE II CYTOSKELETAL 6F (CYTOKERATIN 6F) (CK 6F)
NCBI Description
                   (K6F KERATIN) >gi_2119219_pir__I61771 keratin type II -
                   human >gi 908805 (L42612) keratin type II [Homo sapiens]
                   229620
Seq. No.
                   LIB3196-037-P1-M1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2813965
```

329 BLAST score 9.0e-31 E value

119 Match length 59 % identity

NCBI Description (Z97053) adenosine deaminase (ADA) [Homo sapiens]

229621 Seq. No.

LIB3196-037-P1-M1-A6 Seq. ID

BLASTX Method NCBI GI g4539395 BLAST score 142 7.0e-09 E value 51 Match length 53 % identity

NCBI Description (AL035526) putative protein [Arabidopsis thaliana]

229622 Seq. No.

Seq. ID LIB3196-037-P1-M1-B11

Method BLASTX NCBI GI q464707 BLAST score 516



1.0e-52 E value Match length 105 % identity 95 40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal NCBI Description protein S18.A - Arabidopsis thaliana >gi 405613 emb CAA80684 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273\_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi\_434345\_emb\_CAA82274\_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi 434906 emb CAA82275 (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi\_2505871\_emb\_CAA72909\_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi\_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb Z28701, DNA gb Z23165 from A. thaliana. ESTs gb T21121, gb Z17755, gb R64776 and gb\_R30430 come from this gene. [Arabidopsis thaliana] >gi 4538910 emb CAB39647.1 (AL049482) S18.A ribosomal protein [Arabidopsis thaliana] Seq. No. 229623 LIB3196-037-P1-M1-B12 Seq. ID Method BLASTX NCBI GI q3005063 BLAST score 529 3.0e-54E value Match length 125 83 % identity (AF043324) N-myristoyltransferase 1 [Homo sapiens] NCBI Description 229624 Seq. No. LIB3196-037-P1-M1-B4 Seq. ID Method BLASTX NCBI GI g4056499 BLAST score 139 E value 1.0e-08 Match length 43 58 % identity NCBI Description (AC005896) unknown protein [Arabidopsis thaliana] 229625 Seq. No. LIB3196-037-P1-M1-B8 Seq. ID BLASTX Method NCBI GI g1363944 BLAST score 598 2.0e-62 E value Match length 124 97 % identity type I keratin 16 - human >gi 1195531 bbs\_172338 (S79867) NCBI Description type I keratin 16, K16 [human, epidermal keratinocytes, Peptide, 473 aa] [Homo sapiens] 229626 Seq. No. Seq. ID LIB3196-037-P1-M1-C1

Method BLASTX
NCBI GI g4249382
BLAST score 439
E value 1.0e-43



```
Match length
% identity
                  (AC005966) Strong similarity to gi_3337350 F13P17.3
NCBI Description
                  putative permease from Arabidopsis thaliana BAC
                  gb AC004481. [Arabidopsis thaliana]
                  229627
Seq. No.
                  LIB3196-037-P1-M1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g81546
BLAST score
                  477
E value
                  3.0e-48
Match length
                  103
                  89
% identity
                  alpha-globulin type B precursor (tandem 1) - upland cotton
NCBI Description
                  (fragment)
                  229628
Seq. No.
                  LIB3196-037-P1-M1-C12
Seq. ID
                  BLASTX
Method
                  g762939
NCBI GI
BLAST score
                  614
                  4.0e-64
E value
Match length
                  127
                   92
% identity
                  (Y00057) precursor polypeptide (AA -14 to 747) [Homo
NCBI Description
                  sapiens]
                   229629
Seq. No.
                  LIB3196-037-P1-M1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1843527
BLAST score
                   447
                   1.0e-44
E value
Match length
                   116
% identity
                   78
NCBI Description (U73747) annexin [Gossypium hirsutum]
Seq. No.
                   229630
                   LIB3196-037-P1-M1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g125080
BLAST score
                   533
E value
                   1.0e-54
Match length
                   106
% identity
                   100
                  KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK
NCBI Description
                   14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal
                   - human >gi 386848 (J00124) keratin [Homo sapiens]
                   >gi 4504913 ref NP 000517.1 pKRT14 keratin 14
                   (epidermolysis bullosa simplex, Dowling-Meara, Koebner)
```

Seq. No. 229631

Seq. ID LIB3196-037-P1-M1-D10

Method BLASTX
NCBI GI g3845568
BLAST score 200

Method

BLASTX



```
E value
                   1.0e-15
                  78
Match length
% identity
                  (AB012042) keratin 6 beta [Mus musculus]
NCBI Description
                  229632
Seq. No.
                  LIB3196-037-P1-M1-D11
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1498225
BLAST score
                   309
E value
                   2.0e-28
Match length
                   62
                   100
% identity
                   (Y07569) PHAPI2a protein [Homo sapiens] >gi 1698783
NCBI Description
                   (U70439) silver-stainable protein SSP29 [Homo sapiens]
                   229633
Seq. No.
                   LIB3196-037-P1-M1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g167311
BLAST score
                   496
                   2.0e-50
E value
Match length
                   113
% identity
                  (M83301) 2S albumin storage protein [Gossypium hirsutum]
NCBI Description
                   229634
Seq. No.
                   LIB3196-037-P1-M1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g119339
BLAST score
                   457
E value
                   1.0e-45
                   92
Match length
% identity
                   99
NCBI Description
                  ALPHA ENOLASE (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
                   (NON-NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE)
                   >qi 87368 pir A29170 phosphopyruvate hydratase (EC
                   4.2.1.11) alpha - human >gi 182114 (M14328) alpha enolase
                   (EC 4.2.1.11) [Homo sapiens] >gi 1167843 emb CAA34360_
                   (X16288) alpha-enolase [Homo sapiens]
                   >gi_4503571_ref_NP_001419.1_pEN01_ enolase 1, (alpha)
                   229635
Seq. No.
                   LIB3196-037-P1-M1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1000704
BLAST score
                   465
                   1.0e-46
E value
Match length
                   93
% identity
                   (Z50101) NAD(P) transhydrogenase [Homo sapiens]
NCBI Description
                   >gi_1589396_prf__2211247B nicotinamide nucleotide
                   transhydrogenase [Homo sapiens]
                   229636
Seq. No.
Seq. ID
                   LIB3196-037-P1-M1-D6
```

Method

NCBI GI

BLASTX

g293119



```
NCBI GI
                  q421953
                  272
BLAST score
E value
                  2.0e-29
Match length
                  108
% identity
                  69
                  hypothetical protein 2 - potato transposon Tst1
NCBI Description
                  >gi 21432 emb CAA36614 (X52387) ORF2 [Solanum tuberosum]
Seq. No.
                  229637
Seq. ID
                  LIB3196-037-P1-M1-D8
Method
                  BLASTX
NCBI GI
                  q2944446
BLAST score
                  548
E value
                  2.0e-56
Match length
                  122
                  80
% identity
                  (AF050756) cysteine endopeptidase precursor [Ricinus
NCBI Description
                  communis]
                  229638
Seq. No.
                  LIB3196-037-P1-M1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3041738
BLAST score
                  618
E value
                  1.0e-64
Match length
                  122
% identity
                  97
NCBI Description T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA)
                   (HIV-1 NEF INTERACTING PROTEIN) >gi 2559010 (AF026292)
                  chaperonin containing t-complex polypeptide 1, eta subunit;
                  CCT-eta [Homo sapiens]
                  229639
Seq. No.
                  LIB3196-037-P1-M1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q901998
BLAST score
                  143
                  7.0e-09
E value
                  97
Match length
                  35
% identity
NCBI Description (U23731) TAR DNA-binding protein-43 [Homo sapiens]
                  229640
Seq. No.
Seq. ID
                  LIB3196-037-P1-M1-E3
Method
                  BLASTX
                  g2119228
NCBI GI
BLAST score
                  227
                  9.0e-19
E value
                  111
Match length
                  51
% identity
NCBI Description keratin K4a - human (fragment) >gi 313159 emb CAA47914_
                   (X67683) keratin K4a [Homo sapiens]
                  229641
Seq. No.
Seq. ID
                  LIB3196-037-P1-M1-E6
```

% identity

100



```
BLAST score
                     500
  E value
                     9.0e-51
  Match length
                    121
  % identity
                     83
NCBI Description (L13307) immunoglobulin gamma [Macaca fascicularis]
                    229642
  Seq. No.
                    LIB3196-037-P1-M1-E9
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g1694976
  BLAST score
                    307
  E value
                     3.0e-28
  Match length
                    91
  % identity
                     64
                    (Y09482) HMG1 [Arabidopsis thaliana]
  NCBI Description
                     >gi 2832361 emb CAA74402 (Y14073) HMG protein [Arabidopsis
                    thaliana]
  Seq. No.
                     229643
  Seq. ID
                    LIB3196-037-P1-M1-F2
  Method
                    BLASTX
  NCBI GI
                     g112440
  BLAST score
                    358
  E value
                     4.0e-34
  Match length
                    93
  % identity
                     52
  NCBI Description tropomyosin 1 alpha, brain - rat
  Seq. No.
                     229644
  Seq. ID
                    LIB3196-037-P1-M1-F4
  Method
                    BLASTX
  NCBI GI
                     g4063760
  BLAST score
                     331
  E value
                     5.0e-44
                    118
  Match length
                     73
  % identity
  NCBI Description (AC005561) putative POL3 protein [Arabidopsis thaliana]
  Seq. No.
                     229645
  Seq. ID
                    LIB3196-037-P1-M1-F6
  Method
                    BLASTX
  NCBI GI
                     g3929617
  BLAST score
                     658
  E value
                     3.0e-69
  Match length
                     128
                     99
  % identity
  NCBI Description (U39412) alpha SNAP [Homo sapiens]
                     >gi 4505329 ref NP 003818.1 pNAPA UNKNOWN
                     229646
  Seq. No.
                     LIB3196-037-P1-M1-F8
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                     g125080
  BLAST score
                     517
  E value
                     5.0e-53
  Match length
                     104
```



```
KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK
NCBI Description
                    14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens]
                    >gi_4504913_ref_NP_000517.1_pKRT14 keratin 14
                    (epidermolysis bullosa simplex, Dowling-Meara, Koebner)
                    229647
Seq. No.
                    LIB3196-037-P1-M1-G10
Seq. ID
Method
                    BLASTX
                    g3882321
NCBI GI
BLAST score
                    147
E value
                    2.0e-09
Match length
                    100
                    38
% identity
                    (AB018343) KIAA0800 protein [Homo sapiens]
NCBI Description
                    229648
Seq. No.
                    LIB3196-037-P1-M1-G11
Seq. ID
Method
                    BLASTX
NCBI GI
                    q2494911
BLAST score
                    617
E value
                    2.0e-64
Match length
                    119
                    97
% identity
                    HYPOTHETICAL PROTEIN KIAA0124 >gi 1469171 dbj BAA09473
NCBI Description
                     (D50914) The KIAA0124 gene product is novel. [Homo sapiens]
                    229649
Seq. No.
                    LIB3196-037-P1-M1-G3
Seq. ID
Method
                    BLASTX
NCBI GI
                    q729032
BLAST score
                     4.0e-25
E value
Match length
                    54
                     100
% identity
NCBI Description
                    ADENYLYL CYCLASE-ASSOCIATED PROTEIN 1 (CAP 1)
                    >gi_2137125_pir__I49572 adenylyl cyclase-associated protein
- mouse >gi_293317 (L12367) adenylyl cyclase-associated
                    protein [Mus musculus] >gi_744841_prf__2015321A adenylate cyclase-associated protein [Mus musculus]
                    229650
Seq. No.
                    LIB3196-037-P1-M1-G8
Seq. ID
                    BLASTX
Method
NCBI GI
                    g2500587
BLAST score
                     611
E value
                     8.0e-64
Match length
                     117
                     72
% identity
                    SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53)
NCBI Description
```

>gi\_1082799\_pir\_\_A54964 spliceosome-associated protein SAP-49 - human >gi\_556217 (L35013) spliceosomal protein

[Homo sapiens]

Seq. No. 229651

Seq. ID LIB3196-037-P1-M1-G9

Method BLASTX

NCBI Description



```
NCBI GI
                   q2500587
BLAST score
                   585
                   9.0e-61
E value
Match length
                   117
                   64
% identity
                   SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53)
NCBI Description
                   >gi_1082799_pir__A54964 spliceosome-associated protein
                   SAP-49 - human >gi_556217 (L35013) spliceosomal protein
                   [Homo sapiens]
Seq. No.
                   229652
                   LIB3196-037-P1-M1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3643608
BLAST score
                   195
                   5.0e-15
E value
                   98
Match length
                   39
% identity
NCBI Description (AC005395) hypothetical protein [Arabidopsis thaliana]
                   229653
Seq. No.
                   LIB3196-037-P1-M1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4417310
                   161
BLAST score
E value
                   4.0e-11
                   86
Match length
% identity
                   41
                   (ACO06446) putative Athila retroelement ORF1 protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   229654
Seq. ID
                   LIB3196-037-P1-M1-H4
Method
                   BLASTX
NCBI GI
                   g119172
BLAST score
                   464
                   2.0e-51
E value
Match length
                   108
% identity
                   96
                   ELONGATION FACTOR 2 (EF-2) >gi_2144947_pir__EFHU2
NCBI Description
                   translation elongation factor eEF-2 - human
                   >gi_31106_emb_CAA35829_ (X51466) elongation factor 2 [Homo sapiens] >gi_31108_emb_CAA77750_ (Z11692) human elongation
                   factor 2 [Homo sapiens] >gi_4503483_ref_NP_001952.1_pEEF2_
                   eukaryotic translation elongation factor
Seq. No.
                   229655
Seq. ID
                   LIB3196-037-P1-M1-H5
                   BLASTX
Method
NCBI GI
                   g1730015
BLAST score
                   311
                   1.0e-28
E value
                   82
Match length
                   72
% identity
```

32928

inducing ligand TRAIL [Homo sapiens]

TNF-RELATED APOPTOSIS INDUCING LIGAND (TRAIL PROTEIN)

(APO-2 LIGAND) >gi 1149558 (U37518) TNF-related apoptosis



>qi 1336208 gb AAB01233 (U57059) Apo-2 ligand [Homo sapiens] >gi 4507593\_ref\_NP\_003801.1\_pTNFSF10\_ UNKNOWN

Seq. No. 229656

Seq. ID LIB3196-037-P1-M1-H6

Method BLASTX NCBI GI g2058282 BLAST score 190 E value 2.0e-14 Match length 51

NCBI Description (X97377) atranbpla [Arabidopsis thaliana]

229657 Seq. No.

% identity

Seq. ID LIB3196-037-P1-M1-H7

69

BLASTX Method NCBI GI g3643607 BLAST score 531 E value 2.0e-54 Match length 119 % identity 81

NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 229658

Seq. ID LIB3196-038-P1-M1-A2

Method BLASTX NCBI GI q126682 BLAST score 386 E value 2.0e-37 Match length 74 97 % identity

MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN NCBI Description

> MAD3 >gi 106956 pir A39935 major histocompatibility complex enhance-binding protein MAD3 - human >gi 187291

(M69043) MAD3 [Homo sapiens]

229659 Seq. No.

LIB3196-038-P1-M1-A4 Seq. ID

BLASTX Method NCBI GI g3033397 BLAST score 427 2.0e-42E value 104 Match length 80 % identity

NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]

229660 Seq. No.

Seq. ID LIB3196-038-P1-M1-A5

BLASTX Method NCBI GI q137578 BLAST score 539 2.0e-55 E value Match length 105 100 % identity

NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi 81545 pir S06398 alpha-globulin type A precursor -

upland cotton >gi 167371 (M19378) vicilin precursor



[Gossypium hirsutum] >gi 207906 (M18027) alpha globulin A [Artificial gene] >gi 226119 prf 1410330A vicilin gene A [Saquinus oedipus]

Seq. No. 229661

LIB3196-038-P1-M1-A6 Seq. ID

Method BLASTX NCBI GI q124204 BLAST score 391 5.0e-38 E value Match length 87 87 % identity

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (EIF-2-BETA) >gi\_87941\_pir\_\_A31226 translation initiation factor eIF-2 beta chain - human >gi 109365 pir S13147 protein synthesis factor - rabbit >gi\_182067 (M29536)

translational initiation factor beta subunit [Homo sapiens]

>gi\_227237\_prf\_\_1617105A initiation factor 2beta

[Oryctolagus cuniculus]

>gi\_4503505\_ref\_NP\_003899.1\_pEIF2S2\_ UNKNOWN

Seq. No. 229662

Seq. ID LIB3196-038-P1-M1-A9

Method BLASTX q3334245 NCBI GI BLAST score 228 2.0e-19 E value Match length 53 85 % identity

NCBI Description LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)

(ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi 2909424 emb CAA12028 (AJ224520) Glyoxalase I [Cicer

arietinum]

Seq. No. 229663

Seq. ID LIB3196-038-P1-M1-B10

Method BLASTX NCBI GI g3885334 BLAST score 370 E value 9.0e-36 Match length 94 79 % identity

(AC005623) putative argonaute protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 229664

Seq. ID LIB3196-038-P1-M1-B12

BLASTX Method NCBI GI g3334138 BLAST score 238 2.0e-20 E. value Match length 84 55 % identity

NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi 669003 (U20502) calnexin

[Glycine max]



```
Seq. No.
                   229665
Seq. ID
                   LIB3196-038-P1-M1-B3
Method
                   BLASTX
NCBI GI
                   q3875300
BLAST score
                   144
E value
                   3.0e-09
Match length
                   47
                   62
% identity
NCBI Description
                   (Z68160) Similarity to Yeast putative mitochondrial carrier
                   protein PET8 (SW:PET8_YEAST); cDNA EST CEMSH22F comes from
                   this gene; cDNA EST CEMSH22R comes from this gene; cDNA EST
                   yk331b9.5 comes from this gene [Caenorhabditis e
                   229666
Seq. No.
Seq. ID
                   LIB3196-038-P1-M1-B5
Method
                   BLASTX
NCBI GI
                   q2465923
BLAST score
                   175
E value
                   9.0e-13
Match length
                   50
% identity
                   64
NCBI Description
                   (AF024648) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
Seq. No.
                   229667
Seq. ID
                   LIB3196-038-P1-M1-B6
Method
                   BLASTX
NCBI GI
                   q3834310
BLAST score
                   500
E value
                   7.0e-51
Match length
                   96
% identity
                   100
NCBI Description
                   (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
                   gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464,
                   gb_N37265, gb_H36151, gb_Z34711, gb_AAO40983, and gb_T22122 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   229668
Seq. ID
                   LIB3196-038-P1-M1-B8
Method
                   BLASTX
NCBI GI
                   g2887441
BLAST score
                   467
E value
                   3.0e-47
Match length
                   84
% identity
                   98
NCBI Description
                  (AB007891) KIAA0431 [Homo sapiens]
                   229669
Seq. No.
Seq. ID
                   LIB3196-038-P1-M1-C4
```

Method BLASTX
NCBI GI g4325382
BLAST score 465
E value 9.0e-47
Match length 92
% identity 99

NCBI Description (AF129075) T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA)

[Homo sapiens]

Seq. ID



229670

```
Seq. No.
                  LIB3196-038-P1-M1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q284314
                  673
BLAST score
                  5.0e-71
E value
                  122
Match length
                  100
% identity
                  modulator recognition factor 1 - human (fragment)
NCBI Description
                  >qi 188684 (M62324) modulator recognition factor I [Homo
                  sapiens]
                  229671
Seq. No.
                  LIB3196-038-P1-M1-C8
Seq. ID
                  BLASTX
Method
                  q131162
NCBI GI
                  209
BLAST score
                  7.0e-17
E value
                  42
Match length
                  90
% identity
                  PHOTOSYSTEM I IRON-SULFUR CENTER 1 (PHOTOSYSTEM I SUBUNIT
NCBI Description
                  VII-1) (9 KD POLYPEPTIDE 1) (PSI-C-1)
                  >gi_131163_sp_P07136_PSAC_TOBAC PHOTOSYSTEM I IRON-SULFUR
                   CENTER (PHOTOSYSTEM I SUBUNIT VII) (9 KD POLYPEPTIDE)
                   (PSI-C) >gi_97657_pir__S14967 photosystem I iron-sulfur
                   protein psa\overline{C} - Synechocystis sp. (PCC 6803)
                   >gi 100391_pir__S07170 photosystem I iron-sulfur protein
                   psaC - common tobacco chloroplast >gi_11792_emb_CAA29304_
                   (X05881) 9kd polypeptide (psaC gene product, AA 1 - 81)
                   [Nicotiana tabacum] >gi_47596_emb_CAA37836_ (X53842) 8.9kDa
                   iron-sulfur containing subunit of Photosystem I
                   [Synechocystis sp.] >gi_2924280_emb CAA77433 (Z00044) PSI
                   9kD protein [Nicotiana tabacum]
                   229672
Seq. No.
Seq. ID
                   LIB3196-038-P1-M1-D12
Method
                   BLASTX
                   q224877
NCBI GI
                   453
BLAST score
                   2.0e-45
E value
Match length
                   89
                   96
% identity
NCBI Description deaminase a, adenosine [Homo sapiens]
                   229673
Seq. No.
Seq. ID
                   LIB3196-038-P1-M1-D3
Method
                   BLASTX
NCBI GI
                   g3170190
                   257
BLAST score
E value
                   8.0e-23
Match length
                   70
                   76
% identity
NCBI Description (AF039695) antigen NY-CO-25 [Homo sapiens]
                   229674
Seq. No.
```

LIB3196-038-P1-M1-E10



```
BLASTX
Method
                  g1703446
NCBI GI
                  385
BLAST score
                  2.0e-37
E value
Match length
                  119
                  66
% identity
                  L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
NCBI Description
                  >gi_1076292_pir__S53127 asparaginase - Arabidopsis thaliana
                  >gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis
                  thaliana]
                  229675
Seq. No.
                  LIB3196-038-P1-M1-E12
Seq. ID
                  BLASTX
Method
                  g3915742
NCBI GI
                   448
BLAST score
                   7.0e-45
E value
                   98
Match length
                   88
% identity
                  LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319
NCBI Description
                   (M69188) legumin A [Gossypium hirsutum]
                   >gi 444320_prf__1906369A legumin A:ISOTYPE=D alloallele
                   [Gossypium hirsutum]
                   229676
Seq. No.
                   LIB3196-038-P1-M1-E3
Seq. ID
                   BLASTX
Method
                   g72287
NCBI GI
                   474
BLAST score
                   7.0e-48
E value
                   107
Match length
                   88
% identity
                   beta-globulin A precursor (clone 94) - upland cotton
NCBI Description
                   (fragment) >gi 167377 (M16905) legumin precursor [Gossypium
                   hirsutum]
                   229677
Seq. No.
                   LIB3196-038-P1-M1-E4
Seq. ID
Method
                   BLASTX
                   q284314
NCBI GI
                   606
BLAST score
                   3.0e-63
E value
                   110
Match length
                   100
 % identity
                   modulator recognition factor 1 - human (fragment)
NCBI Description
                   >gi_188684 (M62324) modulator recognition factor I [Homo
                   sapiens]
                   229678
 Seq. No.
                   LIB3196-038-P1-M1-E6
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q2529678
 BLAST score
                   187
                   3.0e-14
 E value
 Match length
                   75
 % identity
 NCBI Description (AC002535) unknown protein [Arabidopsis thaliana]
```



```
229679
Seq. No.
Seq. ID
                   LIB3196-038-P1-M1-E7
Method
                   BLASTX
NCBI GI
                   q137578
BLAST score
                   413
                   9.0e-41
E value
                   98
Match length
                   47
% identity
                   VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                   >gi_81545_pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi_167371 (M19378) vicilin precursor
                    [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                    [Artificial gene] >gi_226119_prf__1410330A vicilin gene A
                    [Saguinus oedipus]
                   229680
Seq. No.
                   LIB3196-038-P1-M1-E8
Seq. ID
Method
                   BLASTX
                   g3641838
NCBI GI
BLAST score
                   409
                   4.0e-40
E value
                   89
Match length
                   88
% identity
                   (AL023094) putative protein (fragment) [Arabidopsis
NCBI Description
                   thaliana]
                   229681
Seq. No.
                   LIB3196-038-P1-M1-F12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1346348
                    464
BLAST score
                    6.0e-47
E value
                    93
Match length
                    99
% identity
                   KERATIN, TYPE II CYTOSKELETAL 6E (CYTOKERATIN 6E) (CK 6E)
NCBI Description
                    (K6E KERATIN) >gi_2119223_pir__I61770 keratin type II - human >gi_908803 (L42611) keratin type II [Homo sapiens]
                    229682
Seq. No.
                    LIB3196-038-P1-M1-F3
Seq. ID
Method
                    BLASTX
NCBI GI
                    g167311
BLAST score
                    513
                    2.0e-52
E value
Match length
                    97
% identity
                    100
NCBI Description (M83301) 2S albumin storage protein [Gossypium hirsutum]
                    229683
Seq. No.
                    LIB3196-038-P1-M1-F4
Seq. ID
Method
                    BLASTX
                    g113944
NCBI GI
BLAST score
                    563
                    3.0e-58
E value
```

121

93

Match length

% identity



```
NCBI Description ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9)
                   (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN)
                   >gi_71756_pir__LUHU annexin I - human
>gi_34388_emb_CAA29338_ (X05908) lipocortin (AA 1-346)
                   [Homo sapiens] >gi_224956_prf__1204261A lipocortin [Homo
                   sapiens] >gi 45021\overline{0}1 ref \overline{NP}_000691.1 pANX1_ annexin I
                   (lipocortin I)
                   229684
Seq. No.
                   LIB3196-038-P1-M1-F7
Seq. ID
                   BLASTX
Method
                   g2827715
NCBI GI
                   279
BLAST score
                   6.0e-25
E value
                   102
Match length
                   60
% identity
                   (AL021684) receptor protein kinase - like protein
NCBI Description
                    [Arabidopsis thaliana]
                   229685
Seq. No.
                   LIB3196-038-P1-M1-F8
Seq. ID
                   BLASTX
Method
                   g2055295
NCBI GI
                   553
BLAST score
                   5.0e-57
E value
Match length
                   117
                    93
% identity
                   (D87438) Similar to a C.elegans protein in cosmid C14H10
NCBI Description
                    [Homo sapiens]
                    229686
Seq. No.
                    LIB3196-038-P1-M1-F9
Seq. ID
                    BLASTX
Method
                    g4467804
NCBI GI
                    513
BLAST score
                    2.0e-52
E value
Match length
                    100
% identity
                    95
                    (AL031678) TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3
NCBI Description
                    PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3).)
                    [Homo sapiens]
                    229687
Seq. No.
                    LIB3196-038-P1-M1-G1
Seq. ID
                    BLASTX
Method
                    q4406814
NCBI GI
BLAST score
                    352
E value
                    9.0e - 34
Match length
                    83
 % identity
                    (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis
 NCBI Description
                    thaliana]
                    229688
 Seq. No.
                    LIB3196-038-P1-M1-G11
 Seq. ID
```

Seq. 1D LIBSIYO-030-FI-MI-GII

Method BLASTX NCBI GI g1169178



```
BLAST score
                   2.0e-12
E value
Match length
                   51
% identity
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN C) >gi_627417_pir__A54204 peptidylprolyl
                   isomerase (EC 5.2.1.8) C precursor - human
                   >gi 547304_bbs_149388 (S71018) cyclophilin C, Cyp-C [human,
                   kidney, Peptide, 212 aa] [Homo sapiens]
                   >qi 4505991 ref NP 000934.1 pPPIC_ peptidylprolyl isomerase
                   C (cyclophilin C); Cyp-C
Seq. No.
                   229689
                   LIB3196-038-P1-M1-G12
Seq. ID
Method
                   BLASTX
                   q2828290
NCBI GI
                   216
BLAST score
                   2.0e-17
E value
                   90
Match length
                   47
% identity
                  (AL021687) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
                   229690
Seq. No.
                   LIB3196-038-P1-M1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2554653
                   486
BLAST score
E value
                   2.0e-49
                   96
Match length
% identity
                   57
NCBI Description Up1, The Two Rna-Recognition Motif Domain Of Hnrnp A1
                   229691
Seq. No.
                   LIB3196-038-P1-M1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4090247
 BLAST score
                   261
E value
                   1.0e-24
Match length
                   133
 % identity
                   53
 NCBI Description (AJ006130) rer [Mus musculus]
                   229692
 Seq. No.
                   LIB3196-038-P1-M1-G7
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g125080
 BLAST score
                   463
 E value
                   9.0e-47
                   94
 Match length
                   100
 % identity
                   KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK
 NCBI Description
```

14) >gi 2144816\_pir\_\_KRHUE keratin, 50K type I cytoskeletal

- human >gi\_386848 (J00124) keratin [Homo sapiens]

>gi\_4504913\_ref\_NP\_000517.1 pKRT14 keratin 14

(epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No. 229693

Match length

88



```
LIB3196-038-P1-M1-G8
Seq. ID
                  BLASTX
Method
                  q2582665
NCBI GI
                  434
BLAST score
                  3.0e-43
E value
                  94
Match length
                  89
% identity
NCBI Description (Z82983) thi [Citrus sinensis]
                  229694
Seq. No.
                  LIB3196-038-P1-M1-H2
Seq. ID
                  BLASTX
Method
                  q1438567
NCBI GI
                  543
BLAST score
                   6.0e-56
E value
Match length
                  104
                   100
% identity
                  (U61266) Rho-associated kinase beta [Rattus norvegicus]
NCBI Description
                   229695
Seq. No.
                  LIB3196-038-P1-M1-H3
Seq. ID
                   BLASTX
Method
                   g683553
NCBI GI
                   155
BLAST score
                   1.0e-10
E value
                   72
Match length
                   51
% identity
                  (Z48450) oleosin-like protein [Citrus sinensis]
NCBI Description
                   >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]
                   229696
Seq. No.
                   LIB3196-038-P1-M1-H6
Seq. ID
                   BLASTX
Method
                   g3264767
NCBI GI
                   379
BLAST score
                   1.0e-36
E value
Match length
                   115
                   62
% identity
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
                   229697
Seq. No.
                   LIB3196-039-P1-M1-A1
Seq. ID
                   BLASTX
Method
                   g2995405
NCBI GI
                   345
BLAST score
                   8.0e-33
E value
Match length
                   96
                   73
 % identity
NCBI Description (Y12432) polyprotein [Ananas comosus]
                   229698
 Seq. No.
                   LIB3196-039-P1-M1-A10
 Seq. ID
                   BLASTX
 Method
                   g131773
 NCBI GI
                   412
 BLAST score
                   2.0e-40
 E value
```

BLAST score

323



```
% identity
                   40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
NCBI Description
                   >gi 82724 pir B30097 ribosomal protein S14 (clone MCH2) -
                   229699
Seq. No.
                   LIB3196-039-P1-M1-A11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g548774
                   257
BLAST score
E value
                   2.0e-22
Match length
                   69
                   72
% identity
                   60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631) ribosomal protein L7A [Oryza sativa]
NCBI Description
                   229700
Seq. No.
Seq. ID
                   LIB3196-039-P1-M1-A3
Method
                   BLASTX
                   q71533
NCBI GI
                    522
BLAST score
E value
                    2.0e-53
Match length
                   106
                    100
% identity.
NCBI Description keratin, 56K type II cytoskeletal - human
                    229701
Seq. No.
                    LIB3196-039-P1-M1-A5
Seq. ID
                   BLASTX
Method
NCBI GI
                    g119172
BLAST score
                    666
                    3.0e-70
E value
Match length
                    127
% identity
                    99
NCBI Description ELONGATION FACTOR 2 (EF-2) >gi_2144947_pir__EFHU2
                    translation elongation factor eEF-2 - human
                    >gi 31106_emb_CAA35829_ (X51466) elongation factor 2 [Homo
                    sapiens] >gi 31108 emb CAA77750 (Z11692) human elongation
                    factor 2 [Homo sapiens] >gi 4503483 ref NP_001952.1 pEEF2
                    eukaryotic translation elongation factor
                    229702
Seq. No.
Seq. ID
                    LIB3196-039-P1-M1-A6
Method
                    BLASTX
NCBI GI
                    g4379025
                    212
BLAST score
                    5.0e-17
E value
                    60
Match length
                    72
% identity
NCBI Description (X03145) pot. ORF VI [Homo sapiens]
                    229703
Seq. No.
Seq. ID
                    LIB3196-039-P1-M1-A9
Method
                    BLASTX
NCBI GI
                    q547753
```

Match length



```
3.0e-30
 E value
                   67
 Match length
                   96
 % identity
                   KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)
 NCBI Description
                   229704
 Seq. No.
                   LIB3196-039-P1-M1-B11
 Seq. ID
                   BLASTX
 Method
                   g2879867
 NCBI GI
                   317
 BLAST score
                   2.0e-29
 E value
                   90
 Match length
                    67
 % identity
                   (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces
 NCBI Description
                   pombe]
                    229705
 Seq. No.
                   LIB3196-039-P1-M1-B3
 Seq. ID
                    BLASTX
 Method
                    g2499087
 NCBI GI
                    470
 BLAST score
                    3.0e-47
 E value
 Match length
                    122
                    67
 % identity
                    UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR
 NCBI Description
                    (DUGT) >gi_1085170_pir__S54723 UDP-glucose--glycoprotein
                    glucosyltransferase - fruit fly (Drosophila sp.) >gi_790585
                    (U20554) UDP-glucose:glycoprotein glucosyltransferase
                    precursor [Drosophila melanogaster]
                    229706
 Seq. No.
                    LIB3196-039-P1-M1-B4
 Seq. ID
 Method
                    BLASTX
                    g4164033
 NCBI GI
                    284
 BLAST score
                    2.0e-25
» E value
 Match length
                    127
 % identity
                    44
                   (AF111075) latrophilin 2 splice variant babbe [Bos taurus]
 NCBI Description
                    229707
 Seq. No.
                    LIB3196-039-P1-M1-B6
 Seq. ID
 Method
                    BLASTX
                    q1130684
 NCBI GI
 BLAST score
                    621
                    5.0e-65
 E value
 Match length
                    120
                    100
 % identity
                   (Z46960) acetohydroxyacid synthase [Gossypium hirsutum]
 NCBI Description
                    229708
 Seq. No.
                    LIB3196-039-P1-M1-B9
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4406225
 BLAST score
                    491
                    9.0e-50
 E value
```



```
% identity
                  (AF104412) proliferating cell nuclear antigen II [Nicotiana
NCBI Description
                  tabacum]
                  229709
Seq. No.
                  LIB3196-039-P1-M1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g729978
                  171
BLAST score
                  2.0e-12
E value
                  50
Match length
                  70
% identity
                  MAD PROTEIN (MAX DIMERIZER) >gi 346245_pir__A45181
NCBI Description
                  Max-binding bHLH-Zip protein Mad - human >gi 187289
                   (L06895) antagonizer of myc transcriptional activity [Homo
                  sapiens] >gi_4505069_ref_NP_002348.1_pMAD_ MAD protein
                   (MAX-binding protein)
                  229710
Seq. No.
                  LIB3196-039-P1-M1-C11
Seq. ID
                  BLASTX
Method
                  g2827550
NCBI GI
                  154
BLAST score
                   3.0e-10
E value
                   51
Match length
                   59
% identity
                  (AL021635) leucine rich repeat receptor kinase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   229711
Seq. No.
                   LIB3196-039-P1-M1-C2
Seq. ID
Method
                   BLASTX
                   g975290
NCBI GI
BLAST score
                   268
                   7.0e-24
E value
Match length
                   79
% identity
                   72
NCBI Description (U24183) phosphofructokinase [Homo sapiens]
                   229712
Seq. No.
Seq. ID
                   LIB3196-039-P1-M1-C3
Method
                   BLASTX
NCBI GI
                   g3860797
BLAST score
                   201
                   7.0e-16
E value
Match length
                   97
% identity
                   41
                  (AJ235271) 30S RIBOSOMAL PROTEIN S9 (rpsI) [Rickettsia
NCBI Description
                   prowazekii]
                   229713
Seq. No.
                   LIB3196-039-P1-M1-C4
Seq. ID
                   BLASTX
Method
                   g4138581
NCBI GI
                   292
BLAST score
```

2.0e-26

96

E value

Match length

BLAST score

E value

7.0e-48



```
% identity
                  (X98474) mitochondrial energy transfer protein [Solanum
NCBI Description
                  tuberosum]
                  229714
Seq. No.
                  LIB3196-039-P1-M1-C5
Seq. ID
                  BLASTX
Method
                  g2352492
NCBI GI
                  339
BLAST score
                  3.0e-32
E value
                  78
Match length
                  81
% identity
                  (AF005047) transport inhibitor response 1 [Arabidopsis
NCBI Description
                  thaliana] >gi_2352494 (AF005048) transport inhibitor
                  response 1 [Arabidopsis thaliana]
                  229715
Seq. No.
                  LIB3196-039-P1-M1-C6
Seq. ID
                  BLASTX
Method
                   g1070474
NCBI GI
                   587
BLAST score
                   5.0e-61
E value
                   119
Match length
                   92
% identity
                  protein-tyrosine kinase (EC 2.7.1.112) fgr - feline sarcoma
NCBI Description
                   virus (strain Gardner-Rasheed) >gi_61543_emb_CAA25063_
                   (X00255) P70 gag gene [Feline sarcoma virus]
                   229716
Seq. No.
                   LIB3196-039-P1-M1-C7
Seq. ID
                   BLASTX
Method
                   g4455211
NCBI GI
                   200
BLAST score
                   1.0e-15
E value
                   85
Match length
                   39
% identity
                  (AL035440) STIG1 like protein [Arabidopsis thaliana]
NCBI Description
                   229717
Seq. No.
                   LIB3196-039-P1-M1-D1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2134892
                   472
BLAST score
                   2.0e-47
E value
                   92
Match length
                   100
 % identity
                   cell surface glycoprotein - human >gi 188256 (M60334) cell
NCBI Description
                   surface glycoprotein [Homo sapiens]
                   >gi 1834460 emb_CAB06609 (Z84814) HLA-DRA*0102 [Homo
                   sapiens]
                   229718
 Seq. No.
                   LIB3196-039-P1-M1-D10
 Seq. ID
                   BLASTX
 Method
                   g2191127
 NCBI GI
                   475
```



```
101
Match length
% identity
                  (AF007269) A IG002N01.1 gene product [Arabidopsis thaliana]
NCBI Description
                  229719
Seq. No.
                  LIB3196-039-P1-M1-D3
Seq. ID
                  BLASTX
Method
                  q2252866
NCBI GI
                  162
BLAST score
                   3.0e-11
E value
                   43
Match length
                   74
% identity
                   (AF013294) contains region of similarity to SYT
NCBI Description
                   [Arabidopsis thaliana]
                   229720
Seq. No.
                   LIB3196-039-P1-M1-D8
Seq. ID
                   BLASTX
Method
                   q2832411
NCBI GI
                   463
BLAST score
                   2.0e-46
E value
                   109
Match length
                   81
% identity
                   (AJ002211) CXC chemokine [Homo sapiens] >gi_2911376
NCBI Description
                   (AF044197) B lymphocyte chemoattractant BLC; B-cell homing
                   chemokine [Homo sapiens] >gi_3169814 (AF029894) Angie [Homo
                   sapiens]
                   229721
Seq. No.
                   LIB3196-039-P1-M1-D9
Seq. ID
                   BLASTX
Method
                   q3600031
NCBI GI
                   228
BLAST score
                   7.0e-19
E value
                   95
Match length
                   60
% identity
                   (AF080119) similar to 2,4-dihydroxyhept-2-ene-1,7-dioic
NCBI Description
                   acid aldolases [Arabidopsis thaliana]
                   229722
 Seq. No.
 Seq. ID
                   LIB3196-039-P1-M1-E11
Method
                   BLASTX
                   g1363944
 NCBI GI
                   607
 BLAST score
                   2.0e-63
 E value
                   121
 Match length
                    100
 % identity
                   type I keratin 16 - human >gi_1195531 bbs 172338 (S79867)
 NCBI Description
                    type I keratin 16, K16 [human, epidermal keratinocytes,
                    Peptide, 473 aa] [Homo sapiens]
                    229723
 Seq. No.
                    LIB3196-039-P1-M1-E12
 Seq. ID
                   BLASTX
 Method
```

32942

g2191150

3.0e-37

384

NCBI GI

E value

BLAST score



```
82
Match length
% identity
NCBI Description (AF007269) similar to mitochondrial carrier family
                   [Arabidopsis thaliana]
                   229724
Seq. No.
                   LIB3196-039-P1-M1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1350945
BLAST score
                   255
E value
                   4.0e-22
Match length
                   64
                   83
% identity
                   40S RIBOSOMAL PROTEIN S17 >gi_1076596_pir__S51665 ribosomal protein S17 - tomato (fragment) >gi_603570_emb_CAA58444_
NCBI Description
                   (X83421) ribosomal protein S17 [Lycopersicon esculentum]
                   229725
Seq. No.
                   LIB3196-039-P1-M1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g730456
BLAST score
                   416
E value
                   6.0e-41
                   98
Match length
                   76
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S19
                   229726
Seq. No.
                   LIB3196-039-P1-M1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3914916
                   637
BLAST score
                   7.0e-67
E value
                   121
Match length
                   100
% identity
NCBI Description
                   40S RIBOSOMAL PROTEIN S4, Y ISOFORM
                   >gi 4432937 dbj BAA21076 (D50105) Y-chromosome linked
                   ribosomal protein S4 [Macaca fuscata]
                    229727
Seq. No.
Seq. ID
                   LIB3196-039-P1-M1-F11
Method
                   BLASTX
NCBI GI
                    g3947719
BLAST score
                    249
E value
                    2.0e-21
Match length
                    53
% identity
                    92 -
                    (AJ012653) ribosomal protein S28 [Prunus persica]
NCBI Description
                    >gi_3947721_emb_CAA10102_ (AJ012654) ribosomal protein S28
                    [Prunus persica] >gi 3947723 emb CAA10103 (AJ012655)
                    ribosomal protein S28 [Prunus persica]
                    229728
Seq. No.
```

Seq. ID LIB3196-039-P1-M1-F12

Method BLASTX NCBI GI g280816 BLAST score 138



9.0e-09 E value Match length 60 50 % identity keratin 13, type I, cytoskeletal, short form - human NCBI Description >gi\_30377\_emb\_CAA36673\_ (X52426) cytokeratin 13 [Homo sapiens] >gi\_3603253 (AF049259) keratin 13 [Homo sapiens] >gi 4504911 ref NP 002265.1 pKRT13 keratin 229729 Seq. No. LIB3196-039-P1-M1-F5 Seq. ID BLASTX Method g1705996 NCBI GI BLAST score 653 1.0e-68 E value 127 Match length 99 % identity COATOMER ALPHA SUBUNIT (ALPHA-COAT PROTEIN) (ALPHA-COP) NCBI Description (HEP-COP) >gi\_2144979\_pir\_ERHUAH coatomer complex alpha chain homolog - human >gi 1002369 (U24105) coatomer protein [Homo sapiens] 229730 Seq. No. LIB3196-039-P1-M1-F7 Seq. ID BLASTX Method g137578 NCBI GI 478 BLAST score 2.0e-48 E value Match length 110 87 % identity VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) NCBI Description >gi\_81545\_pir\_\_S06398 alpha-globulin type A precursor upland cotton >gi\_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi\_207906 (M18027) alpha globulin A [Artificial gene] >gi\_226119\_prf\_\_1410330A vicilin gene A [Saguinus oedipus]

Seq. No. 229731

Seq. ID LIB3196-039-P1-M1-F9

Method BLASTX NCBI GI a266392 594 BLAST score E value 8.0e-62 Match length 118 % identity

TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA NCBI Description

RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON

STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3

GAMMA) >gi\_346215\_pir\_\_A45017 transcription factor ISGF3

qamma chain - human >gi 184653 (M87503) IFN-alpha responsive transcription factor [Homo sapiens]

229732 Seq. No.

LIB3196-039-P1-M1-G2 Seq. ID

Method BLASTX NCBI GI g4105412 BLAST score 309 E value 2.0e-28



Match length 67 87 % identity

NCBI Description (AF045564) development-related protein [Rattus norvegicus]

Seq. No.

229733

Seq. ID

LIB3196-039-P1-M1-G3

Method NCBI GI BLASTX g3777617

BLAST score E value

291

Match length

2.0e-26 73

84

% identity

NCBI Description (AF097709) serine protease [Homo sapiens]

Seq. No.

229734

Seq. ID

LIB3196-039-P1-M1-G5

Method NCBI GI BLAST score BLASTX g137580 604

E value Match length

5.0e-63 119

98

% identity NCBI Description

VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72)

>gi\_72286\_pir\_\_FWCNAB alpha-globulin B precursor (clone C72) - upland cotton >gi 167375 (M16891) vicilin precursor

[Gossypium hirsutum]

Seq. No.

229735

Seq. ID

LIB3196-039-P1-M1-G6

Method BLASTX NCBI GI g123101 BLAST score 330 E value 7.0e-31 Match length 100 % identity 72

NCBI Description NONHISTONE CHROMOSOMAL PROTEIN HMG-14

>gi 107207 pir A33310 nonhistone chromosomal protein HMG-14 - human >gi 306863 (J02621) high mobility group protein 14 [Homo sapiens] >gi 386779 (M21339) high mobility group protein 14 [Homo sapiens] >gi\_3171155 (AF064861)

HMG-14 [Homo sapiens]

Seq. No. Seq. ID

229736

Method

LIB3196-039-P1-M1-G9

NCBI GI

BLASTX

BLAST score

g2995405

345

E value Match length 1.0e-32

109 63

% identity

NCBI Description (Y12432) polyprotein [Ananas comosus]

Seq. No.

229737

Seq. ID

LIB3196-039-P1-M1-H10

Method NCBI GI BLASTX q280816

624

BLAST score



```
E value
                     3.0e-65
 Match length
                    127
 % identity
                    98
 NCBI Description
                    keratin 13, type I, cytoskeletal, short form - human
                    >gi_30377_emb_CAA36673 (X52426) cytokeratin 13 [Homo
sapiens] >gi_3603253 (AF049259) keratin 13 [Homo sapiens]
                    >gi_4504911_ref NP_002265.1 pKRT13 keratin
 Seq. No.
                    229738
Seq. ID
                    LIB3196-039-P1-M1-H11
Method
                    BLASTX
NCBI GI
                    g3717946
BLAST score
                    172
E value
                    2.0e-15 *
Match length
                    81
% identity
                    62
NCBI Description (AJ005901) vag1 [Arabidopsis thaliana]
Seq. No.
                    229739
Seq. ID
                    LIB3196-039-P1-M1-H4
Method
                    BLASTX
NCBI GI
                    g3121828
BLAST score
                    596
E value
                    5.0e-62
Match length
                    124
% identity
                    92
NCBI Description
                    BENE PROTEIN >gi_2135423_pir__I38891 hypothetical protein -
                    human (fragment) >gi_1000712 (U17077) unknown [Homo
                    sapiens]
Seq. No.
                    229740
Seq. ID
                    LIB3196-039-P1-M1-H7
Method
                    BLASTX
NCBI GI
                    g631009
BLAST score
                    355
E value
                    9.0e-34
Match length
                    67
% identity
                    99
NCBI Description G-protein - chicken >gi_2119466_pir__I50230 G protein alpha
                    subunit - chicken >gi_454411 (L\overline{2}455\overline{0}) G protein alpha
                    subunit [Gallus gallus]
Seq. No.
                    229741
Seq. ID
                   LIB3196-039-P1-M1-H8
Method
                   BLASTX
NCBI GI
                   g3396079
BLAST score
                   250
E value
                   1.0e-21
Match length
                   97
% identity
                   47
NCBI Description
                   (AF080173) inositol 1,3,4-trisphosphate 5/6-kinase
                   [Arabidopsis thaliana]
```

Seq. No. 229742

Seq. ID LIB3196-040-P1-M1-A6

Method BLASTX NCBI GI g3745821



BLAST score 660 E value 2.0e-69 Match length 124 % identity 99

NCBI Description Chain A, Tubulin Alpha-Beta Dimer, Electron Diffraction

Seq. No.

229743 Seq. ID LIB3196-040-P1-M1-A8

Method BLASTX NCBI GI q119172 BLAST score 604 E value 5.0e-63 Match length 117 % identity 99

NCBI Description ELONGATION FACTOR 2 (EF-2) >gi\_2144947 pir EFHU2

translation elongation factor eEF-2 - human

>gi\_31106\_emb\_CAA35829\_ (X51466) elongation factor 2 [Homo sapiens] >gi\_31108\_emb\_CAA77750 (Z11692) human elongation factor 2 [Homo sapiens] >gi\_4503483 ref\_NP\_001952.1 pEEF2

eukaryotic translation elongation factor

Seq. No. 229744

Seq. ID LIB3196-040-P1-M1-B10

Method BLASTX NCBI GI q126156 BLAST score 655 E value 6.0e-69 Match length 128 % identity 98

NCBI Description LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)

>gi\_72288\_pir\_\_FWCNBB beta-globulin B precursor (clone 134)

- upland cotton >gi\_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi\_1171335 (U43727) legumin B [Gossypium hirsutum] >gi\_225582\_prf\_\_1306412C storage

protein C134 [Saguinus oedipus]

Seq. No. 229745

Seq. ID LIB3196-040-P1-M1-B7

Method BLASTX NCBI GI g3122673 BLAST score 407 E value 7.0e-40Match length 108 % identity 76

60S RIBOSOMAL PROTEIN L15 >gi\_2245027\_emb\_CAB10447 NCBI Description

(Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No. 229746

Seq. ID LIB3196-040-P1-M1-C10

Method BLASTX NCBI GI g2244979 BLAST score 422 E value 1.0e-41 Match length 122 % identity 68

NCBI Description (Z97340) similarity to enoyl-CoA hydratase [Arabidopsis

thaliana]



Seq. No. 229747

Seq. ID LIB3196-040-P1-M1-C11

Method BLASTX NCBI GI g125105 BLAST score 416 E value 3.0e-41 Match length 83 % identity 99

KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5) NCBI Description

(58 KD CYTOKERATIN) >gi\_88051\_pir\_\_A29904 keratin K5, 58K type II, epidermal (version 1) - human >gi 307082 (M21389)

keratin type II [Homo sapiens]

>gi\_4557890\_ref\_NP\_000415.1\_pKRT5\_ keratin

Seq. No. 229748

Seq. ID LIB3196-040-P1-M1-C2

Method BLASTX NCBI GI g544939 BLAST score 469 E value 4.0e-47Match length 138 % identity 70

NCBI Description (S68736) myosin heavy chain, MHC [rats, CCl4-cirrhotic

liver fat-storing cell line, Peptide, 882 aa] [Rattus sp.]

Seq. No. 229749

Seq. ID LIB3196-040-P1-M1-C4

Method BLASTX NCBI GI g417103 BLAST score 591 E value 2.0e-61 Match length 120 % identity 99

NCBI Description HISTONE H3.2, MINOR >gi\_282871\_pir\_\_S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563 (U09458) histone H3.2 [Medicago sativa]  $>gi_488567$  ( $\overline{U}09460$ ) histone H3.2 [Medicago sativa] >gi\_488569 (\overline{U}09461) histone H3.2 [Medicago sativa] >gi\_488575 (\overline{U}09464) histone H3.2

[Medicago sativa] >gi\_488577 (U09465) histone H3.2 [Medicago sativa] >gi\_510911 emb\_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi\_1435157 emb\_CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >gi\_3885890 (AFO93633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 229750

Seq. ID LIB3196-040-P1-M1-C6

Method BLASTX





```
NCBI GI
                    g728838
BLAST score
                    147
E value
                    2.0e-09
Match length
                    47
 % identity
                    14
NCBI Description ALU SUBFAMILY SX WARNING ENTRY !!!!
Seq. No.
                    229751
Seq. ID
                    LIB3196-040-P1-M1-D1
Method
                    BLASTX
NCBI GI
                    g2414156
BLAST score
                    652
E value
                    1.0e-68
Match length
                    124
% identity
                    100
NCBI Description (Y09787) delta-endotoxin [Bacillus thuringiensis]
Seq. No.
                    229752
Seq. ID
                   LIB3196-040-P1-M1-D10
Method
                    BLASTX
NCBI GI
                    g3915742
BLAST score
                    582
E value
                    2.0e-60
Match length
                    122
% identity
                    90
NCBI Description LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319
                    (M69188) legumin A [Gossypium hirsutum]
                   >gi_444320_prf 1906369A legumin A:ISOTYPE=D alloallele
                    [Gossypium hirsutum]
Seq. No.
                   229753
Seq. ID
                   LIB3196-040-P1-M1-D11
Method
                   BLASTX
NCBI GI
                   g3860274
BLAST score
                   204
E value
                   5.0e-16
Match length
                   53
% identity
                   70
NCBI Description
                   (AC005824) unknown protein [Arabidopsis thaliana]
                   >gi_4314397_gb_AAD15607 (AC006232) putative zinc finger
                   protein [Arabidopsis thaliana]
Seq. No.
                   229754
Seq. ID
                   LIB3196-040-P1-M1-D12
Method
                   BLASTX
NCBI GI
                   g1363944
BLAST score
                   649
E value
                   3.0e-68
Match length
                   129
% identity
                   100
NCBI Description type I keratin 16 - human >gi_1195531_bbs_172338 (S79867) type I keratin 16, K16 [human, epidermal keratinocytes,
                   Peptide, 473 aa] [Homo sapiens]
```

Seq. No. 229755
Seq. ID LIB319

Seq. ID LIB3196-040-P1-M1-D5

Method BLASTX



NCBI GI g1173055 BLAST score 606 E value 3.0e-63 Match length 121 % identity 99

NCBI Description 60S RIBOSOMAL PROTEIN L11 (L5) >gi\_541961\_pir\_\_S42497

ribosomal protein L11.e - alfalfa >gi\_1076504\_pir\_ S51819 RL5 ribosomal protein - alfalfa >gi\_463252\_emb\_CAA55090\_

(X78284) RL5 ribosomal protein [Medicago sativa]

Seq. No. 229756

Seq. ID LIB3196-040-P1-M1-D7

Method BLASTX
NCBI GI g2911060
BLAST score 236
E value 8.0e-20
Match length 95
% identity 36

NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

>gi\_3297826\_emb\_CAA19884.1\_ (AL031032) putative protein

[Arabidopsis thaliana]

Seq. No. 229757

Seq. ID LIB3196-040-P1-M1-D8

Method BLASTX
NCBI GI g106322
BLAST score 578
E value 5.0e-60
Match length 113
% identity 90

NCBI Description hypothetical protein (L1H 3' region) - human

Seq. No. 229758

Seq. ID LIB3196-040-P1-M1-E10

Method BLASTX
NCBI GI g2062154
BLAST score 283
E value 3.0e-25
Match length 101
% identity 61

NCBI Description (AC001645) hypothetical protein [Arabidopsis thaliana]

Seq. No. 229759

Seq. ID LIB3196-040-P1-M1-E2

Method BLASTX
NCBI GI g3820648
BLAST score 305
E value 5.0e-37
Match length 121
% identity 70

NCBI Description (Y12636) allene oxide synthase [Arabidopsis thaliana]

Seq. No. 229760

Seq. ID LIB3196-040-P1-M1-E8

Method BLASTX NCBI GI g400205 BLAST score 646



E value 6.0e-68 Match length 124 % identity 95

NCBI Description PROCOLLAGEN-LYSINE, 2-OXOGLUTARATE 5-DIOXYGENASE PRECURSOR

(LYSYL HYDROXYLASE) >gi\_420086\_pir\_\_A38206

procollagen-lysine 5-dioxygenase (EC 1.14.11.4) precursor - human >gi\_190074 (L06419) lysyl hydroxylase [Homo sapiens] >gi\_4557837\_ref\_NP\_000293.1\_pPLOD\_ procollagen-lysine 5-dioxygenase; lysine hydroxylase; procollagen-lysine,

2-oxoglutarate 5-dioxygenase; lysine, 2-oxoglutarate 5-dioxygenase

Seq. No. 229761

Seq. ID LIB3196-040-P1-M1-F10

Method BLASTX
NCBI GI g1724114
BLAST score 305
E value 7.0e-28
Match length 68
% identity 85

NCBI Description (U80041) Af10-protein [Avena fatua]

Seq. No. 229762

Seq. ID LIB3196-040-P1-M1-F12

Method BLASTX
NCBI GI g4126405
BLAST score 525
E value 1.0e-53
Match length 117
% identity 91

NCBI Description (AB011798) homolog to defender against apoptotic death 1

[Citrus unshiu]

Seq. No. 229763

Seq. ID LIB3196-040-P1-M1-F2

Method BLASTX
NCBI GI g1362819
BLAST score 211
E value 7.0e-17
Match length 114
% identity 40

NCBI Description HPBRII-7 protein - human >gi\_871299\_emb\_CAA47752\_ (X67337)

Human pre-mRNA cleavage factor I 68 kDa subunit [Homo sapiens] >gi\_871301\_emb\_CAA47751\_ (X67336) HPBRII-7 [Homo

sapiens]

Seq. No. 229764

Seq. ID LIB3196-040-P1-M1-F4

Method BLASTX
NCBI GI g1363944
BLAST score 678
E value 1.0e-71
Match length 136
% identity 100

NCBI Description type I keratin 16 - human >gi 1195531 bbs 172338 (S79867)

type I keratin 16, K16 [human, epidermal keratinocytes,

Peptide, 473 aa] [Homo sapiens]

Seq. No.

Seq. ID

229770

LIB3196-040-P1-M1-G2





```
Seq. No.
                   229765
Seq. ID
                   LIB3196-040-P1-M1-F5
Method
                   BLASTX
NCBI GI
                   g3184184
BLAST score
                   544
E value
                   7.0e-56
Match length
                   137
% identity
                   80
NCBI Description
                  (AB002134) airway trypsin-like protease [Homo sapiens]
Seq. No.
                   229766
Seq. ID
                   LIB3196-040-P1-M1-F8
Method
                   BLASTX
NCBI GI
                   q1209756
BLAST score
                   498
E value
                   1.0e-50
Match length
                   126
% identity
                   79
NCBI Description (U43629) integral membrane protein [Beta vulgaris]
Seq. No.
                   229767
Seq. ID
                   LIB3196-040-P1-M1-F9
Method
                   BLASTX
NCBI GI
                   g72287
BLAST score
                   575
E value
                   1.0e-59
Match length
                   109
% identity
                   100
NCBI Description
                  beta-globulin A precursor (clone 94) - upland cotton
                   (fragment) >gi_167377 (M16905) legumin precursor [Gossypium
                   hirsutum]
Seq. No.
                   229768
Seq. ID
                  LIB3196-040-P1-M1-G10
Method
                  BLASTX
NCBI GI
                  q586120
BLAST score
                  231
E value
                  3.0e-19
Match length
                  102
% identity
                  49
NCBI Description
                  TRICHOHYALIN >gi_539701_pir__A45973 trichohyalin - human
                  >gi_292836 (L09190) trichohyalin [Homo sapiens]
Seq. No.
                  229769
Seq. ID
                  LIB3196-040-P1-M1-G11
Method
                  BLASTX
NCBI GI
                  g1101029
BLAST score
                  476
E value
                  5.0e-48
Match length
                  110
% identity
NCBI Description
                  (U30891) pyruvate carboxylase precursor [Homo sapiens]
                  >gi_4505627_ref_NP_000911.1_pPC_ pyruvate carboxylase
```





```
Method
                   BLASTX
NCBI GI
                   g3122232
BLAST score
                   178
E value
                   5.0e-13
Match length
                   99
% identity
                   51
NCBI Description
                   MITOCHONDRIAL HEAT SHOCK 22 KD PROTEIN PRECURSOR
                   >gi_1669866 (U72958) AtHSP23.6-mito [Arabidopsis thaliana]
                   >gi_4454008_emb_CAA23061_ (AL035396) Arabidopsis
                   mitochondrion-localized small heat shock protein
                   (AtHSP23.6-mito) [Arabidopsis thaliana]
Seq. No.
                   229771
Seq. ID
                   LIB3196-040-P1-M1-G5
Method
                   BLASTX
NCBI GI
                   g544184
BLAST score
                   646
E value
                   7.0e-68
Match length
                   133
% identity
                   81
NCBI Description
                  4-ALPHA-GLUCANOTRANSFERASE PRECURSOR (AMYLOMALTASE)
                   (DISPROPORTIONATING ENZYME) (D-ENZYME)
                   >gi_322785_pir__A45049 4-alpha-glucanotransferase (EC
                   2.4.1.25) - potato >gi_296692 emb_CAA48630 (X68664)
                   4-alpha-glucanotransferase [Solanum tuberosum]
Seq. No.
                   229772
Seq. ID
                   LIB3196-040-P1-M1-G7
Method
                   BLASTX
NCBI GI
                   g3115204
BLAST score
                   149
E value
                   1.0e-09
Match length
                   82
% identity
                   46
NCBI Description
                  (Y12059) strong homology to human RING3 sequence [Homo
                   sapiens]
Seq. No.
                   229773
Seq. ID
                  LIB3196-040-P1-M1-G9
Method
                  BLASTX
NCBI GI
                  g2118965
BLAST score
                  631
E value
                   4.0e-66
Match length
                  125
% identity
                  32
NCBI Description polyubiquitin - bovine (fragment) >gi 163573 (M62428)
                  polyubiquitin [Bos taurus]
Seq. No.
                  229774
Seq. ID
                  LIB3196-040-P1-M1-H1
Method
                  BLASTX
NCBI GI
                  g4455253
BLAST score
                  389
E value
                  9.0e-38
Match length
                  110
% identity
NCBI Description
                 (AL035523) superoxide dismutase (EC 1.15.1.1)
```



229775



## (Fe)(fragment) [Arabidopsis thaliana]

Seq. ID LIB3196-040-P1-M1-H10
Method BLASTX
NCBI GI g126156
BLAST score 428
E value 2.0e-42
Match length 120
% identity 71
NCBI Description LEGUMIN B PRECURSOR (

Seq. No.

NCBI Description LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)

>gi\_72288\_pir\_\_FWCNBB beta-globulin B precursor (clone 134)

- upland cotton >gi\_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi\_1171335 (U43727) legumin B [Gossypium hirsutum] >gi\_225582\_prf\_\_1306412C storage

protein C134 [Saguinus oedipus]

Seq. No. 229776

Seq. ID LIB3196-040-P1-M1-H6

Method BLASTX
NCBI GI g3395938
BLAST score 318
E value 2.0e-29
Match length 107
% identity 34

NCBI Description (AF076924) polypyrimidine tract-binding protein homolog

[Arabidopsis thaliana]

Seq. No. 229777

Seq. ID LIB3196-040-P1-M1-H7

Method BLASTX
NCBI GI g2791834
BLAST score 407
E value 6.0e-50
Match length 103
% identity 99

NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta]

Seq. No. 229778

Seq. ID LIB3196-041-P1-M1-A10

Method BLASTX
NCBI GI g3874039
BLAST score 211
E value 7.0e-17
Match length 109
% identity 37

NCBI Description (Z75526) Weak similarity to Staphyloccus autolysin gene

(TR:G765072); cDNA EST EMBL:M89336 comes from this gene; cDNA EST yk505d12.3 comes from this gene [Caenorhabditis

elegans]

Seq. No. 229779

Seq. ID LIB3196-041-P1-M1-A5

Method BLASTX
NCBI GI g4490331
BLAST score 373
E value 7.0e-36





Match length 97 % identity 73 (AL035656) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 229780 Seq. ID LIB3196-041-P1-M1-A7 Method BLASTX NCBI GI g167367 BLAST score 468 E value 5.0e-47 Match length 112 % identity 82 NCBI Description (L08199) peroxidase [Gossypium hirsutum] Seq. No. 229781 Seq. ID LIB3196-041-P1-M1-A8 Method BLASTX NCBI GI g2911247 BLAST score 289 E value 4.0e-26 Match length 70 % identity (AF047863) PNS specific microtubule-associated protein tau, NCBI Description adult isoform [Homo sapiens] Seq. No. 229782 Seq. ID LIB3196-041-P1-M1-B12 Method BLASTX NCBI GI g3914477 BLAST score 317 E value 3.0e-29Match length 56 % identity 100 NCBI Description PROTEASE SERINE-LIKE 1 PRECURSOR (NORMAL EPITHELIAL CELL-SPECIFIC 1) >gi\_1835925\_bbs\_178917 (S82666) serine protease homolog=NES1 [human, mammary epithelial cells, 76N, Peptide, 276 aa] [Homo·sapiens] >gi\_2558912 (AF024605) serine protease-like protease [Homo sapiens] >gi\_3065711 (AF055481) normal epithelial cell-specific 1 [Homo sapiens] >gi\_4506157\_ref\_NP\_002767.1\_pPRSSL1\_ protease, serine-like, Seq. No. 229783 Seq. ID LIB3196-041-P1-M1-B2 Method BLASTX NCBI GI g2459421

BLAST score 410 E value 3.0e-40 Match length 110

% identity 68

NCBI Description (AC002332) putative calcium-binding EF-hand protein

[Arabidopsis thaliana]

Seq. No. 229784

Seq. ID LIB3196-041-P1-M1-B3

Method BLASTX NCBI GI g2995990 BLAST score 209



E value 8.0e-17 Match length 79 % identity 59

NCBI Description (AF053746) dormancy-associated protein [Arabidopsis thaliana] >gi 2995992 (AF053747) dormancy-associated

protein [Arabidopsis thaliana]

Seq. No. 229785

Seq. ID LIB3196-041-P1-M1-B4

Method BLASTX
NCBI GI g3044212
BLAST score 134
E value 6.0e-13
Match length 87
% identity 48

NCBI Description (AF057043) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No. 229786

Seq. ID LIB3196-041-P1-M1-B7

Method BLASTX
NCBI GI g3127127
BLAST score 424
E value 8.0e-42
Match length 101
% identity 88

NCBI Description (AF061016) UDP-glucose dehydrogenase [Homo sapiens]

>gi\_3452405\_emb\_CAA07609 (AJ007702) UDPglucose

dehydrogenase [Homo sapiens]

>gi\_4507813\_ref\_NP\_003350.1\_pUGDH\_ UDP-glucose

dehydrogenase

Seq. No. 229787

Seq. ID LIB3196-041-P1-M1-C10

Method BLASTX
NCBI GI g2832661
BLAST score 154
E value 3.0e-16
Match length 105
% identity 46

NCBI Description (AL021710) pherophorin - like protein [Arabidopsis

thaliana]

Seq. No. 229788

Seq. ID LIB3196-041-P1-M1-C11 Method BLASTX

Method BLASTX
NCBI GI g2522230
BLAST score 238
E value 4.0e-20
Match length 125
% identity 39

NCBI Description (AB007467) retrotransposon-like gene; the first amino acid

was determined to be leucine [Vicia faba]

Seq. No. 229789

Seq. ID LIB3196-041-P1-M1-C5

Method BLASTX NCBI GI g3452507



BLAST score 598 E value 3.0e-62 Match length 132 % identity 86

NCBI Description (AJ010483) CtBP1 protein [Mus musculus]

Seq. No.

229790

Seq. ID LIB3196-041-P1-M1-C6

Method BLASTX
NCBI GI g1350762
BLAST score 348
E value 2.0e-33
Match length 68
% identity 99

NCBI Description 60S RIBOSOMAL PROTEIN L6 (TAX-RESPONSIVE ENHANCER ELEMENT

BINDING PROTEIN 107) (TAXREB107) (NEOPLASM-RELATED PROTEIN

C140) >gi\_2136251\_pir\_\_I51803 TAXREB107 - human

>gi\_433416\_dbj\_BAA04491\_ (D17554) TAXREB107 [Homo sapiens]

Seq. No.

Seq. ID LIB3196-041-P1-M1-C7

229791

Method BLASTX
NCBI GI g3738257
BLAST score 448
E value 1.0e-44
Match length 94
% identity 94

NCBI Description (AB018410) cytosolic phosphoglycerate kinase 1 [Populus

nigra]

Seq. No. 229792

Seq. ID LIB3196-041-P1-M1-C9

Method BLASTX
NCBI GI g1350681
BLAST score 649
E value 3.0e-68
Match length 130
% identity 98

NCBI Description 60S RIBOSOMAL PROTEIN L1 (L4)

Seq. No.

. 229793

Seq. ID LIB3196-041-P1-M1-D1

Method BLASTX
NCBI GI g322750
BLAST score 535
E value 6.0e-55
Match length 105
% identity 100

NCBI Description ubiquitin / ribosomal protein CEP52 - wood tobacco

>gi\_170217 (M74100) ubiquitin fusion protein [Nicotiana

sylvestris]

Seq. No. 229794

Seq. ID LIB3196-041-P1-M1-D10

Method BLASTX NCBI GI g2443887 BLAST score 490

Seq. No.

Seq. ID

229799

LIB3196-041-P1-M1-D9





```
E value
                      1.0e-49
Match length
                     120
% identity
                     78
                     (AC002294) Similar to transcription factor
NCBI Description
                     gb Z46606 1658307 and others [Arabidopsis thaliana]
Seq. No.
                     229795
Seq. ID
                     LIB3196-041-P1-M1-D11
Method
                     BLASTX
NCBI GI
                     g2129604
BLAST score
                     184
E value
                     1.0e-13
Match length
                     50
% identity
                     76
NCBI Description GTP-binding protein 1 - Arabidopsis thaliana
                     >gi_2129607_pir__S71584 GTP-binding protein ATBG1 -
Arabidopsis thaliana >gi_1184981 (U46924) ATGB1
                     [Arabidopsis thaliana]
Seq. No.
                     229796
Seq. ID
                     LIB3196-041-P1-M1-D12
Method
                     BLASTX
NCBI GI
                     g140551
BLAST score
                     564
E value
                     3.0e-58
Match length
                     124
% identity
                     88
NCBI Description
                     HYPOTHETICAL 250 KD PROTEIN (ORF 2131)
                     >gi_81505_pir__S01446 hypothetical protein 2131 - spinach
chloroplast >gi_12246_emb_CAA30743_ (X07908) ORF 2131 (AA
                     1-2131) [Spinacia oleracea]
Seq. No.
                     229797
Seq. ID
                     LIB3196-041-P1-M1-D3
Method
                     BLASTX
NCBI GI
                     g2660676
BLAST score
                     155
E value
                     2.0e-10
Match length
                     32
% identity
                     91
NCBI Description (AC002342) Dreg-2 like protein [Arabidopsis thaliana]
Seq. No.
                     229798
Seq. ID
                     LIB3196-041-P1-M1-D5
Method
                     BLASTX
NCBI GI
                     g125101
BLAST score
                     175
E value
                     1.0e-12
Match length
                     38
% identity
NCBI Description KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4)
                     (CYTOSKELETAL 57 KD KERATIN) >gi_91010_pir__A23518 keratin, 57K type II cytoskeletal - mouse >gi_52785_emb_CAA27207_
                     (X03491) 57 kd keratin (aa 1-524) [Mus musculus]
```





```
Method
                  BLASTX
                  g2317908
NCBI GI
BLAST score
                   471
                   2.0e-47
E value
Match length
                  114
                   41
% identity
NCBI Description (U89959) Unknown protein [Arabidopsis thaliana]
                  229800
Seq. No.
                  LIB3196-041-P1-M1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1350786
                  298
BLAST score
                   4.0e-27
E value
Match length
                   96
% identity
                   64
                  PUTATIVE 60S RIBOSOMAL PROTEIN >gi_285945_dbj_BAA03494
NCBI Description
                   (D14660) KIAA00104 [Homo sapiens] >gi_3947438 (AC005034)
                  ribosomal protein-like [Homo sapiens]
                   229801
Seq. No.
                  LIB3196-041-P1-M1-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4467153
                   524
BLAST score
                   1.0e-53
E value
                   118
Match length
% identity
                   (AL035540) putative thaumatin-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   229802
Seq. No.
                   LIB3196-041-P1-M1-E5
Seq. ID
Method
                   BLASTX
                   g184226
NCBI GI
BLAST score
                   536
                   6.0e-55
E value
Match length
                   109
% identity
                   49
NCBI Description (M83205) HLF2 [Homo sapiens]
                   229803
Seq. No.
                   LIB3196-041-P1-M1-E9
Seq. ID
                   BLASTX
Method
                   q547753
NCBI GI
                   466
BLAST score
                   5.0e-47
E value
                   98
Match length
                   97
% identity
NCBI Description KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)
                   229804
Seq. No.
                   LIB3196-041-P1-M1-F1
Seq. ID
                   BLASTX
Method
                   g122085
NCBI GI
BLAST score
                   432
```

6.0e-43

E value



Match length

NCBI Description

% identity

105

HISTONE H3 >gi\_81641\_pir\_\_S06250 histone H3 - Arabidopsis thaliana >gi\_82482 pir S04099 histone H3 (variant H3R-21) - rice >gi\_1362194\_pir\_\_S57626 histone H3 - maize >gi\_20251\_emb\_CAA31969\_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi\_20253 emb CAA31970 (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi 168493 (M36658) histone H3 (H3C3) [Zea mays] >gi 168495 (M13378) histone H3 [Zea mays] >gi\_168497 (M13379) histone H3 [Zea mays] >gi\_168506 (M35388) histone H3 [Zea mays] >gi\_169655 (M77493) histone H3 [Petroselinum crispum] >gi\_169657 (M77494) histone H3 [Petroselinum crispum] >gi 169659 (M77495) histone H3 [Petroselinum crispum] >gi\_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi\_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi 886738 emb CAA59111 (X84377) histone 3 [Zea mays] >gi  $1\overline{040764}$  (M35 $\overline{387}$ ) histone H3 [Arabidopsis thaliana] >gi 1314779 (U54827) histone H3 homolog [Brassica napus] >gi 1531754 emb CAA57811 (X82414) Histone H3 [Asparagus officinalis] >gi 1667592 (U77296) histone 3 [Oryza sativa] >gi\_3249101 (AC003114) Match to histone H3 gene gb\_M17131 and gb M35387 from A. thaliana. ESTs gb\_H76511 gb\_ $\overline{\text{H}}$ 76255, gb AA7 $\overline{1}$ 2452, gb N65260 and gb T42306 come from this gene. [Arabidopsis thaliana] >gi\_225459\_prf 1303352A histone H3 [Helicoverpa zea] >gi 225839 prf 1314298B histone H3 [Arabidopsis thaliana]

229805 Seq. No. Seq. ID LIB3196-041-P1-M1-F4 Method BLASTX NCBI GI g1652434 BLAST score 303

E value 1.0e-27 Match length 126 % identity 51

NCBI Description (D90905) N-acetylglutamate kinase [Synechocystis sp.]

Seq. No. 229806

Seq. ID LIB3196-041-P1-M1-G12

Method BLASTX NCBI GI q2804273 BLAST score 679 E value 9.0e-72 Match length 131 % identity

NCBI Description (D89980) alpha actinin 4 [Homo sapiens]

Seq. No. 229807

Seq. ID LIB3196-041-P1-M1-G2

Method BLASTX NCBI GI g3127127 BLAST score 190 E value 8.0e-15 46 Match length % identity

(AF061016) UDP-glucose dehydrogenase [Homo sapiens] NCBI Description >gi\_3452405\_emb\_CAA07609 (AJ007702) UDPglucose





```
dehydrogenase [Homo sapiens]
                   >gi_4507813_ref_NP_003350.1_pUGDH_UDP-glucose
                   dehydrogenase
Seq. No.
                   229808
Seq. ID
                  LIB3196-041-P1-M1-G3
Method
                  BLASTX
NCBI GI
                   g167311
BLAST score
                   496
E value
                   2.0e-50
Match length
                   113
% identity
                   86
                   (M83301) 2S albumin storage protein [Gossypium hirsutum]
NCBI Description
                  229809
Seq. No.
Seq. ID
                  LIB3196-041-P1-M1-G4
Method
                  BLASTX
NCBI GI
                  g114549
BLAST score
                  491
E value
                  1.0e-49
Match length
                  128
                  81
% identity
NCBI Description
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
                  >gi_106207_pir__A33370 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain precursor, mitochondrial - human
                  >gi_179281 (M27132) ATP synthase beta subunit precursor
                   [Homo sapiens]
Seq. No.
                  229810
Seq. ID
                  LIB3196-041-P1-M1-G5
Method
                  BLASTX
NCBI GI
                  g167367
BLAST score
                  464
E value
                  1.0e-46
Match length
                  120
% identity
NCBI Description
                  (L08199) peroxidase [Gossypium hirsutum]
                  229811
Seq. No.
Seq. ID
                  LIB3196-041-P1-M1-G6
Method
                  BLASTX
NCBI GI
                  q2765244
BLAST score
                  282
E value
                  3.0e-25
Match length
                  118
```

NCBI Description (Y12807) invertase inhibitor homolog [Arabidopsis thaliana]

Seq. No. 229812

% identity

Seq. ID LIB3196-041-P1-M1-G7

Method BLASTX
NCBI GI g266691
BLAST score 243
E value 8.0e-21
Match length 88
% identity 61

NCBI Description OLEOSIN 16.4 KD >gi\_167361 (L00934) 16.4 kDa oleosin





## [Gossypium hirsutum]

```
229813
Seq. No.
Seq. ID
                   LIB3196-041-P1-M1-G8
Method
                   BLASTX
                   q3650032
NCBI GI
BLAST score
                   279
                   7.0e-25
E value
                   60
Match length
% identity
                   70
                   (AC005396) gibberellin-regulated protein GAST1-like
NCBI Description
                   [Arabidopsis thaliana]
                   229814
Seq. No.
                   LIB3196-041-P1-M1-G9
Seq. ID
Method
                   BLASTX
                   g386850
NCBI GI
                   572
BLAST score
                   3.0e-59
E value
                   115
Match length
                   99
% identity
                  (M19723) keratin K5 [Homo sapiens]
NCBI Description
                   229815
Seq. No.
                   LIB3196-041-P1-M1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3337356
BLAST score
                   364
                   6.0e-35
E value
                   70
Match length
                   97
% identity
                   (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
                   229816
Seq. No.
                   LIB3196-041-P1-M1-H3
Seq. ID
Method
                   BLASTX
                   g544939
NCBI GI
BLAST score
                   465
                   1.0e-46
E value
Match length
                   131
% identity
                   (S68736) myosin heavy chain, MHC [rats, CCl4-cirrhotic
NCBI Description
                   liver fat-storing cell line, Peptide, 882 aa] [Rattus sp.]
                   229817
Seq. No.
Seq. ID
                   LIB3196-041-P1-M1-H4
                   {\tt BLASTX}
Method
                   g3702327
NCBI GI
BLAST score
                   150
                   9.0e-10
E value
Match length
                   92
% identity
                   41
                   (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
```

229818

LIB3196-041-P1-M1-H6

Seq. No. Seq. ID

```
Method
                   BLASTX
                   q4105683
NCBI GI
                   429
BLAST score
                   2.0e-42
E value
                   119
Match length
% identity
                   63
                   (AF049892) unknown [Oryza sativa] >gi_4105692 (AF050155)
NCBI Description
                   embryo-specific protein [Oryza sativa subsp. indica]
                   229819
Seq. No.
                   LIB3196-041-P1-M1-H7
Seq. ID
Method
                   BLASTX
                   g3115374
NCBI GI
BLAST score
                   174
                   9.0e-13
E value
                   90
Match length
% identity
                   46
                   (AF002016) acyl CoA oxidase homolog [Cucurbita sp.]
NCBI Description
                   229820
Seq. No.
                   LIB3196-041-P1-M1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1694976
BLAST score
                   352
                   2.0e-33
E value
                   99
Match length
                   68
% identity
NCBI Description
                   (Y09482) HMG1 [Arabidopsis thaliana]
                   >gi 2832361 emb CAA74402 (Y14073) HMG protein [Arabidopsis
                   thaliana]
                   229821
Seq. No.
                   LIB3196-042-P1-M1-A10
Seq. ID
Method
                   BLASTX
                   g1199772
NCBI GI
                   201
BLAST score
                   9.0e-16
E value
Match length
                   43
% identity
                   84
                   (D83226) extensin like protein [Populus nigra]
NCBI Description
                   >gi_1199774_dbj_BAA11855_ (D83227) extensin like protein
                   [Populus nigra]
                   229822
Seq. No.
                   LIB3196-042-P1-M1-A3
Seq. ID
                   BLASTX
Method
                   g3746652
NCBI GI
BLAST score
                   571
                   4.0e-59
E value
Match length
                   127
                   88
% identity
NCBI Description (AF070523) JWA protein [Homo sapiens]
```

Seq. ID LIB3196-042-P1-M1-A9

229823

Method BLASTX NCBI GI g3334138

Seq. No.

NCBI Description





```
BLAST score
                  535
                  6.0e-55
E value
                  119
Match length
% identity
                  82
                  CALNEXIN HOMOLOG PRECURSOR >gi 669003 (U20502) calnexin
NCBI Description
                  [Glycine max]
                  229824
Seq. No.
                  LIB3196-042-P1-M1-B11
Seq. ID
                  BLASTX
Method
                  g137578
NCBI GI
BLAST score
                  396
                  1.0e-38
E value
                  108
Match length
% identity
                  75
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                  >gi_81545_pir__S06398 alpha-globulin type A precursor -
                  upland cotton >gi 167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                   [Artificial gene] >gi 226119 prf 1410330A vicilin gene A
                   [Saguinus oedipus]
                  229825
Seq. No.
                  LIB3196-042-P1-M1-B3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2498829
BLAST score
                  134
                   3.0e-12
E value
Match length
                  43
% identity
                  88
                  RETINA-SPECIFIC 15.7 KD PROTEIN >gi_2136811_pir__I45978
NCBI Description
                   retina-specific 15.7 kDa protein - bovine >gi_163673
                   (M34915) retina-specific 15.7 kDa protein [Bos taurus]
                   >qi 356830 prf 1211339A protein, retina specific [Bos
                   taurus]
                   229826 .
Seq. No.
                  LIB3196-042-P1-M1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2351035
BLAST score
                   600
                   2.0e-62
E value
                   126
Match length
                   90
% identity
                  (AB004930) Smad 3 [Homo sapiens]
NCBI Description
                   229827
Seq. No.
                  LIB3196-042-P1-M1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2497367
                   372
BLAST score
                   4.0e-68
E value
Match length
                   127
% identity
                  HYPOTHETICAL PROTEIN KIAA0274 >gi 1665813 dbj BAA13403
```

32964

(S55864) [Homo sapiens]

(D87464) Similar to S.cerevisiae hypothetical protein N0330

Match length

% identity





```
Seq. No.
                   229828
                   LIB3196-042-P1-M1-C4
Seq. ID
                   BLASTX
Method
                   g3176726
NCBI GI
BLAST score
                   294
                   1.0e-26
E value
                   93
Match length
                   60
% identity
                   (AC002392) putative serine proteinase [Arabidopsis
NCBI Description
                   thaliana]
                   229829
Seq. No.
                   LIB3196-042-P1-M1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1705678
                   580
BLAST score
E value
                   3.0e-60
                   120
Match length
                   49
 % identity
                   CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
NCBI Description
                   PROTEIN HOMOLOG) (VCP) >gi 862480 (U20213)
                   valosin-containing protein [Glycine max]
Seq. No.
                   229830
                   LIB3196-042-P1-M1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2833388
BLAST score
                   436
                   2.0e-43
E value
                   113
Match length
 % identity
                   75
                   GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR
NCBI Description
                   >gi 629660 pir S43341 ADPglucose--starch
                   glucosyltransferase (EC 2.4.1.21) precursor - cassava
                   >gi_437042_emb_CAA52273_ (X74160) starch (bacterial
                   glycogen) synthase [Manihot esculenta]
 Seq. No.
                   229831
                   LIB3196-042-P1-M1-C8
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g2648442
                   179
 BLAST score
 E value
                   3.0e-13
                   110
Match length
 % identity
                    (AE000959) cell division control protein 48, AAA family
 NCBI Description
                    (cdc48-2) [Archaeoglobus fulgidus]
                   229832
 Seq. No.
                   LIB3196-042-P1-M1-C9
 Seq. ID
Method
                   BLASTX
* NCBI GI
                   g266690
 BLAST score
                   338
                   7.0e-32
E value
```

NCBI GI





```
NCBI Description OLEOSIN 18.2 KD >gi_167363 (L00935) 18.2 kDa oleosin
                   [Gossypium hirsutum] >gi_167365 (L00936) 18.2 kDa oleosin
                   [Gossypium hirsutum]
Seq. No.
                   229833
Seq. ID
                   LIB3196-042-P1-M1-D1
                   BLASTX
Method
NCBI GI
                   q1514614
BLAST score
                   141
                   2.0e-11
E value
Match length
                   119
                   40
% identity
                  (X92842) nuclear protein [Mus musculus]
NCBI Description
                   229834
Seq. No.
Seq. ID
                   LIB3196-042-P1-M1-D5
Method
                   BLASTX
NCBI GI
                   q339743
BLAST score
                   200
                   1.0e-31
E value
                   71
Match length
                   91
% identity
                   (M55913) tumor necrosis factor-beta [Homo sapiens]
NCBI Description
                   >gi 4505031 ref_NP_000586.1,pLTA lymphotoxin alpha
                   (formerly tumor necrosis factor beta)
                   229835
Seq. No.
                   LIB3196-042-P1-M1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3901014
BLAST score
                   234
                   1.0e-19
E value
Match length
                   55
% identity
                   (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                   sylvatica]
                   229836
Seq. No.
Seq. ID
                   LIB3196-042-P1-M1-E11
Method
                   BLASTX
NCBI GI
                   q135858
                   231
BLAST score
                   2.0e-21
E value
                   88
Match length
% identity
                   68
                   TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
NCBI Description
                   >gi 99760_pir__S22201 tonoplast intrinsic protein alpha -
                   Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis
                   thaliana] >gi 166623 (M84343) tonoplast intrinsic protein
                   [Arabidopsis thaliana] >gi 445128_prf 1908432A tonoplast
                   intrinsic protein alpha [Arabidopsis thaliana]
                   229837
Seq. No.
                   LIB3196-042-P1-M1-E6
Seq. ID
                   BLASTX
Method
```

32966

g1707480





```
146
BLAST score
                   3.0e-09
E value
                   71
Match length
                   42
% identity
                  (Y08614) CRM1 [Homo sapiens]
NCBI Description
Seq. No.
                   229838
                   LIB3196-042-P1-M1-E7
Seq. ID
                   BLASTX
Method
                   g729887
NCBI GI
                   552
BLAST score
                   4.0e-57
E value
                   121
Match length
                   98
% identity
                  TYROSINE-PROTEIN KINASE CSK (C-SRC KINASE)
NCBI Description
                   (PROTEIN-TYROSINE KINASE CYL) >gi_88519_pir__JH0559
                   protein-tyrosine kinase (EC 2.7.1.112) CSK - human
                   >gi_30256_emb_CAA42556_ (X59932) c-src-kinase [Homo
                   sapiens] >gi 30315 emb CAA42713 (X60114) put. cytoplasmic
                   tyrosine kinase [Homo sapiens]
                   229839
Seq. No.
Seq. ID
                   LIB3196-042-P1-M1-F2
Method
                   BLASTX
                   g852428
NCBI GI
BLAST score
                   473
                   1.0e-47
E value
Match length
                   101
% identity
                   88
                   (U09202) ornithine decarboxylase antizyme [Homo sapiens]
NCBI Description
                   229840
Seq. No.
Seq. ID
                   LIB3196-042-P1-M1-F5
Method
                   BLASTX
NCBI GI
                   g3877201
BLAST score
                   323
                   5.0e-30
E value
                   123
Match length
% identity
                   48
                   (Z70780) cDNA EST yk465d10.3 comes from this gene; cDNA EST
NCBI Description
                   yk465d10.5 comes from this gene; cDNA EST yk481d9.5 comes
                   from this gene [Caenorhabditis elegans]
                   229841
Seq. No.
                   LIB3196-042-P1-M1-F7
Seq. ID
                   BLASTX
Method
                   g1304227
NCBI GI
                   405
BLAST score
                   1.0e-39
E value
Match length
                   88
                   83
% identity
                   (D63781) Epoxide hydrolase [Glycine max]
NCBI Description
```

>gi\_2764804\_emb\_CAA55293\_ (X78547) epoxide hydrolase

[Glycine max]

Seq. No. 229842

Seq. ID LIB3196-042-P1-M1-G1





```
BLASTX
Method
                  g996057
NCBI GI
BLAST score
                   621
                   6.0e-65
E value
                  125
Match length
                   96
% identity
NCBI Description (X90872) associated to Golgi apparatus [Homo sapiens]
                   229843
Seq. No.
                  LIB3196-042-P1-M1-G2
Seq. ID
                  BLASTX
Method
NCBI GI
                   g728831
BLAST score
                   139
                   9.0e-18
E value
Match length
                   172
                   15
% identity
NCBI Description ALU SUBFAMILY J WARNING ENTRY !!!!
                   229844
Seq. No.
                   LIB3196-042-P1-M1-G3
Seq. ID
                   BLASTX
Method
                   g1336807
NCBI GI
                   310
BLAST score
                   1.0e-28
E value
                   112
Match length
% identity
                   (S81193) CEN=GTP-binding protein homolog
NCBI Description
                   [Antirrhinum=snapdragons, Peptide, 181 aa] [Antirrhinum]
                   >gi_1587482_prf__2206476A CEN gene [Antirrhinum sp.]
                   229845
Seq. No.
                   LIB3196-042-P1-M1-G7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3024889
BLAST score
                   214
                   2.0e-17
E value
Match length
                   87
                   49
% identity
                   HYPOTHETICAL PROTEIN KIAA0288 (HA6116)
NCBI Description
                   >gi 2564324 dbj BAA22957_ (AB006626) KIAA0288 [Homo
                   sapiens]
                   229846
Seq. No.
                   LIB3196-042-P1-M1-H1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q266691
BLAST score
                   265
                   2.0e-23
E value
                   51
Match length
                   100
% identity
                   OLEOSIN 16.4 KD >gi 167361 (L00934) 16.4 kDa oleosin
NCBI Description
                   [Gossypium hirsutum]
                   229847
Seq. No.
                   LIB3196-042-P1-M1-H10
Seq. ID
Method
                   BLASTX
```

q2749943

NCBI GI





```
353-.
BLAST score
                   9.0e-34
E value
                   92
Match length
                   66
% identity
                  (U71244) pathogenesis-related group 5 protein [Brassica
NCBI Description
                  rapa]
                   229848
Seq. No.
                  LIB3196-042-P1-M1-H3
Seq. ID
                   BLASTX
Method
                   g2959872
NCBI GI
                   176
BLAST score
                   8.0e-27
E value
                  73
Match length
                   88
% identity
                  (AJ002308) synaptogyrin 2 [Homo sapiens]
NCBI Description
                   229849
Seq. No.
                   LIB3196-042-P1-M1-H7
Seq. ID
                   BLASTX
Method
                   g37848
NCBI GI
                   216
BLAST score
                   2.0e-17
E value
Match length
                   65
                   69
% identity
                  (X16478) vimentin N-terminal fragment (AA 1-135) [Homo
NCBI Description
                   sapiens]
Seq. No.
                   229850
                   LIB3196-043-P1-M1-A1
Seq. ID
                   BLASTX
Method
                   g2496887
NCBI GI
                   239
BLAST score
                   4.0e-20
E value
                   100
Match length
                   54
% identity .
                   HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III
NCBI Description
                   >gi 732538 (U22832) C09F5.2 gene product [Caenorhabditis
                   elegans]
                   229851
Seq. No.
                   LIB3196-043-P1-M1-A10
Seq. ID
                   BLASTX
Method
                   g123644
NCBI GI
                   591
BLAST score
                   2.0e-61
E value
                   131
Match length
                   92
% identity
                   HEAT SHOCK COGNATE 71 KD PROTEIN >gi_108737_pir__S11456
NCBI Description
                   heat shock cognate protein, 79K - bovine
                   >gi_428_emb_CAA37823_ (X53827) 79KDa heat shock cognate
                   protein [Bos taurus]
                   229852
Seq. No.
                   LIB3196-043-P1-M1-A2
Seq. ID
                   BLASTX
Method
```

32969

g3738257

NCBI GI



BLAST score 483 E value 9.0e-49 Match length 100 % identity 94

NCBI Description (AB018410) cytosolic phosphoglycerate kinase 1 [Populus

nigra]

Seq. No. 229853

Seq. ID LIB3196-043-P1-M1-A4

Method BLASTX
NCBI GI g417031
BLAST score 353
E value 2.0e-33
Match length 70
% identity 99

NCBI Description INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE

NUCLEOTIDE-BINDING PROTEIN 1) >gi\_87609\_pir\_A41268 guanine

nucleotide-binding protein 1 - human >gi 183002 (M55542)

guanylate binding protein isoform I [Homo sapiens]
>gi\_4503939\_ref\_NP\_002044.1\_pGBP1\_ guanylate binding

protein 1, interferon-inducible, 67kD

Seq. No. 229854

Seq. ID LIB3196-043-P1-M1-A5

Method BLASTX
NCBI GI g225580
BLAST score 568
E value 9.0e-59
Match length 126
% identity 88

NCBI Description storage protein C72 [Saguinus oedipus]

Seq. No. 229855

Seq. ID LIB3196-043-P1-M1-B10

Method BLASTX
NCBI GI g1732511
BLAST score 360
E value 2.0e-34
Match length 95
% identity 73

NCBI Description (U62742) Ran binding protein 1 homolog [Arabidopsis

thaliana]

Seq. No. 229856

Seq. ID LIB3196-043-P1-M1-B12

Method BLASTX
NCBI GI g2494238
BLAST score 549
E value 2.0e-56
Match length 130
% identity 87

NCBI Description PROBABLE PEROXISOMAL ENOYL-COA HYDRATASE

>gi\_2135896\_pir\_\_I38882 peroxisomal enoyl-CoA
hydratase-like protein - human >gi\_564065 (U16660)

peroxisomal enoyl-CoA hydratase-like protein [Homo sapiens] >gi\_2623168 (AF030249) putative dienoyl-CoA isomerase [Homo sapiens] >gi\_4503447 ref NP\_001389.1\_pECH1\_ enoyl Coenzyme





## A hydratase 1, peroxisomal

```
229857
Seq. No.
                  LIB3196-043-P1-M1-B2
Seq. ID
                  BLASTX
Method
                  q1200256
NCBI GI
                  507
BLAST score
                  1.0e-51
E value
                  127
Match length
                  77
% identity
                  (X90990) stpk1 protein kinase [Solanum tuberosum]
NCBI Description
                   229858
Seq. No.
                   LIB3196-043-P1-M1-B8
Seq. ID
                   BLASTX
Method
                   q3281851
NCBI GI
BLAST score
                   92
                   1.0e-09
E value
Match length
                   49
% identity
                   (AL031004) RNA lariat debranching enzyme - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   229859
Seq. No.
                   LIB3196-043-P1-M1-B9
Seq. ID
                   BLASTX
Method
                   q683553
NCBI GI
                   247 -
BLAST score
                   4.0e-21
E value
Match length
                   112
                   50
% identity
                   (Z48450) oleosin-like protein [Citrus sinensis]
NCBI Description
                   >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]
                   229860
Seq. No.
                   LIB3196-043-P1-M1-C1
Seq. ID
                   BLASTX
Method
                   g2308997
NCBI GI
                   224
BLAST score
                   1.0e-18
E value
                   44
Match length
% identity
                   (AB004066) DEC1 [Homo sapiens]
NCBI Description
                   >gi_4503299_ref_NP_003661.1_pDEC1_ differentiated Embryo
                   Chondrocyte expressed gene
                   229861
Seq. No.
                   LIB3196-043-P1-M1-C3
Seq. ID
                   BLASTX
Method
                   g539602
NCBI GI
BLAST score
                   691
                   4.0e-73
E value
Match length
                   136
% identity
                   glycine hydroxymethyltransferase (EC 2.1.2.1) precursor,
NCBI Description
                   mitochondrial - human (fragment) >gi_703093 (L11932) serine
```

hydroxymethyltransferase [Homo sapiens]





```
229862
Seq. No.
                  LIB3196-043-P1-M1-C4
Seq. ID
Method
                  BLASTX
                  q2780365
NCBI GI
                  157
BLAST score
                  1.0e-10
E value
                  58
Match length
                  55
% identity
                  (AB007693) Elongin C [Drosophila melanogaster]
NCBI Description
Seq. No.
                  229863
                  LIB3196-043-P1-M1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2507222
BLAST score
                  403
                  2.0e-39
E value
Match length
                  113
                   64
% identity
                  KINASE ASSOCIATED PROTEIN PHOSPHATASE >gi 1709236 (U09505)
NCBI Description
                   kinase associated protein phosphatase [Arabidopsis
                   thaliana]
                   229864
Seq. No.
                  LIB3196-043-P1-M1-C7
Seq. ID
                   BLASTX
Method
                   g3851697
NCBI GI
BLAST score
                   448
E value
                   1.0e-44
                   100
Match length
                   83
% identity
                  (AF100204) putative chemokine receptor [Macaca mulatta]
NCBI Description
                   229865
Seq. No.
                   LIB3196-043-P1-M1-D1
Seq. ID
                   BLASTX
Method
                   g4490295
NCBI GI
                   158
BLAST score
E value
                   1.0e-10
Match length
                   128
                   29
% identity
                  (AL035678) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   229866
Seq. No.
                   LIB3196-043-P1-M1-D5
Seq. ID
                   BLASTX
Method
                   g4455323
NCBI GI
                   521
BLAST score
                   3.0e-53
E value
                   125
Match length
% identity
                   (AL035525) aminopeptidase-like protein [Arabidopsis
NCBI Description
                   thaliana]
```

32972

229867

BLASTX

LIB3196-043-P1-M1-D6

Seq. No.

Seq. ID

Method

Seq. ID

Method

BLASTX





```
NCBI GI
                    q965470
                    658
 BLAST score
                    3.0e-69
 E value
 Match length
                    134
  % identity
                    98
                    (L37033) FK-506 binding protein homologue [Homo sapiens]
 NCBI Description
                    >gi 3395419 (AC005387) FK-506 binding protein homologue
                     [Homo sapiens]
                    229868
  Seq. No.
  Seq. ID
                    LIB3196-043-P1-M1-D8
                    BLASTX
 Method
  NCBI GI
                    g3915742
                    597
  BLAST score
                     4.0e-62
 E value
                    124
  Match length
  % identity
                    91
                    LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319
  NCBI Description
                     (M69188) legumin A [Gossypium hirsutum]
                     >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele
                     [Gossypium hirsutum]
                     229869
  Seq. No.
  Seq. ID
                     LIB3196-043-P1-M1-D9
                     BLASTX
  Method
                     g106322
  NCBI GI
                     120
  BLAST score
                     7.0e-10
  E value
  Match length
                     113
  % identity
                     42
                    hypothetical protein (L1H 3' region) - human
  NCBI Description
                     229870
  Seq. No.
                     LIB3196-043-P1-M1-E10
  Seq. ID
  Method
                     BLASTX
" NCBI GI
                     g2982268
                     399
  BLAST score
                     5.0e-39
  E value
  Match length
                     87
  % identity
                     (AF051217) probable 40S ribosomal protein S15 [Picea
  NCBI Description
                     mariana]
                     229871
  Seq. No.
                     LIB3196-043-P1-M1-E2
  Seq. ID
  Method
                     BLASTX
                     g2289003
  NCBI GI
                     466
  BLAST score
                     8.0e-47
  E value
  Match length
                     127
                     73
  % identity
                     (AC002335) membrane transporter D1 isolog [Arabidopsis
  NCBI Description
                     thaliana]
                     229872
  Seq. No.
                     LIB3196-043-P1-M1-E6
```



q129356 228 2.0e-19 47

% identity NCBI Description

NCBI GI

E value Match length

BLAST score

P3 PROTEIN >gi\_87501\_pir\_\_S01696 gene P3 protein - human >gi 35188 emb\_CAA30998 (X12458) P3 protein (AA 1-1382) [Homo sapiens] >gi 1203976 (L44140) P3 gene product [Homo

sapiens]

229873 Seq. No.

LIB3196-043-P1-M1-E7 Seq. ID

94

Method BLASTX g1399325 NCBI GI 627 BLAST score 1.0e-65 E value Match length 131 % identity

(U41832) MHC class I antigen Mamu A\*07 [Macaca mulatta] NCBI Description

229874 Seq. No.

LIB3196-043-P1→M1-E8 Seq. ID

BLASTX Method NCBI GI q2736151 255 BLAST score 5.0e-22 E value 131 Match length % identity

(AF021935) mytonic dystrophy kinase-related Cdc42-binding NCBI Description

kinase [Rattus norvegicus]

229875 Seq. No.

Seq. ID LIB3196-043-P1-M1-E9

BLASTX Method NCBI GI g417103 533 BLAST score 1.0e-54 E value 107 Match length 100 % identity

HISTONE H3.2, MINOR >gi\_282871\_pir\_\_S24346 histone NCBI Description

H3.3-like protein - Arabidopsis thaliana

>gi 16324 emb CAA42957 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 404825 emb CAA42958 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 488563 (U09458) histone H3.2 [Medicago sativa] >gi\_488567 (U09460) histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2

[Medicago sativa] >gi\_488577 (U09465) histone H3.2

[Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445\_ (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum]

>gi 2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi 3273350 dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AFO93633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi 4490755 emb CAB38917.1\_





## (ALO35708) Histon H3 [Arabidopsis thaliana]

```
229,876
Seq. No.
                  LIB3196-043-P1-M1-F2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4567253
                  166
BLAST score
                  1.0e-11
E value
                  67
Match length
% identity
                   54
                  (AC007070) putative serpin protein [Arabidopsis thaliana]
NCBI Description
                   229877
Seq. No.
                  LIB3196-043-P1-M1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3786016
                   431
BLAST score
                   1.0e-42
E value
                   95
Match length
                   79
% identity
                   (AC005499) putative elongation factor [Arabidopsis
NCBI Description
                   thaliana]
                   229878
Seq. No.
Seq. ID
                   LIB3196-043-P1-M1-F8
Method
                   BLASTX
NCBI GI
                   g4033735
BLAST score
                   693
E value
                   2.0e-73
                   133
Match length
                   98
% identity
                   (AF054284) spliceosomal protein SAP 155 [Homo sapiens]
NCBI Description
Seq. No.
                   229879
                   LIB3196-043-P1-M1-F9
Seq. ID
                   BLASTX
Method
                   g2213610
NCBI GI
                   216
BLAST score
E value
                   2.0e-17
Match length
                   111
                   41
% identity
                   (AC000103) F21J9.4 [Arabidopsis thaliana]
NCBI Description
                   229880
Seq. No.
                   LIB3196-043-P1-M1-G1
Seq. ID
                   BLASTX
Method
                   g2493319
NCBI GI
                   380
BLAST score
                   1.0e-36
E value
                   94
Match length
                   70
% identity
                   MAVICYANIN >gi_1836088_bbs_179249 mavicyanin=12.752 kda
NCBI Description
                   small blue copper-containing stellacyanin-like
                   glycoprotein/type I cupredoxin [Cucurbita pepo=green
                   zucchini, peelings, Peptide, 108 aa]
```

32975

229881





```
LIB3196-043-P1-M1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2864615
BLAST score
                   595
E value
                   6.0e-62
Match length
                   125
% identity
NCBI Description
                   (AL021811) putative protein [Arabidopsis thaliana]
Seq. No.
                   229882
                   LIB3196-043-P1-M1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q88044
                   395
BLAST score
E value
                   1.0e-38
Match length
                   108
                   77
% identity
                   keratin 4, type II, cytoskeletal - human (fragment)
NCBI Description
                   >gi 34073 emb CAA30534 (X07695) cytokeratin 4 (408 AA)
                   [Homo sapiens]
                   229883
Seq. No.
                   LIB3196-043-P1-M1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1346347
BLAST score
                   650
E value
                   2.0e-68
                   132
Match length
                   99
% identity
                   KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D)
NCBI Description
                   (K6D KERATIN) >gi_2119225_pir__I61769 keratin type II -
                   human (fragment) >gi 914833 (L42610) keratin type II [Homo
                   sapiens]
                   229884
Seq. No.
Seq. ID
                   LIB3196-043-P1-M1-G5
Method ~
                   BLASTX
NCBI GI
                   g2431771 <sup>*</sup>
BLAST score
                   157
                   4.0e-11
E value
Match length
                   42
% identity
                   71
                   (U62753) acidic ribosomal protein P2b [Zea mays]
NCBI Description
                   229885
Seq. No.
                   LIB3196-043-P1-M1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3249066
BLAST score
                   234
E value
                   1.0e-19
Match length
                   127
% identity
```

NCBI Description (AC004473) Similar to S. cerevisiae SIK1P protein gb 984964. ESTs gb F15433 and gb AA395158 come from this

gene. [Arabidopsis thaliana]





```
LIB3196-043-P1-M1-H10
Seq. ID
Method
                  BLASTX
                  g2997591
NCBI GI
BLAST score
                  522
                  2.0e-53
E value
                  104
Match length
                   95
% identity
                   (AF020814) glucose-6-phosphate/phosphate-translocator
NCBI Description
                  precursor [Pisum sativum]
                  229887
Seq. No.
                  LIB3196-043-P1-M1-H4
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2435514
BLAST score
                   325
                   3.0e-30
E value
                   108
Match length
% identity
                   (AF024504) Similar to serine/threonine protein kinase;
NCBI Description
                   coded for by A. thaliana cDNA T20930; coded for by A.
                   thaliana cDNA T43472 [Arabidopsis thaliana]
Seq. No.
                   229888
                   LIB3196-043-P1-M1-H9
Seq. ID
Method
                  BLASTX
                   g266691
NCBI GI
                   150
BLAST score
E value
                   4.0e-10
Match length
                   65
% identity
                   OLEOSIN 16.4 KD >gi_167361 (L00934) 16.4 kDa oleosin
NCBI Description
                   [Gossypium hirsutum]
                   229889
Seq. No.
                   LIB3196-044-P1-M1-A3
Seq. ID
                   BLASTX
Method
                   g3342571
NCBI GI
BLAST score
                   140
E value
                   1.0e-08
                   48
Match length
% identity
                   (AF078817) high mobility group protein [Nannospalax
NCBI Description
                   ehrenbergi]
                   229890
Seq. No.
                   LIB3196-044-P1-M1-B2
Seq. ID
                   BLASTX
Method
                   g416662
NCBI GI
BLAST score
                   467
                   6.0e-47
E value
                   120
Match length
% identity
                   21 KD SEED PROTEIN PRECURSOR >gi_99954_pir__S16252 trypsin
NCBI Description
                   inhibitor homolog - soybean >gi 21909 emb CAA39860_
                   (X56509) 21 kDa seed protein [Theobroma cacao]
```

229891

NCBI GI

q82035





```
LIB3196-044-P1-M1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3080426
BLAST score
                   400
E value
                   4.0e-39
Match length
                   113
% identity
NCBI Description
                   (AL022604) putative protein [Arabidopsis thaliana]
                  229892
Seq. No.
                  LIB3196-044-P1-M1-B7
Seq. ID
Method
                  BLASTX
                   g1199772
NCBI GI
                   257
BLAST score
                   3.0e-22
E value
Match length
                  100
                   59
% identity
                   (D83226) extensin like protein [Populus nigra]
NCBI Description
                   >gi_1199774_dbj_BAA11855_ (D83227) extensin like protein
                   [Populus nigra]
                   229893
Seq. No.
Seq. ID
                  LIB3196-044-P1-M1-C1
Method
                  BLASTX
NCBI GI
                   g4008159
BLAST score
                   440
E value
                   8.0e-44
Match length
                  115
                   72
% identity
                  (AB015601) DnaJ homolog [Salix gilgiana]
NCBI Description
                  229894
Seq. No.
                  LIB3196-044-P1-M1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1061040
BLAST score
                   293
E value
                   1.0e-26
Match length
                   89
                   60
% identity
                   (X89867) sterol-C-methyltransferase [Arabidopsis thaliana]
NCBI Description
                   >gi 1587694 prf 2207220A sterol C-methyltransferase
                   [Arabidopsis thaliana]
                   229895
Seq. No.
                  LIB3196-044-P1-M1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g100196
BLAST score
                   462
E value
                   2.0e-46
Match length
                  109
                   80
% identity
NCBI Description chlorophyll a/b-binding protein (cab-11) - tomato
Seq. No.
                  229896
Seq. ID
                  LIB3196-044-P1-M1-C7
Method
                  BLASTX
```



```
BLAST score
                   227
                   6.0e-19
E value
                   107
Match length
                   35
% identity
```

ricin E - castor bean (fragment) >gi\_169715 (M17631) ricin E beta chain [Ricinus communis] >gi\_225896\_prf\_\_1402359A NCBI Description

ricin E [Ricinus communis]

```
229897
Seq. No.
                   LIB3196-044-P1-M1-D11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2662341
BLAST score
                   650
                   2.0e-68
E value
```

124 Match length 100 % identity

(D63580) EF-1 alpha [Oryza sativa] NCBI Description

>gi 2662345\_dbj\_BAA23659\_ (D63582) EF-1 alpha [Oryza satīva] >gi\_2662347\_dbj\_BAA23660\_ (D63583) EF-1 alpha

[Oryza sativa]

229898 Seq. No.

Seq. ID LIB3196-044-P1-M1-D3

BLASTX Method q2498323 NCBI GI 388 BLAST score 1.0e-37 E value 93 Match length

% identity 81

EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY NCBI Description

COMPONENT P85) >gi 1488324 (U65932) extracellular matrix protein 1 [Homo sapiens] >gi\_1488332 (U65938) extracellular

matrix protein 1 [Homo sapiens] >gi\_2654433 (U68186)

extracellular matrix protein 1 [Homo sapiens]

229899 Seq. No.

LIB3196-044-P1-M1-D4 Seq. ID

BLASTX Method NCBI GI g1513059 BLAST score 275 2.0e-24 E value 68 Match length 75 % identity

(D87258) serin protease with IGF-binding motif [Homo NCBI Description

sapiens] >gi 1621244 emb CAA69226 (Y07921) novel serine

protease, PRSS11 [Homo sapiens]

>gi 4506141\_ref\_NP\_002766.1\_pPRSS11\_ protease, serine, 11

(IGF binding)

Seq. No. 229900

LIB3196-044-P1-M1-D6 Seq. ID

BLASTX Method q125077 NCBI GI 496 BLAST score 3.0e-50 E value 128 Match length 81 % identity





```
NCBI Description KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK
                  13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal,
                  long form - human >gi_34033_emb_CAA32786_ (X14640) keratin
                   13 [Homo sapiens]
                  229901
Seq. No.
Seq. ID
                  LIB3196-044-P1-M1-E1
                  BLASTX
Method
                   a3643595
NCBI GI
                   291
BLAST score
                   2.0e-26
E value
                   104
Match length
                   55
% identity
                  (AC005395) putative oleosin protein [Arabidopsis thaliana]
NCBI Description
                   229902
Seq. No.
                   LIB3196-044-P1-M1-E6
Seq. ID
                   BLASTX
Method
                   q3649778
NCBI GI
                   333
BLAST score
                   2.0e-31
E value
                   110
Match length
                   66
% identity
                  (AJ011303) pepc2 [Vicia faba]
NCBI Description
                   229903
Seq. No.
                   LIB3196-044-P1-M1-F10
Seq. ID
                   BLASTX
Method
                   q1363944
NCBI GI
BLAST score
                   385
                   3.0e-37
E value
                   80
Match length
% identity
                   type I keratin 16 - human >gi_1195531_bbs_172338 (S79867)
NCBI Description
                   type I keratin 16, K16 [human, epidermal keratinocytes,
                   Peptide, 473 aa] [Homo sapiens]
                   229904
Seq. No.
                   LIB3196-044-P1-M1-F12
Seq. ID
                   BLASTX
Method
                   g116850
NCBI GI
BLAST score
                   548
                   2.0e-56
E value
                   108
Match length
 % identity
                   COFILIN, NON-MUSCLE ISOFORM >gi_89176_pir__A29240 cofilin -
 NCBI Description
                   pig >gi_164425 (M20866) cofilin [Sus scrofa]
                   229905
 Seq. No.
                   LIB3196-044-P1-M1-F3
 Seq. ID
                   BLASTX
 Method
                   q2131161
 NCBI GI
 BLAST score
                   158
                    1.0e-10
 E value
 Match length
                    60
 % identity
                   4-nitrophenylphosphatase (EC 3.1.3.41) - yeast
 NCBI Description
```





(Saccharomyces cerevisiae) >gi\_1431400\_emb\_CAA98816\_ (Z74284) ORF YDL236w [Saccharomyces cerevisiae]

229906 Seq. No. LIB3196-044-P1-M1-F9 Seq. ID Method BLASTX g1707017 NCBI GI 275 BLAST score

2.0e-24 E value Match length 65 80 % identity

(U78721) RNA helicase isolog [Arabidopsis thaliana] NCBI Description

229907 Seq. No.

LIB3196-044-P1-M1-G3 Seq. ID

BLASTX Method g133041 NCBI GI 614 BLAST score 4.0e-64E value 128 Match length 95 % identity

60S ACIDIC RIBOSOMAL PROTEIN PO (L10E) NCBI Description

>gi\_71137\_pir\_\_R5HUPO acidic ribosomal protein PO - human >gi\_190232 (M17885) acidic ribosomal phosphoprotein (P0) [Homo sapiens] >gi\_2935618\_gb\_AAC05176\_ (AC004263) 60S ACIDIC RIBOSOMAL PROTEIN; match to P05388 (PID:g133041)

[Homo sapiens] >gi\_4506667\_ref\_NP\_000993.1\_pRPLP0\_

ribosomal protein, large, PO

229908 Seq. No.

LIB3196-044-P1-M1-G4 Seq. ID

58

BLASTX Method g662366 NCBI GI BLAST score 341 4.0e-32 E value 107 Match length

% identity NCBI Description (L39786) conglutin gamma [Lupinus angustifolius]

>gi 666056\_emb\_CAA46552\_ (X65601) conglutin gamma [Lupinus

angustifolius]

229909 Seq. No.

LIB3196-044-P1-M1-G5 Seq. ID

Method BLASTX g131805 NCBI GI BLAST score 577 E value 8.0e-60 Match length 116 % identity

RAS-RELATED PROTEIN RAB-11A (RAB-11) (24KG) (YL8) NCBI Description

>gi\_917\_emb\_CAA39799\_ (X56388) rab11 [Canis familiaris] >gi\_35889\_emb\_CAA37300\_ (X53143) ras-like protein (AA 1-216) [Homo sapiens] >gi\_206567 (M75153) ras p21-like small GTP-binding protein [Rattus norvegicus] >gi\_310067



229910



(L19260) tubulovesicle-associated protein [Oryctolagus cuniculus] >gi\_505541\_emb\_CAA40064\_ (X56740) H rab11 small GTP binding protein [Homo sapiens] >gi\_2149975 (AF000231) rab11a [Homo sapiens] >gi\_1089909\_prf\_\_2018147A GTP-binding protein rab11 [Oryctolagus cuniculus]

Seq. No. LIB3196-044-P1-M1-G6 Seq. ID BLASTX Method q407308 NCBI GI 452 BLAST score 2.0e-45 E value 95 Match length 92 % identity

(U02493) 54 kDa protein [Homo sapiens] NCBI Description

>qi 2808511 emb CAA72157 (Y11289) p54nrb [Homo sapiens]

Seq. No. 229911

LIB3196-044-P1-M1-G7 Seq. ID

BLASTX Method g505133 NCBI GI BLAST score 341 3.0e-32E value 118 Match length 66 % identity

(D28557) RYB-a [Rattus norvegicus] NCBI Description

Seq. No. 229912

LIB3196-044-P1-M1-G8 Seq. ID

BLASTX Method g1399319 NCBI GI BLAST score 469 3.0e-47 E value 117 Match length 74 % identity

(U41829) MHC class I antigen Mamu B\*07 [Macaca mulatta] NCBI Description

Seq. No. 229913

LIB3196-044-P1-M1-G9 Seq. ID

BLASTX Method g137578 NCBI GI 513 BLAST score 2.0e-52 E value 118 Match length 87 % identity

VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) NCBI Description

>gi\_81545\_pir\_\_S06398 alpha-globulin type A precursor upland cotton >gi\_167371 (M19378) vicilin precursor

[Gossypium hirsutum] >gi\_207906 (M18027) alpha globulin A [Artificial gene] >gi\_226119\_prf\_\_1410330A vicilin gene A

[Saguinus oedipus]

Seq. No. 229914

LIB3196-044-P1-M1-H3 Seq. ID

BLASTX Method q3123274 NCBI GI BLAST score 333





```
3.0e-31
E value
Match length
                  90
                  73
% identity
                  60S RIBOSOMAL PROTEIN L32 (RP49) >gi 1928968 (U92431)
NCBI Description
                  ribosomal protein 49 [Drosophila melanogaster]
                  >qi 2739301 emb CAA74278 (Y13939) ribosomal protein 49
                  [Drosophila melanogaster]
                  229915
Seq. No.
                  LIB3196-044-P1-M1-H9
Seq. ID
Method
                  BLASTX
                  g3421090
NCBI GI
                  141
BLAST score
                  9.0e-09
E value
Match length
                  31
                  87
% identity
                  (AF043525) 20S proteasome subunit PAE2 [Arabidopsis
NCBI Description
                  thaliana]
                  229916
Seq. No.
                  LIB3196-045-P1-M1-A1
Seq. ID
                  BLASTX
Method
                  g4105275
NCBI GI
                  230
BLAST scoré
                  4.0e-19
E value
                  52
Match length
                  83
% identity
                 (AF044671) MM46 [Homo sapiens]
NCBI Description
                  229917
Seq. No.
                  LIB3196-045-P1-M1-A11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2497542
BLAST score
                  230
                  5.0e-22
E value
                  88
Match length
                  65
% identity
NCBI Description PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR
                  >gi_629696_pir__S44287 pyruvate kinase, plastid - common
                  tobacco >gi 482938 emb CAA82223 (Z28374) Pyruvate kinase;
                  plastid isozyme [Nicotiana tabacum]
                  229918
Seq. No.
                  LIB3196-045-P1-M1-A6
Seq. ID
                  BLASTX
Method
                  g3746069
NCBI GI
                  147
BLAST score
                  2.0e-09
E value
                  100
Match length
                  34
% identity
```

% identity 34
NCBI Description (AC005311) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No. 229919

Seq. ID LIB3196-045-P1-M1-A8

Method BLASTX NCBI GI g3882267

```
281
BLAST score
                   5.0e-25
E value
                   105
Match length
                   60
```

% identity (AB018316) KIAA0773 protein [Homo sapiens] NCBI Description

229920 Seq. No.

LIB3196-045-P1-M1-B4 Seq. ID

BLASTX Method g2623158 NCBI GI BLAST score 614 3.0e-64 E value 121 Match length 93 % identity

(AF030177) N-acetylglucosaminyl transferase component Gpi1 NCBI Description

[Homo sapiens] >gi 2911142 dbj\_BAA24948\_ (AB003723) GPI1

[Homo sapiens]

229921 Seq. No.

LIB3196-045-P1-M1-B5 Seq. ID

BLASTX Method NCBI GI g137578 482 BLAST score 1.0e-48 E value 118 Match length 82 % identity

VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) NCBI Description

>gi\_81545\_pir\_\_S06398 alpha-globulin type A precursor upland cotton >gi 167371 (M19378) vicilin precursor

[Gossypium hirsutum] >gi\_207906 (M18027) alpha globulin A [Artificial gene] >gi\_226119\_prf\_\_1410330A vicilin gene A

[Saguinus oedipus]

229922 Seq. No.

LIB3196-045-P1-M1-B9 Seq. ID

BLASTX Method g1350956 NCBI GI BLAST score 448 1.0e-44E value 94 Match length 93 % identity

40S RIBOSOMAL PROTEIN S20 (S22) NCBI Description

229923 Seq. No.

LIB3196-045-P1-M1-C10 Seq. ID

BLASTX Method NCBI GI g137479 BLAST score 415 8.0e-41 E value Match length 89 98 % identity

VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT NCBI Description

>gi\_107394\_pir\_\_A39367 H+-transporting ATPase (EC 3.6.1.35) chain PKD1 - human >gi\_189676 (M62762) vacuolar H+ ATPase proton channel subunit [Homo sapiens]

>gi\_4502313\_ref\_NP\_001685.1\_pATP6C\_ ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD

Match length





```
229924
 Seq. No.
                    LIB3196-045-P1-M1-C11
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g2981631
 BLAST score
                    210
                     6.0e-17
 E value
                    100
 Match length
                     47
 % identity
 NCBI Description
                   (AB012223) ORF2 [Canis familiaris]
                    229925
 Seq. No.
                    LIB3196-045-P1-M1-C2
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g125105
 BLAST score
                     633
                     2.0e-66
 E value
                     127
 Match length
                     98
 % identity
                    KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5)
 NCBI Description
                     (58 KD CYTOKERATIN) >gi_88051_pir__A29904 keratin K5, 58K
                     type II, epidermal (version 1) - human >gi_307082 (M21389)
                     keratin type II [Homo sapiens]
                     >gi_4557890_ref_NP_000415.1_pKRT5_ keratin
                     229926
 Seq. No.
 Seq. ID
                    LIB3196-045-P1-M1-C3
 Method
                     BLASTX
                     g4314361
NCBI GI
 BLAST score
                     216
                     2.0e-17
 E value
 Match length
                     44
                     95
 % identity
 NCBI Description (AC006340) unknown protein [Arabidopsis thaliana]
                     229927
 Seq. No.
 Seq. ID
                     LIB3196-045-P1-M1-C4
 Method
                     BLASTX
 NCBI GI
                     g126156
 BLAST score
                     400
 E value
                     4.0e-39
 Match length
                     117
  % identity
                     68
                     LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
 NCBI Description
                     >gi 72288 pir FWCNBB beta-globulin B precursor (clone 134)
                     - upland cotton >gi_167373 (M16936) vicilin precursor
                     [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                     protein C134 [Saguinus oedipus]
  Seq. No.
                     229928
                     LIB3196-045-P1-M1-C5
  Seq. ID
 Method
                     BLASTX
 NCBI GI
                     q137578
 BLAST score
                     408
                     5.0e-40
 E value
```





```
% identity
                  72
NCBI Description
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
                  >gi_81545_pir__S06398 alpha-globulin type A precursor -
                  upland cotton >gi 167371 (M19378) vicilin precursor
                  [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                   [Artificial gene] >qi 226119 prf 1410330A vicilin gene A
                   [Saguinus oedipus]
                  229929
Seq. No.
Seq. ID
                  LIB3196-045-P1-M1-C8
Method
                  BLASTX
NCBI GI
                  g4325354
BLAST score
                  259
E value
                  2.0e-25
                  102
Match length
                  56
% identity
NCBI Description
                   (AF128395) contains similarity to retrovirus-related
                  polyproteins and to CCHC zinc finger protein (Pfam:
                  PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana]
                  229930
Seq. No.
                  LIB3196-045-P1-M1-C9
Seq. ID
Method
                  BLASTX
                  g4457221
NCBI GI
BLAST score
                  324
                  3.0e-30
E value
Match length
                  82
% identity
                   (AF127797) putative bZIP DNA-binding protein [Capsicum
NCBI Description
                  chinense]
Seq. No.
                  229931
Seq. ID
                  LIB3196-045-P1-M1-D1
Method
                  BLASTX
NCBI GI
                  g2961372
                  503
BLAST score
E value
                  4.0e-51
Match length
                  99
                  93
% identity
                   (AL022141) putative ribosomal protein L8 [Arabidopsis
NCBI Description
                  thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal
                  protein L2 [Arabidopsis thaliana]
                  229932
Seq. No.
Seq. ID
                  LIB3196-045-P1-M1-D3
Method
                  BLASTX
NCBI GI
                  g227448
BLAST score
                  643
E value
                  1.0e-67
Match length
                  125
% identity
NCBI Description phosphofructokinase [Homo sapiens]
```

229933 Seq. No.

Seq. ID LIB3196-045-P1-M1-D5

Method BLASTX NCBI GI g547753





```
BLAST score
                  436
                  2.0e-43
E value
Match length
                  93
                  . 95
% identity
NCBI Description KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)
Seq. No.
                  229934
                  LIB3196-045-P1-M1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3641870
BLAST score
                  309
                  2.0e-28
E value
Match length
                  116
% identity
                  (AJ011013) hypothetical protein [Cicer arietinum]
NCBI Description
Seq. No.
                  229935
Seq. ID
                  LIB3196-045-P1-M1-D9
Method
                  BLASTX
NCBI GI
                  q4191793
BLAST score
                  406
                  8.0e-40
E value
Match length
                  119
% identity
                  (AC005917) putative zinc finger protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  229936
Seq. ID
                  LIB3196-045-P1-M1-E1
Method
                  BLASTX
NCBI GI
                  g113950
BLAST score
                  557
                  2.0e-57
E value
Match length
                  112
                  59
% identity
                  ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN)
NCBI Description
                   (CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL ANTICOAGULANT
                  PROTEIN IV) (PAP-IV) >gi_71761_pir__LUHU36 annexin II -
                  human >gi 219910 dbj BAA00013 (D00017) lipocortin II [Homo
                  sapiens]
                  229937
Seq. No.
                  LIB3196-045-P1-M1-E2
Seq. ID
                  BLASTX
Method
                  q1174448
NCBI GI
                  385
BLAST score
                  2.0e-37
E value
                  119
Match length
                   61
% identity
                  TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR
NCBI Description
                   (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT)
                   (SSR-ALPHA) >gi 547391 (L32016) alpha-subunit; putative
                   [Arabidopsis thaliana]
```

32987

229938

BLASTX

LIB3196-045-P1-M1-E7

Seq. No.

Seq. ID Method

Match length





```
g2914700
 NCBI GI
 BLAST score
                    315
 E value
                    3.0e-29
 Match length
                    97
 % identity
                    68
                    (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    229939
 Seq. ID
                    LIB3196-045-P1-M1-F1
 Method
                    BLASTX
 NCBI GI
                    g207905
 BLAST score
                    522
 E value
                    2.0e-53
 Match length
                    121
 % identity
                    88
 NCBI Description
                   (M18027) alpha globulin B [Artificial gene]
                    229940
 Seq. No.
                   LIB3196-045-P1-M1-F10
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1362600
 BLAST score
                    192
 E value
                    1.0e-14
 Match length
                    90
 % identity
                    44
NCBI Description
                   anillin - fruit fly (Drosophila melanogaster)
 Seq. No.
                   229941
 Seq. ID
                   LIB3196-045-P1-M1-F11
 Method
                   BLASTX
 NCBI GI
                   g1429226
 BLAST score
                   163
 E value
                   2.0e-11
 Match length
                   32
 % identity
                   91
 NCBI Description
                   (X98861) TFIIA [Arabidopsis thaliana]
 Seq. No.
                   229942
 Seq. ID
                   LIB3196-045-P1-M1-F3
Method
                   BLASTX
NCBI GI
                   g1170567
BLAST score
                   369
E value
                   1.0e-35
Match length
                   74
% identity
                   88
NCBI Description
                   MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)
                   >gi_1085960_pir__S52648 INO1 protein - Citrus paradisi
                   >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]
Seq. No.
                   229943
Seq. ID
                   LIB3196-045-P1-M1-F4
Method
                   BLASTX
NCBI GI
                   g232081
BLAST score
                   572
E value
                   3.0e-59
```





```
% identity
                   96
 NCBI Description FATTY ACID-BINDING PROTEIN, EPIDERMAL (E-FABP)
                   (PSORIASIS-ASSOCIATED FATTY ACID-BINDING-PROTEIN HOMOLOG)
                   (PA-FABP) >gi 2119438 pir I56326 fatty acid binding
                   protein homologue - human >gi 182354 (M94856) fatty acid
                   binding protein homologue [Homo sapiens]
                   >gi 4557581 ref NP 001435.1 pFABP5 fatty acid binding
                   protein 5, psoriasis-associated
 Seq. No.
                   229944
 Seq. ID
                   LIB3196-045-P1-M1-F6
Method
                   BLASTX
NCBI GI
                   g3868758
BLAST score
                   431
 E value
                   9.0e-43
Match length
                   106
                   75
 % identity
NCBI Description
                  (D89802) elongation factor 1B gamma [Oryza sativa]
                   229945
 Seq. No.
                   LIB3196-045-P1-M1-F9
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g461776
BLAST score
                   319
                   1.0e-29
E value
Match length
                   54
 % identity
                   100
NCBI Description
                   CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL
                   PROLINE-RICH SQUAMOUS CELL MARKER) >gi 251369 bbs 108679
                   (S40060) spr1=small proline rich squamous cell marker
                   [Rhesus monkeys, tracheobronchial epithelium, Peptide, 89
                   aa] [Rhesus monkeys] >gi 342297 (M83999) small proline-rich
                   protein [Macaca mulatta]
                   229946
Seq. No.
                   LIB3196-045-P1-M1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1346349
BLAST score
                   544
E value
                   5.0e-56
                   111
Match length
                   100
 % identity
NCBI Description KERATIN, TYPE II CYTOSKELETAL 6F (CYTOKERATIN 6F) (CK 6F)
                   (K6F KERATIN) >gi 2119219 pir I61771 keratin type II -
                   human >gi_908805 (L42612) keratin type II [Homo sapiens]
                   229947
Seq. No.
Seq. ID
                   LIB3196-045-P1-M1-G12
Method
                   BLASTX
                   q116850
```

Method BLASTX
NCBI GI g116850
BLAST score 400
E value 2.0e-39
Match length 89
% identity 88

NCBI Description COFILIN, NON-MUSCLE ISOFORM >gi\_89176\_pir\_\_A29240 cofilin -

pig >gi 164425 (M20866) cofilin [Sus scrofa]

% identity

53





```
Seq. No.
                   229948
Seq. ID
                   LIB3196-045-P1-M1-G4
                   BLASTX
Method
NCBI GI
                   g2507421
BLAST score
                   340
E value
                   5.0e-32
Match length
                   70
                   90
% identity
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi 1800277
NCBI Description
                   (U81042) translation initiation factor [Arabidopsis
                   thaliana] >gi_4490709_emb_CAB38843.1 (AL035680)
                   translation initiation factor [Arabidopsis thaliana]
Seq. No.
                   229949
                   LIB3196-045-P1-M1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1176668
                   191
BLAST score
                   1.0e-14
E value
Match length
                   101
% identity
                   25
NCBI Description
                  HYPOTHETICAL 40.9 KD PROTEIN CO8B11.5 IN CHROMOSOME II
                   >gi 3874172 emb CAA86664 (Z46676) similar to Poly(A) RNA
                   binding protein; cDNA EST EMBL: D65752 comes from this gene;
                   cDNA EST EMBL:D69301 comes from this gene; cDNA EST
                   EMBL:C11188 comes from this gene; cDNA EST EMBL:C13204
                   comes from this gene; cDNA E
Seq. No.
                   229950
Seq. ID
                   LIB3196-045-P1-M1-G7
Method
                   BLASTX
NCBI GI
                   q4432855
BLAST score
                   472
E value
                   1.0e-47
Match length
                   114
% identity
NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]
                   229951
Seq. No.
Seq. ID
                   LIB3196-045-P1-M1-H1
Method
                   BLASTX
NCBI GI
                   g3776005
BLAST score
                   589
E value
                   3.0e-61
Match length
                   121
% identity
NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]
Seq. No.
                   229952
Seq. ID
                  LIB3196-045-P1-M1-H11
Method
                  BLASTX
NCBI GI
                  g232031
BLAST score
                   283
E value .
                   2.0e-25
Match length
                  108
```

NCBI Description ELONGATION FACTOR 1 BETA' >gi 322851 pir S29224





translation elongation factor eEF-1 beta' chain - rice >gi 218161 dbj BAA02253 (D12821) elongation factor 1 beta' [Oryza sativa]

229953 Seq. No.

LIB3196-045-P1-M1-H4 Seq. ID

Method BLASTX NCBI GI g1709442 614 BLAST score 4.0e-64 E value Match length 125 98 % identity

NCBI Description DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT OF

2-OXOGLUTARATE DEHYDROGENASE COMPLEX PRECURSOR (E2) (E2K)

Seq. No. 229954

LIB3196-045-P1-M1-H9 Seq. ID

Method BLASTX NCBI GI g1429226 BLAST score 163 E value 3.0e-11 Match length 32 % identity 91

NCBI Description (X98861) TFIIA [Arabidopsis thaliana]

Seq. No. 229955

LIB3196-046-P1-M1-A10 Seq. ID

Method BLASTX -NCBI GI g2136744 182 BLAST score 1.0e-13 E value 42 Match length 86

% identity

NCBI Description endothelin converting enzyme-2 - bovine (fragment)

229956 Seq. No.

LIB3196-046-P1-M1-A12 Seq. ID

Method BLASTX NCBI GI g2651313 BLAST score 290 E value 2.0e-26 Match length 84 68 % identity

NCBI Description (AC002336) hypothetical protein [Arabidopsis thaliana]

229957 Seq. No.

LIB3196-046-P1-M1-A3 Seq. ID

Method BLASTX NCBI GI g2605714 BLAST score 239 E value 3.0e-20Match length 66 76 % identity

NCBI Description (AF026275) beta-tonoplast intrinsic protein [Arabidopsis

thaliana]

Seq. No. 229958





```
LIB3196-046-P1-M1-A4
Seq. ID
Method ·
                                                 BLASTX
NCBI GI
                                                  g2224691
BLAST score
                                                  268
E value
                                                  1.0e-23
Match length
                                                  102
                                                  53
% identity
NCBI Description
                                                 (AB002373) KIAA0375 [Homo sapiens]
                                                 229959
Seq. No.
                                                 LIB3196-046-P1-M1-A7
Seq. ID
Method
                                                 BLASTX
NCBI GI
                                                  g3047318
BLAST score
                                                  236
E value
                                                  2.0e-20
Match length
                                                  71
% identity
                                                  16
                                                  (AF056625) poly-ubiquitin [Magnaporthe grisea]
NCBI Description
                                                  229960
Seq. No.
Seq. ID
                                                 LIB3196-046-P1-M1-A9
Method
                                                 BLASTX
                                                  g4455335
NCBI GI
                                                  409
BLAST score
E value
                                                  4.0e-40
Match length
                                                  118
% identity
                                                  (AL035525) putative protein [Arabidopsis thaliana]
NCBI Description
                                                  229961
Seq. No.
                                                 LIB3196-046-P1-M1-B10
Seq. ID
                                                 BLASTX
Method
                                                  g1352077
NCBI GI
BLAST score
                                                  328
E value
                                                  1.0e-38
Match length
                                                  103
% identity
                                                  80
                                                 BETA-GALACTOSIDASE PRECURSOR (LACTASE)
NCBI Description
                                                   (EXO-(1-->4)-BETA-D-GALACTANASE) >gi_971485_emb_CAA58734_
                                                   (X83854) putative beta-galactosidase/galactanase
                                                   [Lycopersicon esculentum] >gi_4138139_emb_CAA10174
                                                   (AJ012797) ss-galactosidase [Lycopersicon esculentum]
Seq. No.
                                                  229962
                                                  LIB3196-046-P1-M1-B11
Seq. ID
Method
                                                  BLASTX
NCBI GI
                                                  g122087
BLAST score
                                                  109
                                                  6.0e-12
E value
Match length
                                                  119
% identity
                                                  45
                                                 HISTONE H3 >gi_81849_pir__S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir_A26014 histone H3 - wheat >gi_19607_emb_CAA31964_(X13673) histone H3 (AA 1-136) [Medicago sativa] >gi_19609_emb_CAA31965_(X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_(X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_(X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_(X13674) histone H3 (AB 1-136) [Medicago sativa] >gi_2179_emb_CAA25451_(X13674) histone H3 (AB 1-136) [Medicago sa
NCBI Description
```

(X00937) H3 histone [Triticum aestivum] >gi 488565 (U09459)





histone H3.1 [Medicago sativa] >gi\_2565419 (AF026803) histone H3 [Onobrychis viciifolia]

 Seq. No.
 229963

 Seq. ID
 LIB3196-046-P1-M1-B12

 Method
 BLASTX

 NCBI GI
 g126156

 BLAST score
 670

 E value
 1.0e-70

 Match length
 130

100

NCBI Description LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)

>gi\_72288\_pir\_\_FWCNBB beta-globulin B precursor (clone 134)

- upland cotton >gi\_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi\_1171335 (U43727) legumin B [Gossypium hirsutum] >gi\_225582 prf\_1306412C storage

protein C134 [Saguinus oedipus]

Seq. No. 229964

% identity

Seq. ID LIB3196-046-P1-M1-B6

Method BLASTX
NCBI GI g122007
BLAST score 332
E value 4.0e-31
Match length 90
% identity 74

NCBI Description HISTONE H2A >gi\_100161\_pir\_\_S11498 histone H2A - parsley

>gi\_20448\_emb\_CAA37828 (X53831) H2A histone protein (AA 1

- 149) [Petroselinum crispum]

Seq. No. 229965

Seq. ID LIB3196-046-P1-M1-B7

Method BLASTX
NCBI GI g125077
BLAST score 412
E value 1.0e-50
Match length 116
% identity 96

NCBI Description KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK

13) >gi\_71526\_pir\_\_KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi\_34033\_emb\_CAA32786\_ (X14640) keratin

13 [Homo sapiens]

Seq. No. 229966

Seq. ID LIB3196-046-P1-M1-B8

Method BLASTX
NCBI GI g4510346
BLAST score 514
E value 2.0e-52
Match length 124
% identity 79

NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No. 229967

Seq. ID LIB3196-046-P1-M1-B9

Method BLASTX NCBI GI g132944

NCBI GI

BLAST score





```
BLAST score
                    528
 E value
                    4.0e-54
Match length
                    103
                    94
 % identity
 NCBI Description
                    60S RIBOSOMAL PROTEIN L3 >gi 81658 pir JQ0772 ribosomal
                    protein L3 (ARP2) - Arabidopsis thaliana >qi 806279
                    (M32655) ribosomal protein [Arabidopsis thaliana]
                    229968
 Seq. No.
                    LIB3196-046-P1-M1-C1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q34228
                    317
 BLAST score
                    2.0e-29
 E value
 Match length
                    67
 % identity
                    99
 NCBI Description
                    (X03444) put. lamin A precursor (aa 1-702) [Homo sapiens]
                    >gi 224901 prf 1203377A lamin A [Homo sapiens]
                    229969
 Seq. No.
                    LIB3196-046-P1-M1-C2
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g181967
                    555
 BLAST score
                    4.0e-57
 E value
 Match length
                    131
 % identity
 NCBI Description
                    (M29548) elongation factor 1-alpha [Homo sapiens]
 Seq. No.
                    229970
                    LIB3196-046-P1-M1-C3
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2493130
 BLAST score
                    660
                    2.0e-69
 E value
 Match length
                    128
                    100
 % identity
 NCBI Description
                    VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B
                    SUBUNIT) >gi 459200 (U07053) vacuolar H+-ATPase subunit B
                    [Gossypium hirsutum]
                    229971
 Seq. No.
 Seq. ID
                    LIB3196-046-P1-M1-C4
 Method
                    BLASTX
 NCBI GI
                    q81546
 BLAST score
                    216
 E value
                    1.0e-17
 Match length
                    86
 % identity
                    62
 NCBI Description
                    alpha-globulin type B precursor (tandem 1) - upland cotton
                    (fragment)
                    229972
 Seq. No.
 Seq. ID
                    LIB3196-046-P1-M1-C6
 Method
                    BLASTX
```

32994

q3063698





2.0e-36 E value 130 Match length . 60 % identity NCBI Description (AL022537) putative protein [Arabidopsis thaliana] Seq. No. 229973 LIB3196-046-P1-M1-C7 Seq. ID Method BLASTX NCBI GI g1765899 BLAST score 561 6.0e-58 E value Match length 120 82 % identity NCBI Description (Y07917) Spot 3 protein [Arabidopsis thaliana] >gi 1839244 (U86700) EGF receptor like protein [Arabidopsis thaliana] Seq. No. 229974 LIB3196-046-P1-M1-D1 Seq. ID Method BLASTX NCBI GI q2668557 BLAST score 164 2.0e-11 E value Match length 92 -% identity 47 NCBI Description (U73690) cytosolic IMP-GMP specific 5'-nucleotidase [Bos taurus] Seq. No. 229975 LIB3196-046-P1-M1-D10 Seq. ID Method BLASTX NCBI GI q4090257 430 BLAST score E value 1.0e-42Match length 84 96 % identity NCBI Description (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii] Seq. No. 229976 LIB3196-046-P1-M1-D4 Seq. ID Method BLASTX -NCBI GI q137578 BLAST score 620 E value 8.0e-65 Match length 128 94 % identity NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi\_81545\_pir\_\_S06398 alpha-globulin type A precursor upland cotton >gi\_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi\_207906 (M18027) alpha globulin A

[Artificial gene] >gi 226119 prf 1410330A vicilin gene A

[Saguinus oedipus]

Seq. No. 229977

LIB3196-046-P1-M1-D5 Seq. ID

Method BLASTX g1708239 NCBI GI BLAST score 619





1.0e-64 E value Match length 118 100 % identity HYDROXYMETHYLGLUTARYL-COA SYNTHASE, CYTOPLASMIC (HMG-COA NCBI Description SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi 410028 (L25798) 3-hydroxy-3-methylglutaryl coenzyme A synthase [Homo sapiens] >gi\_4504429\_ref\_NP\_002121.1\_pHMGCS1\_ 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble) Seq. No. 229978 Seq. ID LIB3196-046-P1-M1-D7 Method BLASTX g3377797 NCBI GI BLAST score 440 9.0e-44E value 117 Match length 74 % identity (AF075597) Similar to 60S ribosome protein L19; coded for NCBI Description by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara 229979 Seq. No. Seq. ID LIB3196-046-P1-M1-D9 BLASTX Method NCBI GI g3451473 BLAST score 218 E value 1.0e-17 93 Match length % identity (AL031349) 4-nitrophenylphosphatase [Schizosaccharomyces NCBI Description pombe] 229980 Seq. No. LIB3196-046-P1-M1-E4 Seq. ID Method BLASTX g133027 NCBI GI BLAST score 706 7.0e-75 E value Match length 134 % identity 100 60S RIBOSOMAL PROTEIN L8 >gi 71075 pir\_R5RTL8 ribosomal NCBI Description protein L8 - rat >gi\_478326\_pir\_JN0923 ribosomal protein L8 - human >gi\_57704\_emb\_CAA44071\_ (X62145) ribosomal protein L8 [Rattus rattus] >gi\_433899\_emb\_CAA82248 (Z28407) ribosomal protein L8 [Homo sapiens] >gi\_1527178 (U67771) ribosomal protein L8 [Mus musculus] >gi\_4506663\_ref\_NP\_000964.1\_pRPL8\_ ribosomal protein L8 229981 Seq. No. LIB3196-046-P1-M1-E5

Seq. ID

Method BLASTX NCBI GI g4455335 BLAST score 392 E value 3.0e-38





-87 Match length % identity 82 (AL035525) putative protein [Arabidopsis thaliana] NCBI Description 229982 Seq. No. LIB3196-046-P1-M1-E6 Seq. ID Method BLASTX NCBI GI g2961390 644 BLAST score 1.0e-67 E value Match length 127 % identity 90 (AL022141) beta-galactosidase like protein [Arabidopsis NCBI Description thaliana] Seq. No. 229983 LIB3196-046-P1-M1-E9 Seq. ID Method BLASTX NCBI GI g1362916 BLAST score 560 8.0e-58 E value Match length 127 % identity 87 NCBI Description protein-tyrosine kiņase (EC 2.7.1.112) trkE precursor human >gi 400463 emb CAA52915 (X74979) TrkE [Homo sapiens] >qi 732800 emb CAA82335 (Z29093) receptor tyrosine kinase [Homo sapiens] >gi 1160925 (L57508) receptor kinase [Homo sapiens] >gi  $45034\overline{5}1$  ref NP 001945.1 pEDDR1 epithelial discoidin domain receptor 229984 Seq. No. LIB3196-046-P1-M1-F1 Seq. ID Method BLASTX g2764974 NCBI GI 427 BLAST score 3.0e-42E value 96 Match length % identity NCBI Description (X99906) alpha endosulfine [Homo sapiens] Seq. No. 229985 LIB3196-046-P1-M1-F10 Seq. ID Method BLASTX NCBI GI q140282 140 BLAST score 1.0e-08 E value 28 Match length % identity 93 NCBI Description HYPOTHETICAL 19 KD PROTEIN (ORF 170)

>gi\_1363543\_pir\_\_S58553 hypothetical protein 170 - maize
chloroplast >gi\_12430\_emb\_CAA41108\_ (X58080) ORF170 [Zea
mays] >gi\_902223\_emb\_CAA60287\_ (X86563) ORF170 [Zea mays]

Seq. No. 229986

Seq. ID LIB3196-046-P1-M1-F3

Method BLASTX NCBI GI g2804273

E value

Match length

5.0e-66





```
BLAST score
                   671
                   8.0e-71
E value
Match length
                   129
% identity
                   46
                   (D89980) alpha actinin 4 [Homo sapiens]
NCBI Description
Seq. No.
                   229987
                   LIB3196-046-P1-M1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2997694
BLAST score
                   232
E value
                   2.0e-19
Match length
                   119
% identity
NCBI Description
                   (AF053721) putative retrovirus-related polyprotein
                   [Lithospermum erythrorhizon]
Seq. No.
                   229988
Seq. ID
                   LIB3196-046-P1-M1-F9
Method
                   BLASTX
NCBI GI
                   q1335862
BLAST score
                   554
E value
                   4.0e-57
Match length
                   119
% identity
                   89
NCBI Description
                   (U42608) clathrin heavy chain [Glycine max]
Seq. No.
                   229989
Seq. ID
                   LIB3196-046-P1-M1-G12
Method
                   BLASTX
NCBI GI
                   g1167523
BLAST score
                   319
E value
                   1.0e-30
Match length
                   124
% identity
                   60
                   (D83003) ORF(AA 1-1338) [Nicotiana tabacum]
NCBI Description
                   229990
Seq. No.
Seq. ID
                  LIB3196-046-P1-M1-G2
Method
                   BLASTX
NCBI GI
                   g1171035
BLAST score
                   195
                   4.0e-15
E value
Match length
                   50
% identity
                   68
                  METALLOTHIONEIN-LIKE PROTEIN TYPE 2 PKIWI504
NCBI Description
                   >gi 1086021 pir S48038 metallothionein-like protein - kiwi
                   fruit >gi 450245 (L27813) metallothionein-like protein
                   [Actinidia deliciosa]
                   229991
Seq. No.
                  LIB3196-046-P1-M1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q126156
BLAST score
                   630
```

Seq. ID





```
% identity
                  LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
NCBI Description
                   >gi 72288 pir FWCNBB beta-globulin B precursor (clone 134)
                   - upland cotton >gi 167373 (M16936) vicilin precursor.
                   [Gossypium hirsutum] >gi 1171335 (U43727) legumin B
                   [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                   protein C134 [Saguinus oedipus]
                   229992
Seq. No.
                   LIB3196-046-P1-M1-G7
Seq. ID
                   BLASTX
Method
                   g346219
NCBI GI
BLAST score
                   220
                   6.0e-18
E value
                   77
Match length
                   62
% identity
NCBI Description keratin K4a - human (fragment)
Seq. No.
                   229993
                   LIB3196-046-P1-M1-H2
Seq. ID
                   BLASTX
Method
                   q2134781
NCBI GI
                   201
BLAST score
E value
                   6.0e-16
Match length
                   41
% identity
                   APR peptide - human >gi 2135471 pir 184441 immediate early
NCBI Description
                   response gene - human >gi 219476_dbj BAA14111 (D90070) APR
                   peptide [Homo sapiens]
                   229994
Seq. No.
                   LIB3196-046-P1-M1-H8
Seq. ID
                   BLASTX
Method
                   q125080
NCBI GI
BLAST score
                   470
                   2.0e-47
E value
Match length
                   98
                   98
 % identity
                   KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK
NCBI Description
                   14) >gi 2144816 pir KRHUE keratin, 50K type I cytoskeletal
                   - human >gi_386848 (J00124) keratin [Homo sapiens]
                   >gi 4504913 ref NP 000517.1 pKRT14 keratin 14
                   (epidermolysis bullosa simplex, Dowling-Meara, Koebner)
Seq. No.
                   229995
                   LIB3196-047-P1-M1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2522230
BLAST score
                   276
                   2.0e-24
E value
                   123
Match length
 % identity
                   (AB007467) retrotransposon-like gene; the first amino acid
NCBI Description
                   was determined to be leucine [Vicia faba]
                   229996
Seq. No.
```

LIB3196-047-P1-M1-A4





Method BLASTX g3121828 NCBI GI BLAST score 580 E value 3.0e-60 Match length 121 91 % identity BENE PROTEIN >gi\_2135423 pir I38891 hypothetical protein -NCBI Description human (fragment) >gi\_1000712 (U17077) unknown [Homo sapiens] 229997 Seq. No. LIB3196-047-P1-M1-B10 Seq. ID Method BLASTX NCBI GI g266344 475 BLAST score E value 1.0e-47 Match length 115 83 % identity NCBI Description LEUKOCYTE ELASTASE INHIBITOR (LEI) (MONOCYTE/NEUTROPHIL ELASTASE INHIBITOR) (EI) >gi 284073 pir S27383 elastase inhibitor - human >gi 2997692 (AF053630) monocyte/neutrophil elastase inhibitor [Homo sapiens] 229998 Seq. No. LIB3196-047-P1-M1-B12 Seq. ID Method BLASTX NCBI GI g2224557 BLAST score 331 E value 6.0e - 31Match length 128 52 % identity NCBI Description (AB002306) KIAA0308 [Homo sapiens] 229999 Seq. No. LIB3196-047-P1-M1-B4 Seq. ID Method BLASTX NCBI GI g2605714 BLAST score 229 E value 3.0e-19 Match length 59 % identity 68 NCBI Description (AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana] 230000 Seq. No. LIB3196-047-P1-M1-B7 Seq. ID Method/ BLASTX NCBI GI g207905 543 BLAST score E value 7.0e-56 Match length 121 % identity 86 NCBI Description (M18027) alpha globulin B [Artificial gene]

Seq. No. 230001

Seq. ID LIB3196-047-P1-M1-B8

Method BLASTX

Method

NCBI GI

BLASTX

g1363944

```
g1619300
NCBI GI
                   315
BLAST score
E value
                   3.0e-29
                   79
Match length
                   73
% identity
                   (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   230002
                  LIB3196-047-P1-M1-C2
Seq. ID
Method
                  BLASTX
                   g2605714
NCBI GI
BLAST score
                   238
                   2.0e-20
E value
Match length
                   60
% identity
                   (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   230003
Seq. ID
                   LIB3196-047-P1-M1-C4
Method
                  BLASTX
NCBI GI
                   g226407
BLAST score
                   218
                   5.0e-18
E value
Match length
                   89
% identity
                   48
NCBI Description retrotransposon del1-46 [Lilium henryi]
Seq. No.
                   230004
                   LIB3196-047-P1-M1-C7
Seq. ID
                   BLASTX
Method
                   q1363944
NCBI GI
                   441
BLAST score
                   6.0e-44
E value
                   115
Match length
                   80
% identity
                   type I keratin 16 - human >gi_1195531_bbs_172338 (S79867)
NCBI Description
                   type I keratin 16, K16 [human, epidermal keratinocytes,
                   Peptide, 473 aa] [Homo sapiens]
                   230005
Seq. No.
                   LIB3196-047-P1-M1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4056432
                   187
BLAST score
                   2.0e-14
E value
                   54
Match length
% identity
                   (AC005990) Similar to gi\_2245014 glucosyltransferase
NCBI Description
                   homolog from Arabidopsis thaliana chromosome 4 contig
                   gb Z97341. ESTs gb T20778 and gb AA586281 come from this
                   gene. [Arabidopsis thaliana]
                   230006
Seq. No.
                   LIB3196-047-P1-M1-D5
Seq. ID
```

```
BLAST score 668
E value 2.0e-70
Match length 133
% identity 100
NCBI Description type I keratin 16 - human >gi_1195531_bbs_172338 (S79867)
type I keratin 16, K16 [human, epidermal keratinocytes,
Peptide, 473 aa] [Homo sapiens]
```

Seq. No. 230007 Seq. ID LIB3196-047-P1-M1-D8

Method BLASTX
NCBI GI g2270990
BLAST score 203
E value 6.0e-16
Match length 123
% identity 41

NCBI Description (AF004807) dehydrin [Glycine max]

Seq. No. Seq. ID

230008 LIB3196-047-P1-M1-D9

Method BLASTX
NCBI GI g4056432
BLAST score 175
E value 3.0e-13
Match length 60

% identity 60

NCBI Description (AC005990) Similar to gi 2245014 glucosyltransferase

homolog from Arabidopsis thaliana chromosome 4 contig gb\_Z97341. ESTs gb\_T20778 and gb\_AA586281 come from this

gene. [Arabidopsis thaliana]

Seq. No. 230009

Seq. ID LIB3196-047-P1-M1-E2

Method BLASTX
NCBI GI g3273828
BLAST score 220
E value 5.0e-18
Match length 95
% identity 55

NCBI Description (AF068686) nodule-enhanced malate dehydrogenase [Glycine

max]

Seq. No. 230010

Seq. ID LIB3196-047-P1-M1-F1

Method BLASTX
NCBI GI g730932
BLAST score 511
E value 5.0e-52
Match length 132
% identity 78

NCBI Description PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (TGASE

E3) (TRANSGLUTAMINASE 3) >gi\_307504 (L10386)

transglutaminase E3 [Homo sapiens]

>gi\_4507477\_ref\_NP\_003236.1\_pTGM3\_ transglutaminase 3 (E
polypeptide, protein-glutamine-gamma-glutamyltransferase)

NCBI GI BLAST score

```
Seq. ID
                   LIB3196-047-P1-M1-F12
Method
                   BLASTX
NCBI GI
                   g481131
                   395
BLAST score
                   1.0e-38
E value
                   93
Match length
% identity
                   80
NCBI Description
                   sucrose transport protein SUC2 - Arabidopsis thaliana
                   >gi 407092 emb CAA53150 (X75382) sucrose-proton symporter
                   [Arabidopsis thaliana]
Seq. No.
                   230012
                  LIB3196-047-P1-M1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2813965
BLAST score
                   675
                   3.0e-71
E value
Match length
                  135
% identity
                   96
NCBI Description (Z97053) adenosine deaminase (ADA) [Homo sapiens]
Seq. No.
                   230013
Seq. ID
                  LIB3196-047-P1-M1-F9
Method
                  BLASTX
NCBI GI
                   g3123050
BLAST score
                   510
                  8.0e-52
E value
Match length
                  119
% identity
                  77
NCBI Description
                  HYPOTHETICAL PROTEIN KIAA0064 (HA1355)
                  >gi 498154 dbj BAA06542 (D31764) KIAA0064 [Homo sapiens]
Seq. No.
                  230014
Seq. ID
                  LIB3196-047-P1-M1-G1
Method 4
                  BLASTX
NCBI GI
                  g294668
                  550
BLAST score
E value
                  1.0e-56
Match length
                  113
% identity
                  93
NCBI Description (L13242) beta-ketoacyl-ACP synthase [Ricinus communis]
                  230015
Seq. No.
Seq. ID
                  LIB3196-047-P1-M1-G10
Method
                  BLASTX
NCBI GI
                  g4406763
BLAST score
                  147
E value
                  2.0e-09
                  99
Match length
% identity
NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]
                  230016
Seq. No.
Seq. ID
                  LIB3196-047-P1-M1-G4
                  BLASTX
Method
```

33003

g3935151

Match length

97

```
1.0e-53
E value
Match length
                   126
                   73
% identity
                   (AC005106) T25N20.15 [Arabidopsis thaliana]
NCBI Description
                  230017
Seq. No.
                  LIB3196-047-P1-M1-G5
Seq. ID
                  BLASTX
Method
                   g2492901
NCBI GI
                   504
BLAST score
                   3.0e-51
E value
                   100
Match length
                   55
% identity
NCBI Description
                  THYROID RECEPTOR INTERACTING PROTEIN 9 (TRIP9) >gi 703118
                   (L40407) thyroid receptor interactor [Homo sapiens]
                  >gi 4505385 ref NP 002494.1 pNFKBIB nuclear factor of
                   kappa light polypeptide gene enhancer in B-cells inhibitor,
                  beta
                   230018
Seq. No.
                  LIB3196-047-P1-M1-G6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1778294
                   294
BLAST score
                   1.0e-26
E_value
                   95
Match length
% identity
NCBI Description
                  (U70475) p45 NF-E2 related factor 2 [Mus musculus]
                   230019
Seq. No.
                  LIB3196-047-P1-M1-H4
Seq. ID
                  BLASTX
Method
NCBI GI
                   q1688233
                   155
BLAST score
                   2.0e-10
E value
                  94
Match length
% identity
                  446
NCBI Description (U77655) DNA binding protein homolog [Solanum tuberosum]
Seq. No.
                   230020
                  LIB3196-047-P1-M1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1703447
BLAST score
                   310
                   2.0e-28
E value
                   127
Match length
                   57
% identity
                  L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi 496102
NCBI Description
                   (L19141) L-asparaginase [Lupinus albus]
                   230021
Seq. No.
                  LIB3196-047-P1-M1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q225242
BLAST score
                   476
E value
                   5.0e-48
```

```
% identity
                   93
NCBI Description ORF 1708 [Nicotiana tabacum]
                   230022
Seq. No.
Seq. ID
                   LIB3196-047-P1-M1-H8-
Method
                   BLASTX
NCBI GI
                   g728837
BLAST score
                   149
                   2.0e-09
E value
                   64
Match length
                   13
% identity
NCBI Description ALU SUBFAMILY SQ WARNING ENTRY !!!!
Seq. No.
                   230023
Seq. ID
                  LIB3196-047-P1-M1-H9
Method
                   BLASTX
NCBI GI
                   g548900
BLAST score
                   302
                   1.0e-27
E value
                   127
Match length
% identity
                   45
NCBI Description
                  SUCROSE-BINDING PROTEIN PRECURSOR (SBP)
                   >gi 322691 pir JQ1730 62K sucrose-binding protein
                  precursor - soybean >gi_170064 (L06038) glucose binding
                   protein [Glycine max]
                   230024
Seq. No.
Seq. ID
                  LIB3196-048-P1-M1-A3
Method
                  BLASTX
NCBI GI
                   g113471
BLAST score
                   541
```

E value 1.0e-55

Match length 128 % identity 83

NCBI Description ADRENODOXIN PRECURSOR (ADRENAL FERREDOXIN)

>gi\_476388\_pir\_\_AXHU adrenodoxin precursor - human

>gi\_178086 (J03548) adrenodoxin [Homo sapiens] >gi 182494 (M18003) ferredoxin [Homo sapiens] >gi\_182496 (M34788) ferredoxin [Homo sapiens] >gi\_557734 (M23668) adrenodoxin

[Homo sapiens]

Seq. No. 230025

Seq. ID LIB3196-048-P1-M1-A4

BLASTX Method NCBI GI g49868 BLAST score 662 E value 9.0e-70 Match length 129 % identity 100

NCBI Description (X03765) put. beta-actin (aa 27-375) [Mus musculus]

>gi\_387083 (M12481) cytoplasmic beta-actin [Mus musculus]

Seq. No. 230026

Seq. ID LIB3196-048-P1-M1-A6

Method BLASTX NCBI GI g730832 BLAST score 169





E value 5.0e-12 Match length 53 % identity 57

NCBI Description 8.4 KD SULFUR-RICH PROTEIN PRECURSOR (SE60 PROTEIN)

(PROBABLE PROTEINASE INHIBITOR P322) >gi\_99949\_pir\_\_S24965 probable proteinase inhibitor (Bowman-Birk) p322 - soybean >gi\_18748\_emb\_CAA78359\_ (Z13956) a protein similar to

potato tuber protein p322 homolgous to Bowman-Birk

Proteinase Inhibitor [Glycine max]

Seq. No.

Seq. ID LIB3196-048-P1-M1-A9

230027

Method BLASTX
NCBI GI g2062167
BLAST score 268
E value 1.0e-23
Match length 72
% identity 69

NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis

thaliana]

Seq. No.

230028

Seq. ID LIB3196-048-P1-M1-B1

Method BLASTX
NCBI GI g1706562
BLAST score 142
E value 2.0e-09
Match length 34
% identity 74

NCBI Description EMBRYOGENIC-CELL PROTEIN 40 (ECP40) >gi\_485500\_pir\_\_S33538

embryogenic cell protein ecp40 - carrot

>gi\_311368\_emb\_CAA43906 (X61914) ECP40 [Daucus carota]

Seq. No. 230029

Seq. ID LIB3196-048-P1-M1-B11

Method BLASTX
NCBI GI g3122072
BLAST score 599
E value 2.0e-62
Match length 114
% identity 100

NCBI Description ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION

FACTOR TU) (EF-TU) >gi\_2119922\_pir\_\_I50226 elongation factor 1 alpha - chicken >gi\_488468 (L00677) elongation

factor 1 alpha [Gallus gallus]

Seq. No. 230030

Seq. ID LIB3196-048-P1-M1-B12

Method BLASTX
NCBI GI g462333
BLAST score 648
E value 4.0e-68
Match length 129
% identity 100

NCBI Description HEAT SHOCK FACTOR PROTEIN 1 (HSF 1) (HEAT SHOCK

TRANSCRIPTION FACTOR 1) (HSTF 1) >gi\_87630\_pir\_\_A41137 heat shock transcription factor 1 - human >gi\_184403 (M64673)





## heat shock factor 1 [Homo sapiens]

```
230031
Seq. No.
                   LIB3196-048-P1-M1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g225581
BLAST score
                   406
                   9.0e-40
E value
                   96
Match length
% identity
                   83
NCBI Description
                  storage protein C94 [Saguinus oedipus]
Seq. No.
                   230032
Seq. ID
                  LIB3196-048-P1-M1-B5
Method
                   BLASTX
NCBI GI
                   g1076755
BLAST score
                   176
                   7.0e-13
E value
                   104
Match length
% identity
                   33
NCBI Description
                  protein kinase - rice >gi 450300 (L27821) protein kinase
                   [Oryza sativa]
                   230033
Seq. No.
                  LIB3196-048-P1-M1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4103490
BLAST score
                  171
E value
                   1.0e-12
Match length
                   40
                   90
% identity
NCBI Description
                   (AF024519) glucocorticoid-induced leucine zipper GILZ
                  protein [Mus musculus]
Seq. No.
                  230034
Seq. ID
                  LIB3196-048-P1-M1-B9
Method
                  {\tt BLASTX}
                  g167367
NCBI GI
BLAST score
                  516
E value
                  1.0e-52
Match length
                  115
% identity
NCBI Description
                  (L08199) peroxidase [Gossypium hirsutum]
                  230035
Seq. No.
Seq. ID
                  LIB3196-048-P1-M1-C11
Method
                  BLASTX
NCBI GI
                  g231505
BLAST score
                  573
E value
                  2.0e-59
Match length
                  116
% identity
NCBI Description
                  ACTIN 101 >gi 100419 pir S20093 actin - potato
                  >gi_21534_emb_CAA39281 (X55752) actin [Solanum tuberosum]
Seq. No.
                  230036
                  LIB3196-048-P1-M1-C12
Seq. ID
```

```
BLASTX
Method
NCBI GI
                   q3913425
BLAST score
                   317
                   1.0e-43
E value
Match length
                   116
% identity
                   83
                  PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                   HELICASE >gi 2275203 (AC002337) RNA helicase isolog
                   [Arabidopsis thaliana]
Seq. No.
                   230037
Seq. ID
                  LIB3196-048-P1-M1-C2
Method
                  BLASTX
NCBI GI
                  g2129946
BLAST score
                   340
E value
                   3.0e-32
Match length
                   69
                   99
% identity
NCBI Description
                  ADP-ribosylation factor homolog GTP-binding protein NTGB1 -
                   common tobacco (fragment) >gi 1184987 (U46927) NTGB1
                   [Nicotiana tabacum]
Seq. No.
                  230038
Seq. ID
                  LIB3196-048-P1-M1-C3
Method
                  BLASTX
NCBI GI
                  g3915742
BLAST score
                  365
E value
                  3.0e-35
Match length
                  80
                  85
% identity
                  LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi 167319
NCBI Description
                   (M69188) legumin A [Gossypium hirsutum]
                  >gi 444320 prf 1906369A legumin A:ISOTYPE=D alloallele
                   [Gossypium hirsutum]
Seq. No.
                  230039
Seq. ID
                  LIB3196-048-P1-M1-C4
Method
                  BLASTX
NCBI GI
                  g2135267
BLAST score
                  679
E value
                  9.0e-72
Match length
                  129
                  56
% identity
NCBI Description glucose-regulated protein ERp57/GRP58 - human
                  230040
Seq. No.
Seq. ID
                  LIB3196-048-P1-M1-C9
Method
                  BLASTX
NCBI GI
                  g285057
                  588
BLAST score
E value
                  4.0e-61
Match length
                  106
% identity
                  100
NCBI Description
                  zinc finger protein - mouse (fragment)
```

[Mus musculus]

>gi\_403020\_emb\_CAA47353\_ (X66902) En-2/lacZ fusion protein

```
230041
Seq. No.
Seq. ID
                   LIB3196-048-P1-M1-D1
Method
                   BLASTX
NCBI GI
                   g1064828
BLAST score
                   247
E value
                   1.0e-21
Match length
                   62
% identity
                   84
NCBI Description
                  (D78205) Actin [Ipomoea nil]
Seq. No.
                   230042
                   LIB3196-048-P1-M1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g72287
BLAST score
                   526
E value
                   7.0e-54
Match length
                   116
% identity
                   91
NCBI Description
                  beta-globulin A precursor (clone 94) - upland cotton
                   (fragment) >gi 167377 (M16905) legumin precursor [Gossypium
                  hirsutum]
Seq. No.
                   230043
                  LIB3196-048-P1-M1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1351867
                  559
BLAST score
E value
                   1.0e-57
Match length
                   103
% identity
                   100
NCBI Description
                  ACTIN, CYTOPLASMIC 1 (BETA-ACTIN) >gi 761724 (U20114)
                  beta-actin [Cricetulus griseus]
Seq. No.
                  230044
Seq. ID
                  LIB3196-048-P1-M1-D7
Method
                  BLASTX
NCBI GI
                   g137578
BLAST score
                   461
E value
                   3.0e-46
Match length
                  116
% identity
                  76
NCBI Description
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
                  >gi_81545_pir__S06398 alpha-globulin type A precursor -
                  upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi 207906 (M18027) alpha globulin A
                   [Artificial gene] >gi 226119 prf 1410330A vicilin gene A
                   [Saguinus oedipus]
Seq. No.
                  230045
                  LIB3196-048-P1-M1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g567121
BLAST score
                  171
E value
                  2.0e-12
Match length
                  77
% identity
                  48
NCBI Description
                  (M34024) immunoglobulin heavy chain [Homo sapiens]
```

% identity





```
230046
- Seq. No.
 Seq. ID
                    LIB3196-048-P1-M1-E1
                    BLASTX
 Method
                    g280816
 NCBI GI
 BLAST score
                    612
 E value
                    6.0e-64
                    127
 Match length
                    97
 % identity
                    keratin 13, type I, cytoskeletal, short form - human
 NCBI Description
                    >gi 30377 emb CAA36673 (X52426) cytokeratin 13 [Homo
                    sapiens] >gi 3603253 (AF049259) keratin 13 [Homo sapiens]
                    >gi_4504911_ref_NP_002265.1_pKRT13_ keratin
 Seq. No.
                    230047
 Seq. ID
                    LIB3196-048-P1-M1-E11
 Method
                    BLASTX
 NCBI GI
                    g2129832
 BLAST score
                    578
                    6.0e-60
 E value
 Match length
                    111
 % identity
                    94
 NCBI Description
                    heat shock transcription factor 5 - soybean
                    >gi_671868_emb_CAA87080_ (Z46956) heat shock transcription
                    factor 5 [Glycine max]
 Seq. No.
                    230048
 Seq. ID
                    LIB3196-048-P1-M1-E12
 Method
                    BLASTX
 NCBI GI
                    g3915742
 BLAST score
                    570
                    5.0e-59
 E value
 Match length
                    119
 % identity
                    LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi_167319
 NCBI Description
                    (M69188) legumin A [Gossypium hirsutum]
                    >gi 444320 prf 1906369A legumin A:ISOTYPE=D alloallele
                    [Gossypium hirsutum]
 Seq. No.
                    230049
 Seq. ID
                    LIB3196-048-P1-M1-E2
 Method
                    BLASTX
 NCBI GI
                    g4220534
 BLAST score
                    411
                    2.0e-40
 E value
                    104
 Match length
                    70
 % identity
                    (AL035356) putative protein [Arabidopsis thaliana]
 NCBI Description
                    230050
 Seq. No.
                    LIB3196-048-P1-M1-E6
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3913425
 BLAST score
                    515
 E value
                    1.0e-52
 Match length
                    106
```

NCBI GI

E value

BLAST score

g2369714

3.0e-51

503



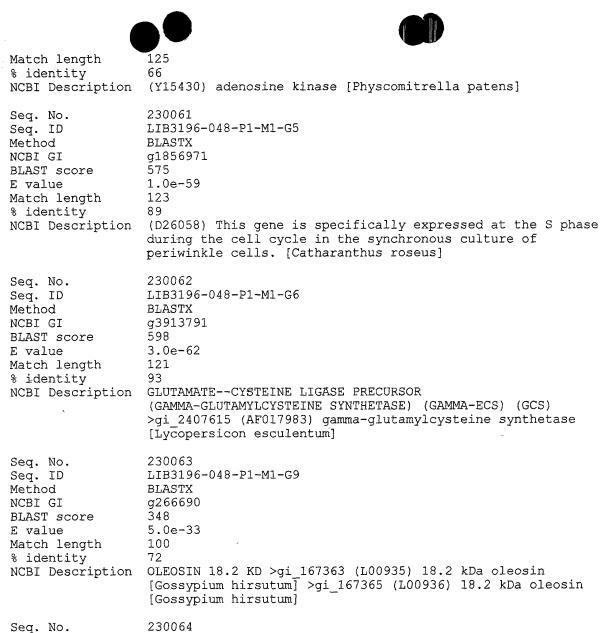
```
NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
                   HELICASE >gi_2275203 (AC002337) RNA helicase isolog
                   [Arabidopsis thaliana]
Seq. No.
                   230051
                  LIB3196-048-P1-M1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3894190
BLAST score
                   240
E value
                   3.0e-20
Match length
                   81
                   54
% identity
NCBI Description
                  (AC005662) putative RNA polymerase [Arabidopsis thaliana]
                  230052
Seq. No.
Seq. ID
                  LIB3196-048-P1-M1-F11
Method
                  BLASTX
NCBI GI
                   g1669533
BLAST score
                  260
E value
                   1.0e-22
Match length
                   93
% identity
                   54
                   (D63643) clathrin coat assembly protein-like [Homo sapiens]
NCBI Description
                  >gi 1770513 emb_CAA67823 (X99458) sigma 3A protein [Homo
                   sapiens] >gi_1923270 (U91932) AP-3 complex sigma3A subunit
                   [Homo sapiens] >gi_3462900 (AF084575) adaptor protein
                   complex-3 sigma3A subunit isoform [Mus musculus]
                   >gi_4502861_ref_NP_001275.1_pCLAPS3_
                   clathrin-associated/assembly/adaptor protein, small 3
                   (22kD)
Seq. No.
                  230053
Seq. ID
                  LIB3196-048-P1-M1-F12
Method
                  BLASTX
NCBI GI
                  g207905
BLAST score
                   644
E value
                  1.0e-67
Match length
                  123
                  100
% identity
NCBI Description
                   (M18027) alpha globulin B [Artificial gene]
                  230054
Seq. No.
Seq. ID
                  LIB3196-048-P1-M1-F2
Method
                  BLASTX
NCBI GI
                  g4049344
BLAST score
                  138
E value .
                  1.0e-08
Match length
                  95
% identity
                  43
NCBI Description
                  (AL034567) putative protein [Arabidopsis thaliana]
                  230055
Seq. No.
Seq. ID
                  LIB3196-048-P1-M1-F7
Method
                  BLASTX
```

```
102
Match length
% identity
                   93
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]
                   230056
Seq. No.
                   LIB3196-048-P1-M1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q115492
BLAST score
                   462
E value
                   2.0e-46
Match length
                   90
% identity
                  CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)
NCBI Description
                   calmodulin-related protein [Petunia hybrida]
                   230057
Seq. No.
                  LIB3196-048-P1-M1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q416585
BLAST score
                   191
E value
                   6.0e-24
                   124
Match length
% identity
                   49
NCBI Description
                  ALCOHOL DEHYDROGENASE, MAJOR >gi_410008_bbs_137224 alcohol
                  dehydrogenase {EC 1.1.1.1} [Alligator
                  mississippiensis=American alligators, liver, Peptide, 374
                  aa]
                   230058
Seq. No.
Seq. ID
                  LIB3196-048-P1-M1-G10
Method
                  BLASTX
NCBI GI
                  g2499946
BLAST score
                   473
E value
                   1.0e-47
Match length
                  120
% identity
NCBI Description
                  URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
                  PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                  DECARBOXYLASE >gi 747980 (U22260) UMP.synthase [Nicotiana
                  tabacum]
Seq. No.
                   230059
Seq. ID
                  LIB3196-048-P1-M1-G2
Method
                  BLASTX
NCBI GI
                  q167311
BLAST score
                  248
E value
                   2.0e-21
Match length
                  78
% identity
NCBI Description
                  (M83301) 2S albumin storage protein [Gossypium hirsutum]
```

Seq. No. 230060

Seq. ID LIB3196-048-P1-M1-G4

Method BLASTX
NCBI GI g2661840
BLAST score 454
E value 2.0e-45



Seq. No. 230064 Seq. ID LIB3196-048-P1-M1-H10

Method BLASTX
NCBI GI g125080
BLAST score 649
E value 3.0e-68

E value 3.0e
Match length 129
% identity 100

NCBI Description KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14) >gi 2144816 pir KRHUE keratin, 50K type I cytoskeletal

- human >gi 386848 (J00124) keratin [Homo sapiens] >gi 4504913 ref NP 000517.1 pKRT14 keratin 14

(epidermolysis bullosa simplex, Dowling-Meara, Koebner)

Seq. No. 230065

Seq. ID LIB3196-048-P1-M1-H11

% identity

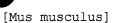
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Method
                   BLASTX
NCBI GI
                   q1694673
BLAST score
                   416
E value
                   6.0e-41
Match length
                   95
% identity
                   85
NCBI Description
                   (D89052) proton-ATPase-like protein [Homo sapiens]
Seq. No.
                   230066
                   LIB3196-048-P1-M1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g547752
BLAST score
                   196
E value
                   4.0e-15
Match length
                   70
% identity
                   47
NCBI Description
                   KERATIN, TYPE II CYTOSKELETAL 2 ORAL (CYTOKERATIN 2P) (K2P)
                   (CK 2P) >gi 2119218 pir I53169 cytokeratin 2 - human
                   >gi 181390 (M99063) cytokeratin 2 [Homo sapiens]
Seq. No.
                   230067
Seq. ID
                   LIB3196-048-P1-M1-H3
Method
                   BLASTX
NCBI GI
                   g133041
BLAST score
                   522
E value
                   2.0e-53
Match length
                   102
                   99
% identity
NCBI Description
                   60S ACIDIC RIBOSOMAL PROTEIN PO (L10E)
                   >gi_71137_pir__R5HUPO acidic ribosomal protein PO - human
                   >gi_19023\overline{2} (M17885) acidic ribosomal phosphoprotein (P0)
                   [Homo sapiens] >gi_2935618_gb_AAC05176_ (AC004263) 60S
                   ACIDIC RIBOSOMAL PROTEIN; match to P05388 (PID:g133041)
                   [Homo sapiens] >gi 4506667 ref NP 000993.1 pRPLP0
                   ribosomal protein, large, PO
Seq. No.
                   230068
Seq. ID
                   LIB3196-048-P1-M1-H5
Method
                   BLASTX
NCBI GI
                   g549063
BLAST score
                   370
E value
                   1.0e-35
Match length
                   94
                   73
% identity
NCBI Description
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
                   factor homolog - rice >gi_303835_dbj_BAA02151 (D12626)
                   21kd polypeptide [Oryza sativa]
                   230069
Seq. No.
Seq. ID
                   LIB3196-048-P1-M1-H7
Method
                   BLASTX
NCBI GI
                   q2388585
BLAST score
                   295
E value
                   3.0e-38
Match length
                   119
```

```
(AC000098) Similar to Caenorhabditis unknown protein
NCBI Description
                  T03F1.1 (gb_U88169). [Arabidopsis thaliana]
                  230070
Seq. No.
                  LIB3196-049-P1-M1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1220196
BLAST score
                  521
                  3.0e-53
E value
Match length
                  121
% identity
                  85
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
                  230071
Seq. No.
                  LIB3196-049-P1-M1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3421134
                  478
BLAST score
                  3.0e-48
E value
                  126
Match length
% identity
                  (AF045666) arginine decarboxylase [Theobroma cacao]
NCBI Description
                  230072
Seq. No.
                  LIB3196-049-P1-M1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1778370
BLAST score
                  512
                  4.0e-52
E value
                  130
Match length
                  74
% identity
NCBI Description (U77678) asparagine synthetase 2 [Glycine max]
                  230073
Seq. No.
                  LIB3196-049-P1-M1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2493852
BLAST score
                  291
                  3.0e - 26
E value
Match length
                  63
                  84
% identity
                  CYTOCHROME C OXIDASE POLYPEPTIDE VC
NCBI Description
                  >gi_1070356_emb_CAA92107_ (Z68091) cytochrome c oxidase, Vc
                  subunit [Hordeum vulgare]
                  230074
Seq. No.
                  LIB3196-049-P1-M1-A7
Seq. ID
Method
                  BLASTX
                  g3641837
NCBI GI
BLAST score
                  176
E value
                  3.0e-13
Match length
                  58
                  69
% identity
                   (AL023094) Nonclathrin coat protein gamma - like protein
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No.

```
LIB3196-049-P1-M1-A9
   Seq. ID
                      BLASTX
   Method
                      g72287
   NCBI GI
   BLAST score
                      292
   E value
                      2.0e-26
   Match length
                      71
                      85
   % identity
                     beta-globulin A precursor (clone 94) - upland cotton
   NCBI Description
                      (fragment) >gi_167377 (M16905) legumin precursor [Gossypium
                      hirsutum]
                      230076
   Seq. No.
                      LIB3196-049-P1-M1-B11
   Seq. ID
   Method
                      BLASTX
                      g126156
   NCBI GI
   BLAST score
                      625
                      2.0e-65
   E value
                      127
   Match length
                      91
   % identity
                      LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
   NCBI Description
                      >gi 72288 pir FWCNBB beta-globulin B precursor (clone 134)
                      - upland cotton >gi_167373 (M16936) vicilin precursor
                      [Gossypium hirsutum] >gi_1171335 (U43727) legumin B
                      [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                      protein C134 [Saguinus oedipus]
   Seq. No.
                      230077
                      LIB3196-049-P1-M1-B12
   Seq. ID
                      BLASTX
   Method
                      g2369714
   NCBI GI
                      617
   BLAST score
   E value
                      2.0e-64
                      127
   Match length
                      93
   % identity
                     (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                      230078
   Seq. No.
   Seq. ID
                      LIB3196-049-P1-M1-B2
   Method
                      BLASTX
   NCBI GI
                      g2894611
                      148
   BLAST score
                      2.0e-09
   E value
   Match length
                      50
   % identity
                      66
                      (AL021889) putative protein [Arabidopsis thaliana]
   NCBI Description
                      230079
   Seq. No.
   Seq. ID
                      LIB3196-049-P1-M1-B3
   Method
                      BLASTX
   NCBI GI
                      g476850
                      610
   BLAST score
                      1.0e-63
   E value
   Match length
                      136
   % identity
                      90
                      heat shock cognate protein 70 - mouse >gi_309319 (M19141)
   NCBI Description
                      heat shock protein 70 cognate [Mus musculus]
                      >gi 1661134 gb AAB18391.1 (U73744) heat shock 70 protein
```





```
230080
Seq. No.
Seq. ID
                  LIB3196-049-P1-M1-B4
Method
                  BLASTX
                  g476850
NCBI GI
                  234
BLAST score
                  1.0e-19
E value
                  83
Match length
                  64
% identity
                  heat shock cognate protein 70 - mouse >gi 309319 (M19141)
NCBI Description
                  heat shock protein 70 cognate [Mus musculus]
                  >gi 1661134_gb_AAB18391.1_ (U73744) heat shock 70 protein
                   [Mus musculus]
                  230081
Seq. No.
Seq. ID
                  LIB3196-049-P1-M1-C2
                  BLASTX
Method
NCBI GI
                  g3452572
                  227
BLAST score
                  1.0e-18
E value
                  47
Match length
                  94
% identity
NCBI Description (AB011399) AF-6 [Homo sapiens]
                  230082
Seq. No.
Seq. ID
                  LIB3196-049-P1-M1-C3
Method
                  BLASTX
NCBI GI
                  g4204303
BLAST score
                  310
                  2.0e-28
E value
                  70
Match length
                  81
% identity
                  (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  230083
Seq. No.
                  LIB3196-049-P1-M1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2460200
BLAST score
                  170
E value
                   4.0e-12
Match length
                   61
% identity
NCBI Description
                   (AF020833) eukaryotic translation initiation factor 3
                  subunit [Homo sapiens]
Seq. No.
                  230084
                  LIB3196-049-P1-M1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4206196
BLAST score
                  241
E value
                  2.0e-20
Match length
                  80
                  55
% identity
```

NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana]

```
230085
Seq. No.
                  LIB3196-049-P1-M1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q167311
BLAST score
                  413
                  6.0e-48
E value
Match length
                  111
% identity
                  89
                  (M83301) 2S albumin storage protein [Gossypium hirsutum]
NCBI Description
                  230086
Seq. No.
Seq. ID
                  LIB3196-049-P1-M1-D1
Method
                  BLASTX
NCBI GI
                  g3702286
BLAST score
                  251
E value
                  1.0e-21
Match length
                  50
% identity
                  (AC005787) R33374_1 [Homo sapiens]
NCBI Description
                  230087
Seq. No.
                  LIB3196-049-P1-M1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3646426
BLAST score
                  394
                  3.0e-38
E value
Match length
                  79
% identity
NCBI Description
                   (AJ223355) mitochondrial dicarboxylate carrier [Rattus
                  norvegicus]
                  230088
Seq. No.
                  LIB3196-049-P1-M1-D6
Seq. ID
Method
                  BLASTX
                  g1170644
NCBI GI
BLAST score
                   342
                   3.0e-32
E value
                  132
Match length
% identity
                  17
                  RING CANAL PROTEIN (KELCH PROTEIN) >gi 577276 (L08483) ring
NCBI Description
                   canal protein [Drosophila melanogaster]
                   230089
Seq. No.
                  LIB3196-049-P1-M1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3193299
                   442
BLAST score
                   6.0e-44
E value
Match length
                   116
% identity
                   (AF069298) Arabidopsis poly(ADP-ribose) polymerase
NCBI Description
                   (GB:Z48243) [Arabidopsis thaliana]
                   230090
Seq. No.
                  LIB3196-049-P1-M1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2129842
```

E value

```
BLAST score
                   174
E value
                   1.0e-12
Match length
                   53
                   58
% identity
                   SE60 protein - soybean >gi_509769_emb_CAA79164_ (Z18359)
NCBI Description
                   seed-specific low molecular weight sulfur-rich protein
                   [Glycine max]
                   230091
Seq. No.
                   LIB3196-049-P1-M1-F11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2708738
                   210
BLAST score
                   9.0e-17
E value
Match length
                   60
% identity
                   (AC003952) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   230092
Seq. No.
                   LIB3196-049-P1-M1-F12
Seq. ID
                   BLASTX
Method
                   g549063
NCBI GI
BLAST score
                   426
                   4.0e-42
E value
                   99
Match length
% identity
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
                   factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
                   230093
Seq. No.
                   LIB3196-049-P1-M1-F2
Seq. ID
Method
                   BLASTX
                   g4033735
NCBI GI
                   596
BLAST score
                   5.0e-62
E value
                   125
Match length
% identity
                   90
                   (AF054284) spliceosomal protein SAP 155 [Homo sapiens]
NCBI Description
                   230094
Seq. No.
                   LIB3196-049-P1-M1-F6
Seq. ID
                   BLASTX
Method
                   q4098129
NCBI GI
                   652
BLAST score
                   1.0e-68
E value
Match length
                   127
                   94
% identity
                   (U73588) sucrose synthase [Gossypium hirsutum]
NCBI Description
                   230095
Seq. No.
                   LIB3196-049-P1-M1-F7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2244734
                   512
BLAST score
                   3.0e-52
```



% identity



```
102
Match length
                   98
% identity
                   (D88414) actin [Gossypium hirsutum]
NCBI Description
                   230096
Seq. No.
                   LIB3196-049-P1-M1-F9
Seq. ID
Method
                   BLASTX
                   q4210948
NCBI GI
BLAST score
                   505
                   2.0e-51
E value
                   118
Match length
% identity
                  (AF085275) DnaJ protein [Hevea brasiliensis]
NCBI Description
                   230097
Seq. No.
Seq. ID
                   LIB3196-049-P1-M1-G1
Method
                   BLASTX
NCBI GI
                   q123571
BLAST score
                   583
                   2.0e-60
E value
                   123
Match length
                   88
% identity
                   HEAT SHOCK 27 KD PROTEIN (HSP 27) (STRESS-RESPONSIVE
NCBI Description
                   PROTEIN 27) (SRP27) (ESTROGEN-REGULATED 24 KD PROTEIN) (28
                   KD HEAT SHOCK PROTEIN) >gi_662841 (L39370) heat shock
                   protein 27 [Homo sapiens]
                   230098
Seq. No.
Seq. ID
                   LIB3196-049-P1-M1-G10
Method
                   BLASTX
NCBI GI
                   q3201969
BLAST score
                   446
                   2.0e-44
E value
Match length
                   109
                   71
% identity
                   (AF068332) submergence induced protein 2A [Oryza sativa]
NCBI Description
                   230099
Seq. No.
Seq. ID
                   LIB3196-049-P1-M1-G11
Method
                   BLASTX
NCBI GI
                   g72287
                   691
BLAST score
E value
                   3.0e-73
Match length
                   127
                   100
% identity
                   beta-globulin A precursor (clone 94) - upland cotton
NCBI Description
                   (fragment) >gi 167377 (M16905) legumin precursor [Gossypium
                   hirsutum]
                   230100
Seq. No.
                   LIB3196-049-P1-M1-G4
Seq. ID
                   {\tt BLASTX}
Method
NCBI GI
                   g3258569
BLAST score
                   338
                   8.0e-32
E value
Match length
                   73
```

```
NCBI Description (U89959) Similar to yeast general negative regulator of
                   transcription subunit 1 [Arabidopsis thaliana]
                  230101
Seq. No.
                  LIB3196-049-P1-M1-G5
Seq. ID
                  BLASTX
Method
                  g2244734
NCBI GI
                   649
BLAST score
                   3.0e-68
E value
Match length
                  128
                   100
% identity
                  (D88414) actin [Gossypium hirsutum]
NCBI Description
Seq. No.
                  230102
                  LIB3196-049-P1-M1-G6
Seq. ID
Method
                  BLASTX
                   g1363944
NCBI GI
BLAST score
                   662
                   1.0e-69
E value
                   134
Match length
                   99
% identity
                  type I keratin 16 - human >gi_1195531_bbs_172338 (S79867)
NCBI Description
                   type I keratin 16, K16 [human, epidermal keratinocytes,
                  Peptide, 473 aa] [Homo sapiens]
Seq. No.
                   230103
Seq. ID
                  LIB3196-049-P1-M1-G7
Method
                  BLASTX
                  g3746652
NCBI GI
                   239
BLAST score
                   4.0e-20
E value
Match length
                   48
% identity
                   100
                   (AF070523) JWA protein [Homo sapiens]
NCBI Description
                   230104
Seq. No.
                   LIB3196-049-P1-M1-G9
Seq. ID
Method
                   BLASTX
                   g4417306
NCBI GI
                   277
BLAST score
                   1.0e-24
E value
                   119
Match length
                   49
% identity
                   (AC006446) putative Athila retroelement ORF1 protein
NCBI Description
                   [Arabidopsis thaliana]
                   230105
Seq. No.
                   LIB3196-049-P1-M1-H1
Seq. ID
Method
                   BLASTX
                   g107554
NCBI GI
BLAST score
                   612
                   6.0e-64
E value
Match length
                   121
% identity
                  pyruvate kinase (EC 2.7.1.40) isozyme M2 - human >gi_338827
NCBI Description
                   (M26252) cytosolic thyroid hormone-binding protein (EC
                   2.7.1.40) [Homo sapiens]
```

Match length

```
230106
Seq. No.
                  LIB3196-049-P1-M1-H10
Seq. ID
                  BLASTX
Method
                  q3757517
NCBI GI
                  181
BLAST score
                  2.0e-13
E value
                  118
Match length
                  5
% identity
                  (AC005167) putative salt-inducible protein [Arabidopsis
NCBI Description
                  thaliana]
                   230107
Seq. No.
                  LIB3196-049-P1-M1-H11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q137578
                   496
BLAST score
                   3.0e-50
E value
                   126
Match length
                   78
% identity
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                   >gi_81545_pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                   [Artificial gene] >gi_226119_prf__1410330A vicilin gene A
                   [Saguinus oedipus]
Seq. No.
                   230108
                   LIB3196-049-P1-M1-H6
Seq. ID
Method
                   BLASTX
                   g3329386
NCBI GI
                   605
BLAST score
                   5.0e-63
E value
Match length
                   117
                   97
% identity
                   (AF038958) synaptic glycoprotein SC2 spliced variant [Homo
NCBI Description
                   sapiens]
Seq. No.
                   230109
                   LIB3196-049-P1-M1-H7
Seq. ID
Method
                   BLASTX
                   g2072626
NCBI GI
                   380
BLAST score
                   1.0e-36
E value
                   123
Match length
% identity
                   (Y12904) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3281856_emb_CAA19751_ (AL031004) Transcription factor
                   II homolog [Arabidopsis thaliana]
                   230110
Seq. No.
                   LIB3196-049-P1-M1-H8
Seq. ID
                   BLASTX
Method
                   g1565225
NCBI GI
                   150
BLAST score
                   9.0e-10
E value
                   29
```

E value

2.0e-56

```
% identity
                  (X95572) salt-tolerance protein [Arabidopsis thaliana]
NCBI Description
                  230111
Seq. No.
                  LIB3196-050-P1-M1-A1
Seq. ID
Method
                  BLASTX
                  g547753
NCBI GI
BLAST score
                  511
                  4.0e-52
E value
Match length
                  110
% identity
NCBI Description KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)
                  230112
Seq. No.
                  LIB3196-050-P1-M1-A10
Seq. ID
Method
                  BLASTX
                  g1346342
NCBI GI
                  314
BLAST score
                  6.0e-29
E value
                  63
Match length
                  97
% identity
                  KERATIN, TYPE I CYTOSKELETAL 17 (CYTOKERATIN 17) (K17) (CK
NCBI Description
                  17) (VERSION 2) >gi_186685 (M28439) keratin type 16 [Homo
                  sapiens]
                  230113
Seq. No.
                  LIB3196-050-P1-M1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417440
BLAST score
                  525
E value
                  1.0e-53
Match length
                  125
% identity
                  DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS)
NCBI Description
                   [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK);
                  GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR)
                   (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE)
                   (GLUTAMYL-GAMMA-SEMIALDEHYDE ... >gi 423821_pir__A46295
                  delta 1-pyrroline-5-carboxylate synthetase - moth bean
                  230114
Seq. No.
                  LIB3196-050-P1-M1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334320
BLAST score
                  518
E value
                   2.0e-56
Match length
                  119
% identity
                  40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
NCBI Description
                  ribosome-associated protein p40 [Glycine max]
Seq. No.
                  230115
Seq. ID
                  LIB3196-050-P1-M1-A8
                  BLASTX
Method
NCBI GI
                  g2499575
BLAST score
                  547
```

```
112
Match length
                   92
% identity
                   PROTEIN KINASE C, MU TYPE (NPKC-MU) >gi_1362911_pir__A53215
NCBI Description
                   protein kinase C (EC 2.7.1.-) mu - human
                   >gi_438373_emb_CAA53384_ (X75756) protein kinase C mu [Homo
sapiens] >gi_4506075_ref_NP_002733.1_pPRKCM_ protein kinase
                   C, mu
                   230116
Seq. No.
                   LIB3196-050-P1-M1-A9
Seq. ID
Method
                   BLASTX
                   g547753
NCBI GI
                   685
BLAST score
                   2.0e-72
E value
Match length
                   141
                   99
% identity
                   KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)
NCBI Description
                   230117
Seq. No.
                   LIB3196-050-P1-M1-B2
Seq. ID
                   BLASTX
Method
                   g1163177
NCBI GI
BLAST score
                   670
                   1.0e-70
E value
                   132
Match length
                   29
% identity
NCBI Description
                    (U33818) inducible poly(A)-binding protein [Homo sapiens]
                   >gi_2801403 (U75686) polyadenylate binding protein [Homo
                   sapiens] >gi_1585757_prf__2201474A inducible
                   poly(A)-binding protein [Homo sapiens]
                   >gi 4504715_ref_NP_003810.1_pIPABP__ UNKNOWN
Seq. No.
                   230118
                   LIB3196-050-P1-M1-B3
Seq. ID
                   BLASTX
Method
                   g4204277
NCBI GI
BLAST score
                   522
                   3.0e-53
E value
Match length
                   110
% identity
                   81
                    (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   230119
Seq. No.
                   LIB3196-050-P1-M1-B7
Seq. ID
Method
                   BLASTX
                   g3745822
NCBI GI
                   592
BLAST score
                   1.0e-61
E value
                   114
Match length
                   100
% identity
                   Chain B, Tubulin Alpha-Beta Dimer, Electron Diffraction
NCBI Description
                   230120
Seq. No.
                   LIB3196-050-P1-M1-B8
Seq. ID
Method
                   BLASTX
                   g3687243
NCBI GI
                   245
BLAST score
```

```
7.0e-21
E value
Match length
                   61
                   79
% identity
NCBI Description
                   (AC005169) putative ribosomal protein [Arabidopsis
                   thaliana]
                   230121
Seq. No.
                   LIB3196-050-P1-M1-B9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2739383
BLAST score
                   450
                   7.0e-45
E value
                   103
Match length
                   79
% identity
                   (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
                   230122
Seq. No.
                   LIB3196-050-P1-M1-C1
Seq. ID
                   BLASTX
Method
                   g126156
NCBI GI
                   585
BLAST score
                   1.0e-60
E value
                   136
Match length
                   84
% identity
                   LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
NCBI Description
                   >gi 72288 pir FWCNBB beta-globulin B precursor (clone 134)
                  - upland cotton >gi_167373 (M16936) vicilin precursor
                   [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                   protein C134 [Saguinus oedipus]
                   230123
Seq. No.
                   LIB3196-050-P1-M1-C2
Seq. ID
                   BLASTX
Method
                   g2792220
NCBI GI
                   320
BLAST score
                   1.0e-29
E value
Match length
                   134
                    47
% identity
                    (AF032688) NBS-LRR type resistance protein [Oryza sativa]
NCBI Description
                   230124
Seq. No.
                   LIB3196-050-P1-M1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g117501
                    553
BLAST score
                    6.0e-57
E value
                   104
Match length
                    98
% identity
                   CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60)
NCBI Description
                    (52 KD RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A)
                   >gi_87015_pir__A37047 calreticulin precursor - human
                    >gi_179882 (M84739) calreticulin [Homo sapiens] >gi_1337487
                    (M32294) Ro ribonucleoprotein autoantigen (Ro/SS-A)
                   precursor [Homo sapiens] >gi 1905911 (AD000092)
```

calreticulin [Homo sapiens]

Method

BLASTX

```
230125
Seq. No.
                  LIB3196-050-P1-M1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2493144
                  391
BLAST score
                  5.0e-38
E value
                  96
Match length
                  83
% identity
                  VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE
NCBI Description
                   16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__$60132
                  H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
                   (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585)
                   vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
                  thaliana]
                  230126
Seq. No.
                  LIB3196-050-P1-M1-C5
Seq. ID
Method
                  BLASTX
                   q2584787
NCBI GI
                   231
BLAST score
                   3.0e-19
E value
                   104
Match length
% identity
                   45
                   (X95762) Aminopeptidase P-like [Homo sapiens]
NCBI Description
Seq. No.
                   230127
                   LIB3196-050-P1-M1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q126156
                   567
BLAST score
                   1.0e-58
E value
                   109
Match length
                   100
% identity
                  LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
NCBI Description
                   >gi 72288_pir__FWCNBB beta-globulin B precursor (clone 134)
                   - upland cotton >gi_167373 (M16936) vicilin precursor
                   [Gossypium hirsutum] >gi_1171335 (U43727) legumin B
                   [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                   protein C134 [Saguinus oedipus]
Seq. No.
                   230128
                   LIB3196-050-P1-M1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1174621
BLAST score
                   166
E value
                   1.0e-11
                   78
Match length
                  -47
% identity
                   T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA)
NCBI Description
                   (CCT-THETA) >gi_1083259_pir__JC4073 TCP-1 containing
                   cytosolic chaperonin (CCT) theta chain - mouse
                   >gi_695625_emb_CAA85521_ (Z37164) CCTtheta, theta subunit
                   of the chaperonin containing TCP-1 (CCT) [Mus musculus]
                   230129
Seq. No.
                   LIB3196-050-P1-M1-C9
Seq. ID
```

```
g88047
NCBI GI
                  193
BLAST score
E value
                  7.0e - 15
Match length
                  40
% identity
                  100
NCBI Description keratin, 46K type I cytoskeletal - human
                  230130
Seq. No.
                  LIB3196-050-P1-M1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455177
BLAST score
                  485
E value
                  5.0e-49
                  132
Match length
                  68
% identity
                   (AL035521) putative protein [Arabidopsis thaliana]
NCBI Description
                  230131
Seq. No.
                  LIB3196-050-P1-M1-D10
Seq. ID
                  BLASTX
Method
                  g120649
NCBI GI
                  467
BLAST score
                  5.0e-47
E value
                  89
Match length
                  99
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
NCBI Description
                  >gi_625203_pir__DEHUG3 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - human >gi_182861 (M17851)
                  glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]
                  >gi_182863 (J02642) glyceraldehyde 3-phosphate
                  dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi_182977
                   (M33197) glyceraldehyde-3-phosphate dehydrogenase (EC
                   1.2.1.12) [Homo sapiens] >gi_182981 (J04038)
                  glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]
                  >gi_224880_prf__1203217A
                  dehydrogenase, glyceraldehydephosphate [Homo sapiens]
Seq. No.
                  230132
Seq. ID
                  LIB3196-050-P1-M1-D11
Method
                  BLASTX
                   g2369714
NCBI GI
                   588
BLAST score
                   4.0e-61
E value
Match length
                   118
                   92
% identity
                   (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                  230133
Seq. No.
                  LIB3196-050-P1-M1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g137578
BLAST score
                   473
                   1.0e-47
E value
Match length
                   134
% identity
                   44
NCBI Description
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
                   >gi 81545_pir__S06398 alpha-globulin type A precursor -
```

```
[Artificial gene] >gi_226119_prf__1410330A vicilin gene A
                   [Saguinus oedipus]
                  230134
Seq. No.
                  LIB3196-050-P1-M1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351867
BLAST score
                   715
                   6.0e-76
E value
Match length
                  133
                  100
% identity
                  ACTIN, CYTOPLASMIC 1 (BETA-ACTIN) >gi 761724 (U20114)
NCBI Description
                  beta-actin [Cricetulus griseus]
Seq. No.
                  230135
                  LIB3196-050-P1-M1-D4
Seq. ID
                  BLASTX
Method
                  q3860275
NCBI GI
                  147
BLAST score
                   3.0e-15
E value
                  88
Match length
% identity
                   (AC005824) putative GTP-binding protein [Arabidopsis
NCBI Description
                   thaliana] >gi_4314395_gb_AAD15605_ (AC006232) putative
                   terminal flower 1 (TFL1) [Arabidopsis thaliana]
                   >gi 4521159 dbj BAA75933.1_ (AB024712) ATC [Arabidopsis
                   thaliana] >gi 4521161_dbj_BAA75931.1_ (AB024714) ATC
                   [Arabidopsis thaliana] >gi_4521163_dbj_BAA75932.1_
                   (AB024715) ATC [Arabidopsis thaliana]
Seq. No.
                   230136
                   LIB3196-050-P1-M1-D5
Seq. ID
                   BLASTX
Method
                   g137578
NCBI GI
                   715
BLAST score
                   6.0e-76
E value
Match length
                   134
                   100
% identity
                   VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                   >gi 81545 pir S06398 alpha-globulin type A precursor -
                   upland cotton >gi 167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                   [Artificial gene] >gi 226119 prf 1410330A vicilin gene A
                   [Saguinus oedipus]
                   230137
Seq. No.
Seq. ID
                   LIB3196-050-P1-M1-D8
Method
                   BLASTX
NCBI GI
                   g3746127
BLAST score
                   403
                   2.0e-39
E value
                   98
Match length
                   79
% identity
                  (U76253) E25B protein [Mus musculus]
NCBI Description
```

upland cotton >gi\_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi\_207906 (M18027) alpha globulin A

```
230138
                  LIB3196-050-P1-M1-D9
Seq. ID
Method
                  BLASTX
                  q2078298
NCBI GI
BLAST score
                  563
                  4.0e-58
E value
Match length
                  133
% identity
                  (U97257) glyceraldehyde 3-phosphate dehydrogenase
NCBI Description
                   [Lycopersicon esculentum]
                  230139
Seq. No.
                  LIB3196-050-P1-M1-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1754538
BLAST score
                  450
                  7.0e-45
E value
Match length
                  93
% identity
                   (U66894) ESX [Homo sapiens] >gi 1841523 (U73843) ESE-1b
NCBI Description
                   [Homo sapiens] >qi 2338756 (AF017307) Ets-related
                   transcription factor [Homo sapiens] >gi_2384740 (AF016295)
                   Ets transcription factor [Homo sapiens] >gi_2459797
                   (U97156) epthelial-specific ets protein [Homo sapiens]
                   230140
Seq. No.
                  LIB3196-050-P1-M1-E12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4006924
BLAST score
                   162
                   1.0e-11
E value
Match length
                   76
                   41
% identity
                   (Z99708) beta-galactosidase like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   230141
                   LIB3196-050-P1-M1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1169534
BLAST score
                   451
E value
                   1.0e-61
                   130
Match length
% identity
                   ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir__S39203
                   phosphopyruvate hydratase (EC 4.2.1.11) - castor bean
                   >gi 433609 emb_CAA82232_ (Z28386) enolase [Ricinus
                   communis]
                   230142
Seq. No.
                   LIB3196-050-P1-M1-E6
Seq. ID
Method
                   BLASTX
                   q106903
NCBI GI
                   213
BLAST score
                   5.0e-17
E value
                   82
Match length
```

```
% identity
                  line-1 protein ORF2 - human
NCBI Description
                   230143
Seq. No.
                  LIB3196-050-P1-M1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2431769
BLAST score
                   227
                   6.0e-19
E value
Match length
                   58
                   76
% identity
                  (U62752) acidic ribosomal protein Pla [Zea mays]
NCBI Description
                   230144
Seq. No.
                  LIB3196-050-P1-M1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g167367
                   525
BLAST score
                   9.0e-54
E value
                   115
Match length
                   90
% identity
                   (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                   230145
Seq. No.
                   LIB3196-050-P1-M1-F10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g683553
BLAST score
                   238
                   5.0e-20
E value
                   109
Match length
                   50
% identity
                   (Z48450) oleosin-like protein [Citrus sinensis]
NCBI Description
                   >gi 1582679_prf__2119230A oleosin homolog [Citrus sinensis]
                   230146
Seq. No.
                   LIB3196-050-P1-M1-F3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3915742
                   539
BLAST score
E value
                   2.0e-55
                   114
Match length
                   90
% identity
                   LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi 167319
NCBI Description
                   (M69188) legumin A [Gossypium hirsutum]
                   >qi 444320 prf 1906369A legumin A:ISOTYPE=D alloallele
                   [Gossypium hirsutum]
                   230147
Seq. No.
                   LIB3196-050-P1-M1-F5
Seq. ID
                   BLASTX
Method
                   g4539335
NCBI GI
                   427
BLAST score
                   3.0e-42
E value
                   131
Match length
                   62
% identity
                  (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
```

```
230148
Seq. No.
                  LIB3196-050-P1-M1-F7
Seq. ID
                  BLASTX
Method
                  g547751
NCBI GI
                  632
BLAST score
                  3.0e-66
E value
                  129
Match length
% identity
                  KERATIN, TYPE I CYTOSKELETAL 17 (CYTOKERATIN 17) (K17) (CK
NCBI Description
                  17) (39.1) (VERSION 1) >gi_422802_pir__S30433 keratin 17,
                  cytoskeletal - human >gi_30379_emb_CAA79626_ (Z19574)
                  cytokeratin 17 [Homo sapiens] >gi_34075_emb_CAA44451_
                   (X62571) keratin related product [Homo sapiens]
                   >gi 4557701 ref_NP_000413.1_pKRT17_ keratin
                  230149
Seq. No.
                  LIB3196-050-P1-M1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3288823
BLAST score
                   376
                   3.0e-36
E value
Match length
                  84
                   83
% identity
                   (AF063852) FUS5 [Arabidopsis thaliana]
NCBI Description
                   230150
Seq. No.
                   LIB3196-050-P1-M1-G3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g478818
BLAST score
                   231
                   3.0e-19
E value
Match length
                   109
                   40
% identity
                   strictosidine synthase - Rauvolfia mannii (fragment)
NCBI Description
                   >gi 21097 emb CAA45025_ (X63431) strictosidine synthase
                   [Rauvolfia mannii]
                   230151
Seq. No.
Seq. ID
                   LIB3196-050-P1-M1-G5
Method
                   BLASTX
                   g464707
NCBI GI
                   570
BLAST score
                   5.0e-59
E value
Match length
                   116
                   96
% identity
                   40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal
NCBI Description
                   protein S18.A - Arabidopsis thaliana
                   >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                   [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)
                   S18 ribosomal protein [Arabidopsis thaliana]
                   >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
                   [Arabidopsis thaliana] >gi 434906 emb CAA82275_ (Z28962)
                   S18 ribosomal protein [Arabidopsis thaliana]
                   >gi 2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A
                   [Arabidopsis thaliana] >gi 3287678 (AC003979) Match to
                   ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A.
                   thaliana. ESTs gb T21121, gb Z17755, gb R64776 and
```

```
protein [Arabidopsis thaliana]
                   230152
Seq. No.
                   LIB3196-050-P1-M1-G9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1350944
                   389
BLAST score
                   8.0e-38
E value
                   80
Match length
                   96
% identity
                   40S RIBOSOMAL PROTEIN S17
NCBI Description
Seq. No.
                   230153
                   LIB3196-050-P1-M1-H1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1663706
                   529
BLAST score
                   4.0e-54
E value
                   100
Match length
                   94
% identity
                   (D87685) similar to human transcription factor TFIIS
NCBI Description
                    (S34159). [Homo sapiens]
                   230154
Seq. No.
                   LIB3196-050-P1-M1-H10
Seq. ID
Method
                   BLASTX
                   g71533
NCBI GI
                   158
BLAST score
                   3.0e-11
E value
                   53
Match length
                   68
% identity
                   keratin, 56K type II cytoskeletal - human
NCBI Description
                   230155
Seq. No.
                   LIB3196-050-P1-M1-H12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g232139
                   282
BLAST score
                   2.0e-25
E value
                   62
Match length
                   87
% identity
                   GUANINE NUCLEOTIDE-BINDING PROTEIN, ALPHA-15 SUBUNIT
NCBI Description
                    (ALPHA-16) >gi_106195_pir__A41096 GTP-binding regulatory
                   protein alpha-\overline{1}6 chai\overline{n} - \overline{hu}man >gi_182892 (M63904)
                    G-alpha-16 protein [Homo sapiens]
                   >gi_4504039_ref_NP_002059.1_pGNA15_ guanine nucleotide
                   binding protein (G protein), alpha 15 (Gq class)
                    230156
Seq. No.
                   LIB3196-050-P1-M1-H3
Seq. ID
                   BLASTX
Method
                    g3319958
NCBI GI
                    445
BLAST score
                    3.0e-44
E value
```

gb R30430 come from this gene. [Arabidopsis thaliana]
>gI 4538910 emb CAB39647.1\_ (AL049482) S18.A ribosomal

137

Match length

Seq. No.

Seq. ID

```
% identity
                  (AJ228139) VAKTI precursor [Homo sapiens]
NCBI Description
                  230157
Seq. No.
                  LIB3196-050-P1-M1-H5
Seq. ID
                  BLASTX
Method
                  q3510462
NCBI GI
                  141
BLAST score
                  6.0e-09
E value
                  27
Match length
                  93
% identity
                  (AF019767) zinc finger protein [Homo sapiens]
NCBI Description
                  >gi 4508021_ref_NP_003895.1_pZNF259__UNKNOWN
Seq. No.
                  230158
                  LIB3196-050-P1-M1-H6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q125080
                  677
BLAST score
                  2.0e-71
E value
                  138
Match length
% identity
                  KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK
NCBI Description
                  14) >gi 2144816 pir KRHUE keratin, 50K type I cytoskeletal
                  - human >gi 386848 (J00124) keratin [Homo sapiens]
                  >gi 4504913 ref NP 000517.1 pKRT14 keratin 14
                   (epidermolysis bullosa simplex, Dowling-Meara, Koebner)
Seq. No.
                  230159
                  LIB3196-050-P1-M1-H7
Seq. ID
Method
                  BLASTX
                  q125080
NCBI GI
BLAST score
                  581
E value
                  2.0e-60
                  115
Match length
                  100
% identity
                  KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK
NCBI Description
                  14) >gi 2144816 pir__KRHUE keratin, 50K typė I cytoskeletal
                   - human >gi 386848 (J00124) keratin [Homo sapiens]
                  >gi 4504913 ref NP 000517.1_pKRT14_ keratin 14
                   (epidermolysis bullosa simplex, Dowling-Meara, Koebner)
                  230160
Seq. No.
                  LIB3196-050-P1-M1-H8
Seq. ID
Method
                  BLASTX
                  q125887
NCBI GI
                   224
BLAST score
                   2.0e-18
E value
                   125
Match length
                   42
% identity
                   ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
NCBI Description
                   >gi 82092 pir S04765 LAT52 protein precursor - tomato
                   >gi 295812 emb CAA33854 (X15855) LAT52 [Lycopersicon
                   esculentum]
                   230161
```

LIB3196-050-P1-M1-H9

```
BLASTX
 Method
NCBI GI
                      q2655037
                      627
 BLAST score
                      1.0e-65
 E value
 Match length
                      133
 % identity
                      (AF019952) tumor suppressing STF cDNA 1 [Homo sapiens]
 NCBI Description
                      >gi_4507703_ref_NP_003301.1_pTSSC1_ tumor suppressing
                      subtransferable candidate
                      230162
 Seq. No.
                      LIB3196-052-P1-M1-A11
 Seq. ID
                      BLASTX
 Method
                      g2605714
 NCBI GI
                      221
 BLAST score
                      4.0e-18
 E value
                      59
 Match length
 % identity
                      (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
 NCBI Description
                      thaliana]
                      230163
 Seq. No.
                      LIB3196-052-P1-M1-A4
 Seq. ID
                      BLASTX
 Method
                      g1346348
 NCBI GI
                      665
 BLAST score
                      4.0e-70
 E value
                      135
 Match length
                      99
  % identity
                      KERATIN, TYPE II CYTOSKELETAL 6E (CYTOKERATIN 6E) (CK 6E)
 NCBI Description
                      (K6E KERATIN) >gi_2119223_pir__I61770 keratin type II - human >gi_908803 (L42611) keratin type II [Homo sapiens]
                      230164
  Seq. No.
                      LIB3196-052-P1-M1-B1
  Seq. ID
                      BLASTX
 Method
                      g2982259
 NCBI GI
  BLAST score
                      504
 E value
                      2.0e-51
 Match length
                      101
  % identity
                      (AF051212) probable 60s ribosomal protein L13a [Picea
  NCBI Description
                      mariana]
                      230165
  Seq. No.
                      LIB3196-052-P1-M1-B11
  Seq. ID
                      BLASTX
  Method
  NĈBI GI
                      g1173267
                      241
  BLAST score
                      1.0e-20
  E value
                      91
  Match length
                      59
  % identity
                      40S RIBOSOMAL PROTEIN S5 >gi_1362935_pir__S55916 ribosomal
  NCBI Description
                      protein S5 - human >gi_550021 (U14970) ribosomal protein S5 [Homo sapiens] >gi_1096942 prf_2113200E ribosomal protein
                      S5 [Homo sapiens] >gi_4506729_ref_NP_001000.1_pRPS5_
                      ribosomal protein S5
```

```
230166
Seq. No.
                  LIB3196-052-P1-M1-B2
Seq. ID
                  BLASTX
Method
                  g1169475
NCBI GI
                  255
BLAST score
                  1.0e-23
E value
                  87
Match length
                  71
% identity
                 ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION
NCBI Description
                  FACTOR TU) (EF-TU) >gi 556301 (M22432) elongation factor Tu
                  [Mus musculus]
                  230167
Seq. No.
                  LIB3196-052-P1-M1-B4
Seq. ID
Method
                  BLASTX
                  q2492860
NCBI GI
BLAST score
                  511
                  4.0e-52
E value
                  127
Match length
                  76
% identity
                  GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 2 PRECURSOR (GSA
NCBI Description
                  2) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 2) (GSA-AT 2)
                  >qi 498914 (U10278) glutamate-1-semialdehyde
                  aminotransferase [Arabidopsis thaliana]
                  230168
Seq. No.
Seq. ID
                  LIB3196-052-P1-M1-B6
Method
                  BLASTX
                  g3122833
NCBI GI
                  365
BLAST score
                  3.0e-35
E value
Match length
                  81
% identity
                  90
NCBI Description 40S RIBOSOMAL PROTEIN S5 >gi 1685071 (U78085) ribosomal
                  protein S5 [Mus musculus]
                  230169
Seq. No.
                  LIB3196-052-P1-M1-C1
Seq. ID
Method
                  BLASTX
                  g1587477
NCBI GI
                   347
BLAST score
                   6.0e-33
E value
                  107
Match length
                   71
% identity
NCBI Description TCOF1 gene [Homo sapiens]
                   230170
Seq. No.
                  LIB3196-052-P1-M1-C11
Seq. ID
Method
                  BLASTX
                   g207905
NCBI GI
BLAST score
                   558
E value
                   1.0e-57
Match length
                   126
                   89
% identity
NCBI Description (M18027) alpha globulin B [Artificial gene]
```

```
Seq. No.
                  230171
                  LIB3196-052-P1-M1-C12
Seq. ID
                  BLASTX
Method
                  g1465772
NCBI GI
                  592
BLAST score
                  1.0e-61
E value
                  130
Match length
                  85
% identity
                   (U61232) cofactor E [Homo sapiens]
NCBI Description
                  >gi 4507375_ref_NP_003184.1_pTBCE_ tubulin-specific
                   chaperone e
                   230172
Seq. No.
                  LIB3196-052-P1-M1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1363944
                   264
BLAST score
                   1.0e-38
E value
                   115
Match length
                   80
% identity
                   type I keratin 16 - human >gi_1195531_bbs_172338 (S79867)
NCBI Description
                   type I keratin 16, K16 [human, epidermal keratinocytes,
                   Peptide, 473 aa] [Homo sapiens]
                   230173
Seq. No.
                   LIB3196-052-P1-M1-C4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1346348
BLAST score
                   656
                   4.0e-69
E value
                   132
Match length
                   99
% identity
                   KERATIN, TYPE II CYTOSKELETAL 6E (CYTOKERATIN 6E) (CK 6E)
NCBI Description
                   (K6E KERATIN) >gi 2119223_pir__I61770 keratin type II -
                   human >gi_908803 (L42611) keratin type II [Homo sapiens]
                   230174
Seq. No.
                   LIB3196-052-P1-M1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4469023
                   523
BLAST score
                   2.0e-53
E value
                   116
Match length
                   88
% identity
                   (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
                   230175
Seq. No.
                   LIB3196-052-P1-M1-C7
Seq. ID
                   BLASTX
Method
                   g1587477
NCBI GI
BLAST score
                   151
                   5.0e-10
E value
                   83
Match length
                   49
% identity
                   TCOF1 gene [Homo sapiens]
NCBI Description
```

Seq. No.

```
LIB3196-052-P1-M1-C8
 Seq. ID
                   BLASTX
 Method
                   g1363944
 NCBI GI
                    583
 BLAST score
                    1.0e-60
 E value
                   118
 Match length
                    98
 % identity
                   type I keratin 16 - human >gi_1195531_bbs_172338 (S79867)
 NCBI Description
                    type I keratin 16, K16 [human, epidermal keratinocytes,
                    Peptide, 473 aa] [Homo sapiens]
                    230177
 Seq. No.
                    LIB3196-052-P1-M1-D11
 Seq. ID
                    BLASTX
 Method
                    g2982303
 NCBI GI
                    564
 BLAST score
                    3.0e-58
 E value
                    127
 Match length
                    82
 % identity
                    (AF051236) hypothetical protein [Picea mariana]
 NCBI Description
                    230178
 Seq. No.
                    LIB3196-052-P1-M1-D12
 Seq. ID
                    BLASTX
 Method
                    g1705654
 NCBI GI
                    630
- BLAST score
                    5.0e-66
 E value
 Match length
                    128
                    96
 % identity
                    80 KD NUCLEAR CAP BINDING PROTEIN (NCBP 80 KD SUBUNIT)
 NCBI Description
                    (CBP80) >gi 1082651_pir__S50082 nuclear cap binding protein
                    - human >gi_563368_emb_CAA56334_ (X80030) cap binding
                    protein [Homo sapiens] >gi_577628_dbj_BAA06769_ (D32002)
                    nuclear cap binding protein [Homo sapiens]
                    >qi 4505343 ref NP 002477.1_pNCBP_ nuclear cap binding
                    protein, 80kD
                    230179
 Seq. No.
                    LIB3196-052-P1-M1-D2
 Seq. ID
                    BLASTX
 Method
                    g730565
 NCBI GI
                    646
 BLAST score
                    7.0e-68
 E value
                    122
 Match length
                    100
 % identity
                    60S RIBOSOMAL PROTEIN L3 >gi_423069_pir__S34195 ribosomal
 NCBI Description
                    protein L3 - human >gi_313659_emb_CAA51839_ (X73460)
                    ribosomal protein L3 [Homo sapiens]
                    >gi_3850177_emb_CAA18450_ (AL022326) dJ333H23.1.1 (60S
                    Ribosomal Protein L3) [Homo sapiens]
                    >gi_4506649_ref_NP_000958.1_pRPL3_ ribosomal protein L3
                    230180
 Seq. No.
                    LIB3196-052-P1-M1-D3
 Seq. ID
                    BLASTX
 Method
                    g1173104
 NCBI GI
                    438
 BLAST score
```

.

```
2.0e-43
E value
                   93
Match length
                   77
% identity
                   RIBONUCLEASE 2 PRECURSOR >gi 289210 (M98336) ribonuclease
NCBI Description
                   [Arabidopsis thaliana] >gi_2\overline{6}42160 (AC003000) ribonuclease,
                   RNS2 [Arabidopsis thaliana]
                   230181
Seq. No.
                   LIB3196-052-P1-M1-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g553182
BLAST score
                   332
                   5.0e-31
E value
Match length
                   78
                   81
% identity
NCBI Description (M99703) class II AP endonuclease [Homo sapiens]
                   230182
Seq. No.
                   LIB3196-052-P1-M1-E1
Seq. ID
                   BLASTX
Method
                   g170354
NCBI GI
BLAST score
                   231
                   2.0e-19
E value
                   53
Match length
                   18
% identity
NCBI Description (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
                   230183
Seq. No.
                   LIB3196-052-P1-M1-E10
Seq. ID
                   BLASTX
Method
                   g3860247
NCBI GI
BLAST score
                   549
                   1.0e-56
E value
                   123
Match length
% identity
                   (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   230184
                   LIB3196-052-P1-M1-E4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2160694
BLAST score
                    623
E value
                    3.0e-65
Match length
                   126
 % identity
                   (U73528) B' regulatory subunit of PP2A [Arabidopsis
NCBI Description
                   thaliana]
 Seq. No.
                    230185
                   LIB3196-052-P1-M1-E5
 Seq. ID
Method
                   BLASTX
 NCBI GI
                    q116026
 BLAST score
                    450
                    7.0e-45
 E value
Match length
                   113
                    83
 % identity
NCBI Description CD63 ANTIGEN (MELANOMA-ASSOCIATED ANTIGEN ME491)
```

Seq. No.

Seq. ID

Method

NCBI GI

E value

Seq. No.

Seq. ID

Method

NCBI GI

E value

Seq. No.

Seq. ID

Method NCBI GI

E value

Seq. No.

Seq. ID Method

NCBI GI

E value

BLAST score

Match length

% identity

Seq. No.

Seq. ID

BLAST score

Match length

% identity

BLAST score

Match length % identity

BLAST score

Match length

% identity

```
(LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 3) (LAMP-3)
                   (OCULAR MELANOMA-ASSOCIATED ANTIGEN) (OMA81H)
                   (GRANULOPHYSIN) >gi_2144873_pir__I38016 melanoma-associated
                   antigen CD63 - human >gi_34527_emb CAA30792_ (X07982) ME491 antigen precursor (AA -1 to 237) [Homo sapiens] >gi_189384
                   (M59907) melanoma-associated antigen [Homo sapiens]
                   >gi_246539_bbs_93790 (S93788) ocular melanoma-associated
                   antigen, OMA81H [human, uveal melanoma, Peptide, 238 aa]
                   [Homo sapiens] >gi_430756_emb_CAA44519_ (X62654) ME491
                   /CD63 antigen [Homo sapiens]
                   >gi_4502679_ref_NP_001771.1_pCD63_ CD63 antigen (melanoma 1
                   antigen)
                   230186
                   LIB3196-052-P1-M1-E6
                   BLASTX
                   g2245108
                   441
                   6.0e-44
                   110
                   75
                  (Z97343) EREBP-4 homolog [Arabidopsis thaliana]
NCBI Description
                   230187
                   LIB3196-052-P1-M1-E7
                   BLASTX
                   q167311
                   563
                   4.0e-58
                   126
                   87
                  (M83301) 2S albumin storage protein [Gossypium hirsutum]
NCBI Description
                   230188
                   LIB3196-052-P1-M1-F11
                   BLASTX
                   g3435312
                   497
                   1.0e-51
                   131
                   (AF083255) RNA helicase-related protein [Homo sapiens]
NCBI Description
                   230189
                   LIB3196-052-P1-M1-F12
                   BLASTX
                   q2493439
                   230
                   4.0e-19
                   46
                   100
                   CALCYPHOSINE >gi 1359717 emb CAA66609 (X97966)
NCBI Description
                   calcyphosine [Homo sapiens] >gi 3075376 (AC004602)
                   CAYP HUMAN; RD25 [Homo sapiens]
                   230190
```

LIB3196-052-P1-M1-F3

Match length

```
Method
                   BLASTX
NCBI GI
                   g266690
BLAST score
                   357
E value
                   5.0e-34
Match length
                   106
                    71
% identity
                   OLEOSIN 18.2 KD >gi_167363 (L00935) 18.2 kDa oleosin [Gossypium hirsutum] >gi_167365 (L00936) 18.2 kDa oleosin
NCBI Description
                    [Gossypium hirsutum]
Seq. No.
                    230191
                   LIB3196-052-P1-M1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                    q728837
BLAST score
                    146
E value
                    8.0e-10
                    90
Match length
                    25
% identity
NCBI Description ALU SUBFAMILY SQ WARNING ENTRY !!!!
                    230192
Seq. No.
                   LIB3196-052-P1-M1-F7
Seq. ID
Method
                    BLASTX
NCBI GI
                    g4138912
                    270
BLAST score
                    8.0e-24
E value
                    55
Match length
                    84
% identity
NCBI Description (AF059487) expansin precursor [Lycopersicon esculentum]
                    230193
Seq. No.
                    LIB3196-052-P1-M1-F9
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2317910
BLAST score
                    460
E value
                    4.0e-46
Match length
                    127
% identity
                    65
                   (U89959) CER1 protein [Arabidopsis thaliana]
NCBI Description
                    230194
Seq. No.
Seq. ID
                    LIB3196-052-P1-M1-G10
                    BLASTX
Method
                    g2145023
NCBI GI
                    225
BLAST score
E value
                    2.0e-18
Match length
                    112
% identity
                   (U97700) 15.5 kDa oleosin [Sesamum indicum]
NCBI Description
                    230195
Seq. No.
                    LIB3196-052-P1-M1-G11
Seq. ID
Method
                    BLASTX
                    g2145023
NCBI GI
BLAST score
                    178
                    5.0e-13
E value
                    97
```

Match length

```
% identity
                   (U97700) 15.5 kDa oleosin [Sesamum indicum]
NCBI Description
                    230196
Seq. No.
                    LIB3196-052-P1-M1-G12
Seq. ID
                    BLASTX
Method
                    g1076457
NCBI GI
BLAST score
                    484
                    7.0e-49
E value
                    107
Match length
                    88
% identity
                    small GTP-binding protein - rape >gi_289370 (L12395) small
NCBI Description
                    GTP-binding protein [Brassica napus]
                    230197
Seq. No.
                    LIB3196-052-P1-M1-G4
Seq. ID
                    BLASTX
Method
                    g4115931
NCBI GI
                    248
BLAST score
                    3.0e-21
E value
Match length
                    104
                    54
% identity
                   (AF118223) contains similarity to Guillardia theta ABC
NCBI Description
                    transporter (GB:AF041468) [Arabidopsis thaliana]
                    230198
Seq. No.
                    LIB3196-052-P1-M1-G5
Seq. ID
                    BLASTX
Method
                    g2459441
NCBI GI
                    277
BLAST score
                    1.0e-24
E value
Match length
                    80
                    70
% identity
                    (AC002332) putative SWI/SNF complex subunit BAF170
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                    230199
                    LIB3196-052-P1-M1-G8
Seq. ID
Method
                    BLASTX
NCBI GI
                    g125080
                    581
BLAST score
E value
                    3.0e-60
                    116
Match length
% identity
                    KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK
NCBI Description
                    14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal - human >gi_386848 (J00124) keratin [Homo sapiens] >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14
                    (epidermolysis bullosa simplex, Dowling-Meara, Koebner)
                    230200
Seq. No.
                    LIB3196-052-P1-M1-H10
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1732511
BLAST score
                    176
                    4.0e-13
E value
```

BLAST score

```
% identity
                   (U62742) Ran binding protein 1 homolog [Arabidopsis
NCBI Description
                   thaliana]
                   230201
Seq. No.
                   LIB3196-052-P1-M1-H4
Seq. ID
                   BLASTX
Method
                   g126156
NCBI GI
                   411
BLAST score
                   2.0e-40
E value
                   82
Match length
                   100
% identity
                   LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
NCBI Description
                   >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134)
                   - upland cotton >gi_167373 (M16936) vicilin precursor
                   [Gossypium hirsutum] >gi_1171335 (U43727) legumin B
                   [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                   protein C134 [Saguinus oedipus]
                   230202
Seq. No.
                   LIB3196-052-P1-M1-H5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q741804
                   474
BLAST score
                   1.0e-47
E value
                   113
Match length
                   80
% identity
NCBI Description protein RAKc [Rattus norvegicus]
                   230203
Seq. No.
                   LIB3196-052-P1-M1-H6
Seq. ID
                   BLASTX
Method
                   g167311
NCBI GI
BLAST score
                   521
                   3.0e-53
E value
                   114
Match length
                   89
% identity
                   (M83301) 2S albumin storage protein [Gossypium hirsutum]
NCBI Description
                   230204
Seq. No.
                   LIB3196-052-P1-M1-H7
Seq. ID
                   BLASTX
Method
                   g3915961
NCBI GI
                    597
BLAST score
                    4.0e-62
E value
                    128
Match length
                    92
% identity
                   HYPOTHETICAL 267 KD PROTEIN (ORF 2280)
NCBI Description
                    >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana
tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical
                   protein [Nicotiana tabacum]
                    230205
Seq. No.
                    LIB3196-052-P1-M1-H9
Seq. ID
                    BLASTX
Method
                    g137578
NCBI GI
                    527
```

```
E value
                   6.0e-54
                  123
Match length
                   88
% identity
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                  >gi_81545_pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                   [Artificial gene] >gi_226119_prf__1410330A vicilin gene A
                   [Saguinus oedipus]
                   230206
Seq. No.
                   LIB3196-053-P1-M1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4469019
BLAST score
                   421
                   2.0e-41
E value
Match length
                   89
% identity
                  (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
                   230207
Seq. No.
                   LIB3196-053-P1-M1-A2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g136140
BLAST score
                   151
                   8.0e-10
E value
                   86
Match length
% identity
                   PUTATIVE AC9 TRANSPOSASE >gi_72973_pir__TQZMCA probable
NCBI Description
                   transposase - maize transposon Ac9
                   230208
Seq. No.
                   LIB3196-053-P1-M1-A5
Seq. ID
                   BLASTX
Method
                   g2147165
NCBI GI
                   529
BLAST score
                   4.0e-54
E value
                   103
Match length -
                   58
 % identity
                   calmodulin - Bidens pilosa >gi_939860_emb_CAA61980_
NCBI Description
                   (X89890) Calmodulin [Bidens pilosa]
                   230209
 Seq. No.
                   LIB3196-053-P1-M1-A6
 Seq. ID
 Method
                   BLASTX
                   g1916850
 NCBI GI
                   187
 BLAST score
                   5.0e-14
 E value
                   113
 Match length
 % identity
                   47
                   (U83463) scaffold protein Pbp1 [Homo sapiens]
 NCBI Description
 Seq. No.
                   230210
                   LIB3196-053-P1-M1-A8
 Seq. ID
                   BLASTX
 Method
                   g3283166
 NCBI GI
```

299

BLAST score

```
4.0e-27
E value
                   112
Match length
                   54
% identity
                   (AF057526) erythrocyte membrane protein Rh50 [Mus musculus]
NCBI Description
                   >gi_3329467 (AF065395) Rh50-like protein [Mus musculus]
                   >gi_3445508_dbj_BAA32441_ (AB015192) 50 kD glycoprotein
                   (Rh50) [Mus musculus]
                   230211
Seq. No.
                   LIB3196-053-P1-M1-B10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2970051
                   579
BLAST score
                   4.0e-60
E value
                   122
Match length
                   92
% identity
                  (AB012110) ARG10 [Vigna radiata]
NCBI Description
                   230212
Seq. No.
                   LIB3196-053-P1-M1-B11
Seq. ID
                   BLASTX
Method
                   g2078529
NCBI GI
                   527
BLAST score
                   6.0e-54
E value
                   123
Match length
                   80
% identity
                   (U89505) Hlark [Homo sapiens]
NCBI Description
                   >gi_4506445_ref_NP_002887.1_pRBM4_ RNA binding motif ...
                   protein
                   230213
Seq. No.
                   LIB3196-053-P1-M1-B2
Seq. ID
                   BLASTX
Method
                   g3193222
NCBI GI
                   169
BLAST score
                   6.0e-12
E value
Match length
                   37
                   89
% identity
                   (AF068687) malate dehydrogenäse [Glycine max]
NCBI Description
                   230214
Seq. No.
                   LIB3196-053-P1-M1-B5
Seq. ID
Method
                   BLASTX
                   g2191175
NCBI GI
BLAST score
                   160
                   7.0e-11
E value
                   125
Match length
                   52
% identity
                   (AF007270) A IG002P16.24 gene product [Arabidopsis
NCBI Description
                   thaliana]
                   230215
Seq. No.
                   LIB3196-053-P1-M1-B8
Seq. ID
Method
                   BLASTX
                   g2443869
NCBI GI
                   518
BLAST score
                   7.0e-53
E value
```

Seq. ID

```
104
Match length
                   99
% identity
                  (AC002985) epsilon-COP [Homo sapiens]
NCBI Description
                   230216
Seq. No.
                  LIB3196-053-P1-M1-B9
Seq. ID
                   BLASTX
Method
                   g4097714
NCBI GI
                   656
BLAST score
                   5.0e-69
E value
Match length
                   139
                   90
% identity
NCBI Description (U67734) cPLA2 interacting protein [Homo sapiens]
                   230217
Seq. No.
                   LIB3196-053-P1-M1-C1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1381394
                   432
BLAST score
                   4.0e-43
E value
                   89
Match length
                   91
% identity
NCBI Description (U40989) tat interactive protein [Homo sapiens]
                   230218
Seq. No.
                   LIB3196-053-P1-M1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4467128
BLAST score
                   280
                   6.0e-25
E value
                   79
Match length
                   68
% identity
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]
                   230219
Seq. No.
                   LIB3196-053-P1-M1-C3
Seq. ID
                   BLASTX
Method
                   g1161926
NCBI GI
BLAST score
                   575
                   1.0e-59
E value
                   119
Match length
                   87
% identity
                   (U34392) alpha-carboxyltransferase aCT-1 precursor [Glycine
NCBI Description
                   max]
                   230220
Seq. No.
                   LIB3196-053-P1-M1-C4
Seq. ID
                   BLASTX
Method
                   g2558938
NCBI GI
BLAST score
                   286
                   1.0e-25
E value
Match length
                   131
                   49
 % identity
                   (AF024625) arm repeat containing protein [Brassica napus]
NCBI Description
                   230221
Seq. No.
```

LIB3196-053-P1-M1-C6

```
BLASTX
Method
                   q2244847
NCBI GI
                   147
BLAST score
                   2.0e-09
E value
                   91
Match length
                   42
% identity
                   (Z97337) hydroxyproline-rich glycoprotein homolog
NCBI Description
                   [Arabidopsis thaliana]
                   230222
Seq. No.
                   LIB3196-053-P1-M1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2654435
                   565
BLAST score
                   6.0e-61
E value
Match length
                   133
                   82
% identity
                   (U68187) extracellular matrix protein 1 [Homo sapiens]
NCBI Description
                   230223
Seq. No.
                   LIB3196-053-P1-M1-D1
Seq. ID
                   BLASTX
Method
                   g88052
NCBI GI
                   694
BLAST score
                   2.0e-73
E value
                   139
Match length
                   100
% identity
                   keratin K5, 58K type II, epidermal (version 2) - human
NCBI Description
                   (fragment)
                   230224
Seq. No.
                   LIB3196-053-P1-M1-D10
Seq. ID
                   BLASTX
Method
                   g2642448
NCBI GI
                   156
BLAST score
                   2.0e-10
E value
                   43
Match length
                   47
% identity
                   (AC002391) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3169187 (AC004401) hypothetical protein [Arabidopsis
                   thaliana]
                   230225
Seq. No.
                   LIB3196-053-P1-M1-D12
Seq. ID
                   BLASTX
Method
                   g266691
NCBI GI
                   398
BLAST score
                   8.0e-39
E value
                   119
Match length
                   71
% identity
                   OLEOSIN 16.4 KD >gi_167361 (L00934) 16.4 kDa oleosin
NCBI Description
                   [Gossypium hirsutum]
                   230226
Seq. No.
                   LIB3196-053-P1-M1-D2
Seq. ID
Method
                   BLASTX
                   g1653016
NCBI GI
```

```
154
BLAST score
                  4.0e-10
E value
                  87
Match length
                  40
% identity
NCBI Description (D90910) hypothetical protein [Synechocystis sp.]
                  230227
Seq. No.
                  LIB3196-053-P1-M1-D4
Seq. ID
                  BLASTX
Method
                  g4510363
NCBI GI
BLAST score
                  212
                  2.0e-34
E value
Match length
                  89
                  84
% identity
                  (AC007017) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  230228
Seq. No.
                  LIB3196-053-P1-M1-D9
Seq. ID
                  BLASTX
Method
                  g1085384
NCBI GI
                  299
BLAST score
                  3.0e-27
E value
                  79
Match length
                  65
% identity
                  Sm protein F - human >gi_806564_emb_CAA59688_ (X85372) Sm
NCBI Description
                  protein F [Homo sapiens]
                  >gi_4507131_ref_NP_003086.1_pSNRPF_ small nuclear
                  ribonucleoprotein polypeptide F
                  230229
Seq. No.
                  LIB3196-053-P1-M1-E10
Seq. ID
                  BLASTX
Method
                   g2662343
NCBI GI
                   633
BLAST score
                   2.0e-66
E value
                   126
Match length
                   96
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                   230230
Seq. No.
                   LIB3196-053-P1-M1-E12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g464707
BLAST score
                   521
                   3.0e-53
E value
                   106
Match length
                   95
% identity
                   40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal
NCBI Description
                   protein S18.A - Arabidopsis thaliana
                   >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                   [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)
                   S18 ribosomal protein [Arabidopsis thaliana]
                   >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein *
                   [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)
                   S18 ribosomal protein [Arabidopsis thaliana]
                   >gi 2505871 emb CAA72909 (Y12227) ribosomal protein S18A
```

E value

Match length

```
[Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal
protein [Arabidopsis thaliana]
 230231
```

```
Seq. No.
                   LIB3196-053-P1-M1-E4
Seq. ID
Method
                   BLASTX
                   g2134892
NCBI GI
BLAST score
                   340
                   2.0e-32
E value
                   76
Match length
                   89
% identity
                  cell surface glycoprotein - human >gi_188256 (M60334) cell
NCBI Description
                   surface glycoprotein [Homo sapiens]
                   >gi 1834460 emb CAB06609_ (Z84814) HLA-DRA*0102 [Homo
                   sapiens]
                   230232
Seq. No.
                   LIB3196-053-P1-M1-E5
Seq. ID
                   BLASTX
Method
                   g30851
NCBI GI
                   192
BLAST score
                   4.0e-15
E value
Match length
                   38
% identity
                   97
                  (X62421) homologue to E.coli DnaJ protein [Homo sapiens]
NCBI Description
                   230233
Seq. No.
                   LIB3196-053-P1-M1-E6
Seq. ID
                   BLASTX
Method
                   g3414809
NCBI GI
                   150
BLAST score
                   4.0e-10
E value
Match length
                   76
% identity
                   49
                  (AF061529) rjs [Mus musculus]
NCBI Description
                   230234
Seq. No.
                   LIB3196-053-P1-M1-F10
Seq. ID
                   BLASTX
Method
                   g2245138
NCBI GI
                   185
BLAST score
                   7.0e-14
E value
                   63
Match length
                   62
 % identity
                   (Z97344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   230235
 Seq. No.
                   LIB3196-053-P1-M1-F12
 Seq. ID
                   BLASTX
Method
                   g4539005
NCBI GI
                   250
BLAST score
                   2.0e-21
```

```
% identity
                  (AL049481) putative oxidoreductase [Arabidopsis thaliana]
NCBI Description
                   230236
Seq. No.
                   LIB3196-053-P1-M1-G11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g126156
                   313
BLAST score
E value
                   7.0e-29
                   109
Match length
                   60
% identity
                   LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
NCBI Description
                   >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134)
                   - upland cotton >gi_167373 (M16936) vicilin precursor
                   [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                   protein C134 [Saguinus oedipus]
                   230237
Seq. No.
                   LIB3196-053-P1-M1-G12
Seq. ID
                   BLASTX
Method
                   g226120
NCBI GI
                   218
BLAST score
                   1.0e-17
E value
                   83
Match length
                    54
% identity
NCBI Description vicilin gene B [Saguinus oedipus]
                    230238
Seq. No.
                   LIB3196-053-P1-M1-G3
Seq. ID
                   BLASTX
Method
                    g1346347
NCBI GI
                    498
BLAST score
                    2.0e-50
E value
                    102
Match length
% identity
NCBI Description KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D)
                    (K6D KERATIN) >gi_2119225_pir__I61769 keratin type II -
                    human (fragment) \overline{>}gi 9148\overline{3}3 (\overline{L4}2610) keratin type II [Homo
                    sapiens]
                    230239
Seq. No.
                    LIB3196-053-P1-M1-G5
Seq. ID
                    BLASTX
Method
                    g122106
NCBI GI
                    398
BLAST score
                    6.0e-39
E value
                    80
Match length
                    100
% identity
                    HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize
NCBI Description
                    >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana
                    >gi_2119028_pir__S60475 histone H4 - garden pea
                    >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum
                    aestivum] >gi 166740 (M17132) histone H4 [Arabidopsis
                    thaliana] >gi 166742 (M17133) histone H4 [Arabidopsis
                    thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays]
                    >gi 168501 (M13370) histone H4 [Zea mays] >gi_168503
```

E value

4.0e-09

```
>gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
                     >gi 4580385 gb AAD24364.1_AC007184_4 (AC007184) histone H4
                     [Arabidopsis thaliana] >gi_225838_prf__1314298A histone H4
                     [Arabidopsis thaliana]
 Seq. No.
                     230240
 Seq. ID
                     LIB3196-053-P1-M1-G6
 Method
                     BLASTX
 NCBI GI
                     q4263779
                     353
 BLAST score
                     2.0e-33
 E value
 Match length
                     104
 % identity
                     66
 NCBI Description (AC006068) hypothetical protein [Arabidopsis thaliana]
                     230241
 Seq. No.
                     LIB3196-053-P1-M1-H10
 Seq. ID
 Method
                     BLASTX
 NCBI GI
                     q106322
 BLAST score
                     197
 E value
                     2.0e-21
                     87
 Match length
                     59
 % identity
 NCBI Description hypothetical protein (L1H 3' region) - human
                     230242
 Seq. No.
                     LIB3196-053-P1-M1-H4
 Seq. ID
 Method
                     BLASTX
                     g1363944
 NCBI GI
                     695
 BLAST score
 E value
                     1.0e-73
                     139
Match length
  % identity
                     type I keratin 16 - human >gi_1195531_bbs_172338 (S79867)
type I keratin 16, K16 [human, epidermal keratinocytes,
NCBI Description
                     Peptide, 473 aa] [Homo sapiens]
                     230243
  Seq. No.
                     LIB3196-053-P1-M1-H8
  Seq. ID
 Method
                     BLASTX
  NCBI GI
                     g4512699
  BLAST score
                     396
                     1.0e-38
  E value
 Match length
                     115
  % identity
                     (AC006569) putative NADH-ubiquinone oxireductase
  NCBI Description
                     [Arabidopsis thaliana]
                     230244
  Seq. No.
                     LIB3196-053-P1-M1-H9
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g3861068
  BLAST score
                     145
```

(M13377) histone H4 [Zea mays] >gi\_498898 (U10042) histone

H4 homolog [Pisum sativum] >gi\_1806285\_emb\_CAB01914\_(Z79638) histone H4 homologue [Sesbania rostrata]

```
65
Match length
                   45
% identity
                  (AJ235272) unknown [Rickettsia prowazekii]
NCBI Description
                   230245
Seq. No.
                  LIB3196-054-P1-M1-A1
Seq. ID
Method
                   BLASTX
                   g1236083
NCBI GI
BLAST score
                   398
                   8.0e-39
E value
Match length
                   123
                   69
% identity
                  (U49507) Lisch7 [Mus musculus]
NCBI Description
                   230246
Seq. No.
                   LIB3196-054-P1-M1-A11
Seq. ID
                   BLASTX
Method
                   g2578033
NCBI GI
                   544
BLAST score
                   6.0e-56
E value
                   109
Match length
                   92
% identity
NCBI Description (X97016) omega-6 desaturase [Gossypium hirsutum]
                   230247
Seq. No.
                   LIB3196-054-P1-M1-A12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2443751
                   136
BLAST score
                   7.0e-09
E value
Match length
                   83
                   54
% identity
                   (AF020303) fumarase [Arabidopsis thaliana] >gi_2529676
NCBI Description
                   (AC002535) putative fumarase [Arabidopsis thaliana]
                   230248
Seq. No.
Seq. ID
                   LIB3196-054-P1-M1-A4
Method
                   BLASTX
                   g1336807
NCBI GI
                   337
BLAST score
                   1.0e-31
E value
Match length
                   119
% identity
                   58
                   (S81193) CEN=GTP-binding protein homolog
NCBI Description
                   [Antirrhinum=snapdragons, Peptide, 181 aa] [Antirrhinum]
                   >gi 1587482_prf__2206476A CEN gene [Antirrhinum sp.]
Seq. No.
                   230249
                   LIB3196-054-P1-M1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2702281
BLAST score
                   147
E value
                   2.0e-09
Match length
                   59
% identity
                   51
                   (AC003033) putative protein disulfide isomerase precursor
NCBI Description
```

[Arabidopsis thaliana]

Match length

```
230250
Seq. No.
Seq. ID
                  LIB3196-054-P1-M1-A7
Method
                  BLASTX
                  g225280
NCBI GI
                  339
BLAST score
                  5.0e-32
E value
                  72
Match length
% identity
NCBI Description rpoC-like ORF 548 [Nicotiana tabacum]
                  230251
Seq. No.
                  LIB3196-054-P1-M1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3024646
                  602
BLAST score
                  1.0e-62
E value
                  119
Match length
                  98
% identity
                  STEROL REGULATORY ELEMENT BINDING PROTEIN-2 (SREBP-2)
NCBI Description
                   (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 2)
                  >gi_1082805_pir__A54962 sterol regulatory element binding
                  protein 2 precursor - human >gi 451330 (U02031) sterol
                  regulatory element binding protein-2 [Homo sapiens]
                  230252
Seq. No.
                  LIB3196-054-P1-M1-B1
Seq. ID
                  BLASTX
Method
                   g113950
NCBI GI
                   623
BLAST score
                   3.0e-65
E value
Match length
                   126
% identity
                  ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN)
NCBI Description
                   (CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL ANTICOAGULANT
                   PROTEIN IV) (PAP-IV) >gi_71761_pir__LUHU36 annexin II -
                   human >gi_219910_dbj_BAA00013_ (D00017) lipocortin II [Homo
                   sapiens]
                   230253
Seq. No.
                   LIB3196-054-P1-M1-B11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1136402
                   326
BLAST score
                   3.0e - 30
E value
                   112
Match length
                   62
% identity
                   (D79993) similar to hypothetical protein L8167.6 of
NCBI Description
                   Saccharomyces cerevisiae. [Homo sapiens]
                   230254
Seq. No.
                   LIB3196-054-P1-M1-B12
Seq. ID
Method
                   BLASTX
                   g399413
NCBI GI
                   691
BLAST score
                   4.0e-73
E value
```

NCBI Description

```
% identity
                     ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION
NCBI Description
                     FACTOR TU) (EF-TU) >gi_72869_pir__EFRB1 translation
                     elongation factor eEF-1 alpha chain - rabbit
                     >gi 1070665_pir__EFHU1 translation elongation factor eEF-1
alpha-1 chain - human >gi 1551_emb_CAA44162_ (X62245)
elongation factor 1 alpha [Oryctolagus cuniculus]
                     >gi_31098_emb_CAA27245 (X03558) EF-1 alpha (aa 1-463)
[Homo sapiens] >gi_181963 (J04617) elongation factor
                     EF-1-alpha [Homo sapiens] >gi 495221 (U09823) elongation
                     factor 1 alpha [Oryctolagus cuniculus]
                     >gi_4503471_ref_NP_001393.1_pEEF1A1_ eukaryotic translation
                     elongation factor 1 alpha
                     230255
Seq. No.
                     LIB3196-054-P1-M1-B2
Seq. ID
                     BLASTX
Method
                     q280816
NCBI GI
                     661
BLAST score
                     1.0e-69
E value
                     134
Match length
% identity
                     keratin 13, type I, cytoskeletal, short form - human
NCBI Description
                     >gi_30377_emb_CAA36673_ (X52426) cytokeratin 13 [Homo sapiens] >gi_3603253 (AF049259) keratin 13 [Homo sapiens]
                     >gi_4504911_ref_NP_002265.1_pKRT13_ keratin
                     230256
Seq. No.
                     LIB3196-054-P1-M1-B6
Seq. ID
                     BLASTX
Method
                     g3282092
NCBI GI
BLAST score
                     165
                      1.0e-11
E value
                      108
Match length
% identity
NCBI Description (AJ007446) hypothetical protein [Thermotoga neapolitana]
                      230257
Seq. No.
                      LIB3196-054-P1-M1-B7
Seq. ID
                      BLASTX
Method
                      q3309082
NCBI GI
BLAST score
                      544
                      6.0e-56
E value
Match length
                      125
% identity
                      (AF076251) calcineurin B-like protein 1 [Arabidopsis
NCBI Description
                      thaliana]
Seq. No.
                      230258
                      LIB3196-054-P1-M1-B8
Seq. ID
Method
                      BLASTX
NCBI GI
                      g183663
BLAST score
                      167
                      1.0e-11
E value
Match length
                      32
 % identity
                      (M99422) glutathione transferase [Homo sapiens]
```

```
230259
  Seq. No.
                      LIB3196-054-P1-M1-C11
  Seq. ID
                      BLASTX
  Method
  NCBI GI
                      g2921213
                      462
  BLAST score
                      2.0e-46
  E value
                      123
  Match length
                      73
  % identity
                      (AF026150) beta-ketoacyl-ACP synthase IIIA [Perilla
  NCBI Description
                      frutescens]
                      230260
  Seq. No.
                      LIB3196-054-P1-M1-C3
  Seq. ID
                      BLASTX
  Method
  NCBI GI
                      q2244975
                      499
  BLAST score
                      1.0e-50
  E value
                      125
  Match length
                      73
  % identity
                     (Z97340) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
                      230261
  Seq. No.
                      LIB3196-054-P1-M1-C4
  Seq. ID
                      BLASTX
  Method
                      g125077
  NCBI GI
  BLAST score
                      367
                      4.0e-35
  E value
                      76
  Match length
                      91
   % identity
                      KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK
  NCBI Description
                      13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal, long form - human >gi_34033_emb_CAA32786_ (X14640) keratin
                      13 [Homo sapiens]
                      230262
   Seq. No.
   Seq. ID
                      LIB3196-054-P1-M1-C6
Method
                      BLASTX
                      g2583129
   NCBI GI
                      297
   BLAST score
                      5.0e-27
   E value
   Match length
                      81
                      70
   % identity
                       (AC002387) putative methionine aminopeptidase [Arabidopsis
   NCBI Description
                      thaliana]
                      230263
   Seq. No.
                      LIB3196-054-P1-M1-C7
   Seq. ID
                      BLASTX
   Method
   NCBI GI
                      g2145023
                      167
   BLAST score
                      1.0e-11
   E value
                      71
   Match length
   % identity
                      (U97700) 15.5 kDa oleosin [Sesamum indicum]
   NCBI Description
```

230264

Seq. No.

```
LIB3196-054-P1-M1-D1
Seq. ID
                    BLASTX
Method
                    q3024665
NCBI GI
                    199
BLAST score
                    2.0e-15
E value
                    116
Match length
                    40
% identity
                    STRICTOSIDINE SYNTHASE 3 PRECURSOR >gi_1754987 (U43946)
NCBI Description
                    strictosidine synthase [Arabidopsis thaliana]
                    230265
Seq. No.
                    LIB3196-054-P1-M1-D10
Seq. ID
                    BLASTX
Method
                    q3128168
NCBI GI
                    171
BLAST score
                    3.0e-12
E value
                    43
Match length
                    60
% identity
                     (AC004521) putative carboxyl-terminal peptidase
NCBI Description
                     [Arabidopsis thaliana]
                    230266
Seq. No.
                    LIB3196-054-P1-M1-D11
Seq. ID
                    BLASTX
Method
                    g1223922
NCBI GI
                     305
BLAST score
                     6.0e-28
E value
Match length ·
                     67
                     81
% identity
                     (U49445) Vigna radiata vicilin peptidohydrolase [Vigna
NCBI Description
                     radiata]
                     230267
Seq. No.
                     LIB3196-054-P1-M1-D12
Seq. ID
                     BLASTX
Method
                     g3875242
NCBI GI
                     207
BLAST score
E value
                     2.0e-16
                     85
Match length
% identity
                     (Z75532) similar to mitochrondrial carrier protein; cDNA
NCBI Description
                     EST yk264h5.5 comes from this gene [Caenorhabditis elegans]
                     230268
 Seq. No.
                     LIB3196-054-P1-M1-D2
 Seq. ID
                     BLASTX
Method
                     g137578
NCBI GI
                     547
 BLAST score
                     2.0e-56
E value
                     125
Match length
                     86
 % identity
                     VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                     >gi_81545_pir__S06398 alpha-globulin type A precursor -
upland cotton >gi_167371 (M19378) vicilin precursor
[Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                     [Artificial gene] >gi_226119_prf 1410330A vicilin gene A
```

[Saguinus oedipus]

```
230269
Seq. No.
                  LIB3196-054-P1-M1-D3
Seq. ID
Method
                  BLASTX
                  g115833
NCBI GI
                  460
BLAST score
                  4.0e-46
E value
                  117
Match length
                  77
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR
NCBI Description
                   (CAB-10A) (LHCP) >gi_100195_pir__S11877 chlorophyll
                  a/b-binding protein Cab10A - tomato >gi_170394 (M32605)
                  a-binding protein [Lycopersicon esculentum]
                  230270
Seq. No.
                  LIB3196-054-P1-M1-D4
Seq. ID
                  BLASTX
Method
                  g3080405
NCBI GI
                   290
BLAST score
                   4.0e-26
E value
                  100
Match length
                   57
% identity
                  (AL022603) Lsd1 like protein [Arabidopsis thaliana]
NCBI Description
                  ->gi 4455269_emb CAB36805.1_ (AL035527) Lsd1 like protein
                   [Arabidopsis thaliana]
                   230271
Seq. No.
                   LIB3196-054-P1-M1-D6
Seq. ID
Method
                  BLASTX
                   q3885334
NCBI GI
                   596
BLAST score
                   5.0e-62
E value
                   125
Match length
% identity
                   (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                   thaliana]
                   230272
Seq. No.
                   LIB3196-054-P1-M1-D9
Seq. ID
Method
                   BLASTX
                   q421876
NCBI GI
                   364
BLAST score
                   8.0e-35
E value
Match length
                   114
                   66
% identity
                   probable ATP synthase chain - soybean
NCBI Description
                   -
>gi_396230_emb_CAA52349_ (X74296) putative ATP synthase
                   subunit [Glycine max]
                   230273
Seq. No.
                   LIB3196-054-P1-M1-E1
Seq. ID
                   BLASTX
Method
                   g4415936
NCBI GI
                   218
BLAST score
                   1.0e-17
E value
                   55
Match length
                   71
% identity
```

```
NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]
                  230274
Seq. No.
                  LIB3196-054-P1-M1-E10
Seq. ID
                  BLASTX
Method
                  q3080416
NCBI GI
                  182
BLAST score
                  1.0e-13
E value
                  41
Match length
                  85
% identity
                  (AL022604) UDP-galactose transporter - like protein
NCBI Description
                   [Arabidopsis thaliana]
                  230275
Seq. No.
                  LIB3196-054-P1-M1-E11
Seq. ID
Method
                  BLASTX
                  g1888357
NCBI GI
                  515
BLAST score
                  1.0e-52
E value
                  123
Match length
                   75
% identity
                   (X98130) alpha-mannosidase [Arabidopsis thaliana]
NCBI Description
                  >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase
                  precursor [Arabidopsis thaliana]
                   230276
Seq. No.
                  LIB3196-054-P1-M1-E2
Seq. ID
Method
                   BLASTX
                   g125080
NCBI GI
                   238
BLAST score
                   5.0e-20
E value
                   120
Match length
                   45
% identity
                   KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK
NCBI Description
                   14) >gi_2144816_pir__KRHUE keratin, 50K type I cytoskeletal
                   - human >gi_386848 (J00124) keratin [Homo sapiens]
                   >gi_4504913_ref_NP_000517.1_pKRT14_ keratin 14
                   (epidermolysis bullosa simplex, Dowling-Meara, Koebner)
                   230277
Seq. No.
                   LIB3196-054-P1-M1-E4
Seq. ID
                   BLASTX
Method
                   g3540195
NCBI GI
                   604
BLAST score
                   5.0e-63
E value
                   122
Match length
                   44
% identity
                   (AC004260) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   230278
Seq. No.
                   LIB3196-054-P1-M1-E7
Seq. ID
                   BLASTX
Method
                   g2160158
NCBI GI
                   213
BLAST score
                   3.0e-17
E value
                   48
Match length
```

81

% identity

```
NCBI Description (AC000132) Similar to elongation factor 1-gamma
                   (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]
                   230279
Seq. No.
                  LIB3196-054-P1-M1-E8
Seq. ID
                   BLASTX
Method
                   g115421
NCBI GI
                   685
BLAST score
                   2.0e-72
E value
                   133
Match length
                   30
% identity
                  NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
NCBI Description
                   >gi_319925_pir__IJBOCN N-cadherin precursor - bovine
                   (fragment) >gi_664894_emb_CAA37677_ (X53615) N-cadherin
                   [Bos taurus]
                   230280
Seq. No.
                   LIB3196-054-P1-M1-E9
Seq. ID
                   BLASTX
Method
                   g1703377
NCBI GI
                   246
BLAST score
                   6.0e-21
E value
                   45
Match length
                   100
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_951146 (U31350)
                   ADP-ribosylation factor 1 [Xenopus laevis]
Seq. No.
                   230281
                   LIB3196-054-P1-M1-F5
Seq. ID
                   BLASTX
Method
                   q2443314
NCBI GI
                   158
BLAST score
                   7.0e-21
E value
                   98
Match length
                   59
% identity
NCBI Description (D63774) keratin 14 [Rattus norvegicus]
                   230282
Seq. No.
                   LIB3196-054-P1-M1-F8
Seq. ID
                   BLASTX
Method
                   q3128177
NCBI GI
                   528
BLAST score
                    4.0e-54
E value
                   125
Match length
                    82
 % identity
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
                    230283
 Seq. No.
                    LIB3196-054-P1-M1-F9
 Seq. ID
                    BLASTX
 Method
                    g1199772
 NCBI GI
                    245
 BLAST score
                    7.0e-21
 E value
                    51
 Match length
 % identity
                    86
 NCBI Description (D83226) extensin like protein [Populus nigra]
```

```
>gi 1199774 dbj_BAA11855_ (D83227) extensin like protein
                   [Populus nigra]
                  230284
Seq. No.
                  LIB3196-054-P1-M1-G1
Seq. ID
                  BLASTX
Method
                   q559703
NCBI GI
                   605
BLAST score
                   4.0e-63
E value
                  133
Match length
                   89
% identity
                  (D38549) ha1025 is new [Homo sapiens]
NCBI Description
                   230285
Seq. No.
                   LIB3196-054-P1-M1-G11
Seq. ID
Method
                   BLASTX
                   q2459421
NCBI GI
BLAST score
                   411
                   2.0e-40
E value
                   110
Match length
                   68
% identity
                   (AC002332) putative calcium-binding EF-hand protein
NCBI Description
                   [Arabidopsis thaliana]
                   230286
Seq. No.
                   LIB3196-054-P1-M1-G3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g100001
BLAST score
                   450
                   6.0e-45
E value
                   121
Match length
                   72
% identity
                   endopeptidase C1 - kidney bean >gi_1345573_emb_CAA40073_
NCBI Description
                   (X56753) endopeptidase (EP-C1) [Phaseolus vulgaris]
                   230287
Seq. No.
                   LIB3196-054-P1-M1-G7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2655420
BLAST score
                   440
E value
                   9.0e-44
                   109
Match length
                   76
% identity
                   (AF035414) heat shock cognate protein HSC70 [Brassica
NCBI Description
                   napus]
                   230288
Seq. No.
                   LIB3196-054-P1-M1-G8
Seq. ID
                   BLASTX
Method
                   g2507455
NCBI GI
                   578
BLAST score
                   6.0e-60
E value
                   125 -
Match length
                   92
% identity
                   FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE
NCBI Description
                   SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir__A43350
                   formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach
```

```
[Spinacia oleracea]
                   230289
Seq. No.
                   LIB3196-054-P1-M1-H2
Seq. ID
                   BLASTX
Method
                   q799177
NCBI GI
                   163
BLAST score
                   3.0e-11
E value
                   122
Match length
                   39
% identity
                   (U22055) 100 kDa coactivator [Homo sapiens]
NCBI Description
                   230290
Seq. No.
                   LIB3196-054-P1-M1-H3
Seq. ID
                   BLASTX
Method
                   q473949
NCBI GI
BLAST score
                   182
                   2.0e-13
E value
Match length
                   36
                   97
% identity
                   (D29958) KIAA0116 [Homo sapiens]
NCBI Description
                   230291
Seq. No.
Seq. ID
                   LIB3196-054-P1-M1-H7
                   BLASTX
Method
                   q266690
NCBI GI
BLAST score
                   360
                   2.0e-34
E value
Match length
                   101
                   73
% identity
                   OLEOSIN 18.2 KD >gi_167363 (L00935) 18.2 kDa oleosin
NCBI Description
                   [Gossypium hirsutum] >gi_167365 (L00936) 18.2 kDa oleosin
                   [Gossypium hirsutum]
                   230292
Seq. No.
                   LIB3196-055-P1-M1-A12
Seq. ID -
Method
                   BLASTX
NCBI GI
                   g2462749
BLAST score
                   403
                   2.0e-39
E value
                   81
Match length
                   94
% identity
                   (AC002292) Putative Serine/Threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   230293
Seq. No.
                   LIB3196-055-P1-M1-A2
Seq. ID
                   BLASTX
Method
                   g135858
NCBI GI
                   467
BLAST score
                   6.0e-47
E value
                   119
Match length
                   78
% identity
                   TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP)
NCBI Description
                   >gi_99760_pir__S22201 tonoplast intrinsic protein alpha -
                   Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551)
```

>gi 170145 (M83940) 10-formyltetrahydrofolate synthetase

tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi\_166623 (M84343) tonoplast intrinsic protein [Arabidopsis thaliana] >gi\_445128\_prf\_\_1908432A tonoplast intrinsic protein alpha [Arabidopsis thaliana]

```
230294
  Seq. No.
                     LIB3196-055-P1-M1-A6
  Seq. ID
                     BLASTX
  Method
                     g730526
  NCBI GI
                     358
  BLAST score
                     4.0e - 34
  E value
                     117
  Match length
                     62
  % identity
                     60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
  NCBI Description
                     >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis
                     thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein
                     [Arabidopsis thaliana]
                     230295
  Seq. No.
                     LIB3196-055-P1-M1-A7
  Seq. ID
                     BLASTX
  Method
                     g4006875
  NCBI GI
  BLAST score
                     197
                     2.0e-15
  E value
                     91
  Match length
                     48
  % identity
                    (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
   Seq. No.
                     230296
                     LIB3196-055-P1-M1-A8
   Seq. ID
                     BLASTX
  Method
                     q2388689
  NCBI GI
                     136
  BLAST score
                      9.0e-12
  E value
                     86
  Match length
                     53
   % identity
                     (AF016633) GH1 protein [Glycine max]
   NCBI Description
   Seq. No.
                      230297
                     LIB3196-055-P1-M1-B1
   Seq. ID
                      BLASTX
   Method
                      g2137162
   NCBI GI
                      288
   BLAST score
                      5.0e-26
   E value
                      97
   Match length
                      70
   % identity
                      BAP31 protein - mouse >gi 1487986 emb CAA57414 (X81816)
   NCBI Description
                      BAP31 [Mus musculus]
                      230298
   Seq. No.
                      LIB3196-055-P1-M1-B3
   Seq. ID
                      {\tt BLASTX}
   Method
                      g1742951
   NCBI GI
                      278
   BLAST score
                      1.0e-24
   E value
                      61
   Match length
                      89
   % identity
```

```
NCBI Description (Y09817) Ca2+-ATPase [Arabidopsis thaliana]
                   230299
Seq. No.
                   LIB3196-055-P1-M1-B5
Seq. ID
                   BLASTX
Method
                   g129899
NCBI GI
                   302
BLAST score
                   4.0e-28
E value
                   78
Match length
                   77
% identity
                   PROSTAGLANDIN G/H SYNTHASE 1 PRECURSOR (CYCLOOXYGENASE -1)
NCBI Description
                   (COX-1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 1)
                   (PROSTAGLANDIN H2 SYNTHASE 1) (PGH SYNTHASE 1) (PGHS-1)
                   (PHS 1) >gi_88488_pir__JH0259 prostaglandin-endoperoxide synthase (EC 1.14.99.1) 1 precursor - human >gi_189887
                   (M59979) prostaglandin endoperoxide synthase [Homo sapiens]
                   >gi_243972_bbs_78221 (S78220) prostaglandin endoperoxide
                   synthase, cyclooxygenase [human, platelets, Peptide, 599
                   aa] [Homo sapiens] >gi_249626_bbs_103946 (S36271)
                   prostaglandin G/H synthase, \overline{PGG/HS} [human, lung fibroblast,
                   Peptide, 599 aa] [Homo sapiens]
                   230300
Seq. No.
                   LIB3196-055-P1-M1-C1
Seq. ID
                   BLASTX
Method
                   q1524121
NCBI GI
                   157
BLAST score
                   2.0e-10
E value
                   56
Match length
                   57
% identity
                   (X96539) malate dehydrogenase [Mesembryanthemum
NCBI Description
                    crystallinum]
                    230301
Seq. No.
                    LIB3196-055-P1-M1-C12
Seq. ID
                    BLASTX
Method
                    g1809248
NCBI GI
                    319
BLAST score
E value
                    1.0e-29
                    124
Match length
                    56
% identity
                   (U51586) siah binding protein 1 [Homo sapiens]
NCBI Description
Seq. No.
                    230302
                    LIB3196-055-P1-M1-C3
Seq. ID
                    BLASTX
Method
                    g2739383
NCBI GI
                    377
BLAST score
                    2.0e-36
E value
                    119
Match length
 % identity
                    (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
                    230303
 Seq. No.
                    LIB3196-055-P1-M1-C5
 Seq. ID
                    BLASTX
 Method
```

g1708480

NCBI GI

```
BLAST score
                  233
                  2.0e-33
E value
                  108
Match length
                  76
% identity
                  IMPORTIN ALPHA-2 SUBUNIT (KARYOPHERIN ALPHA-2 SUBUNIT)
NCBI Description
                   (SRP1-ALPHA) (RAG COHORT PROTEIN 1) >gi_2135835_pir__A56516
                  nuclear localization sequence receptor SRP1 alpha - human
                  >gi 791185 (U09559) Rch1 [Homo sapiens] >gi 899539 (U28386)
                  hSRPlalpha [Homo sapiens]
                   >gi_4504897_ref_NP_002257.1_pKPNA2_ karyopherin alpha 2
                   (RAG cohort 1, importin alpha 1)
                   230304
Seq. No.
                   LIB3196-055-P1-M1-D12
Seq. ID
                   BLASTX
Method
                   g126396
NCBI GI
                   644
BLAST score
                   1.0e-67
E value
                   125
Match length
                   94
% identity
                  ARACHIDONATE 15-LIPOXYGENASE (ARACHIDONATE OMEGA-6
NCBI Description
                   LIPOXYGENASE) (15-LOX) >gi_86878_pir__A31349 arachidonate
                   15-lipoxygenase (EC 1.13.11.33) - human >gi_307135 (M23892)
                   15-lipoxygenase [Homo sapiens] >gi_1872525 (U88317)
                   15-lipoxygenase [Homo sapiens]
                   >gi 4502055 ref_NP_001131.1_pALOX15_ arachidonate
                   15-lipoxygenase
                   230305
Seq. No.
                   LIB3196-055-P1-M1-D5
Seq. ID
                   BLASTX
Method
                   q72287
NCBI GI
                   629
BLAST score
                   6.0e-66
E value
                   121
Match length
% identity
                   beta-globulin A precursor (clone 94) - upland cotton
NCBI Description
                   (fragment) >gi_167377 (M16905) legumin precursor [Gossypium
                   hirsutum]
                   230306
Seq. No.
                   LIB3196-055-P1-M1-E12
Seq. ID
                   BLASTX
Method
                   g125887
NCBI GI
                   164
BLAST score
                   2.0e-11
E value
                   89
Match length
                   45
% identity
                   ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
NCBI Description
                   >gi_82092_pir__S04765 LAT52 protein precursor - tomato
                   >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon
                   esculentum]
                   230307
 Seq. No.
                   LIB3196-055-P1-M1-E2
Seq. ID
                   BLASTX
Method
                   g683553
NCBI GI
```

```
210
BLAST score
                   8.0e-17
E value
                   97
Match length
                   48
% identity
                   (Z48450) oleosin-like protein [Citrus sinensis]
NCBI Description
                   >gi 1582679_prf__2119230A oleosin homolog [Citrus sinensis]
                   230308
Seq. No.
                   LIB3196-055-P1-M1-E8
Seq. ID
                   BLASTX
Method
                   g167311
NCBI GI
                   316
BLAST score
                    3.0e-29
E value
                   71
Match length
                   85
% identity
                   (M83301) 2S albumin storage protein [Gossypium hirsutum]
NCBI Description
Seq. No.
                    230309
                   LIB3196-055-P1-M1-F1
Seq. ID
                    BLASTX
Method
                    g4262140
NCBI GI
                    143
BLAST score
                    2.0e-12
E value
Match length
                    77
                    58
% identity
                    (AC005275) putative C-type U1 snRNP [Arabidopsis thaliana]
NCBI Description
                    230310
Seq. No.
                    LIB3196-055-P1-M1-F11
Seq. ID
                    BLASTX
Method
                    q3643595
NCBI GI
                    303
BLAST score
                    1.0e-27
E value
                    110
Match length
                    54
% identity
                    (AC005395) putative oleosin protein [Arabidopsis thaliana]
NCBI Description
                    230311
Seq. No.
                    LIB3196-055-P1-M1-F12
Seq. ID
Method
                    BLASTX
                    g125105
NCBI GI
                    562
BLAST score
                    5.0e-58
E value
                    122
Match length
                    92
% identity
                    KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5) (K5) (CK 5)
NCBI Description
                    (58 KD CYTOKERATIN) >gi_88051_pir__A29904 keratin K5, 58K type II, epidermal (version 1) - human >gi_307082 (M21389)
                    keratin type II [Homo sapiens]
                    >gi_4557890_ref_NP_000415.1_pKRT5_ keratin
                    230312
Seq. No.
                    LIB3196-055-P1-M1-F3
Seq. ID
                    BLASTX
Method
                    g1732417
NCBI GI
                    246
BLAST score
                    6.0e-21
E value
```

NCBI Description

```
Match length
                     98
                    56
% identity
NCBI Description (U47924) DRPLA [Homo sapiens]
                    230313
Seq. No.
                    LIB3196-055-P1-M1-F5
Seq. ID
Method
                    BLASTX
                     g2746719
NCBI GI
                     149
BLAST score
                     1.0e-09
E value
                     45
Match length
                     64
% identity
                    (AF038386) histone H2B [Capsicum annuum]
NCBI Description
                     230314
Seq. No.
                     LIB3196-055-P1-M1-G1
Seq. ID
                     BLASTX
Method
NCBI GI
                     q4102715
                     454
BLAST score
                     2.0e-45
E value
                     113
Match length
                     77
% identity
NCBI Description (AF015287) serine protease [Homo sapiens]
                     230315
Seq. No.
                     LIB3196-055-P1-M1-G11
Seq. ID
                     BLASTX
Method
NCBI GI
                     g113287
BLAST score
                     498
                     2.0e-50
E value
                     96
Match length
                     95
% identity
                     ACTIN, ALPHA SKELETAL MUSCLE (ALPHA-ACTIN 1)
NCBI Description
                     >gi_71610_pir__ATHU actin, skeletal muscle - human
                     >gi_71612_pir__ATRT actin, skeletal muscle - rat
                     >gi_71613_pir__ATCH actin alpha, skeletal muscle - chicken
                     >gi 90264 pir A24904 actin, skeletal muscle - mouse
>gi 55577 emb CAA24529 (V01218) actin [Rattus norvegicus]
>gi 63029 emb CAA24753 (V01507) a-actin [Gallus gallus]
>gi 178029 (J0008) alpha-actin [Homo sapiens] >gi 309088
                      (M1\overline{2}866) actin [Mus musculus] >gi_337746 (M20543)
                     alpha-skeletal actin precursor [Homo sapiens] >gi_387081
                     (M12347) alpha-actin [Mus musculus] >gi_790202 (U16368)
                     skeletal alpha actin [Sus scrofa] >gi_223503_prf__0809315A
                     actin [Rattus norvegicus]
                     >gi_4501881_ref_NP_001091.1_pACTA1_ actin, alpha 1,
                     skeletal muscle
                     230316
 Seq. No.
                     LIB3196-055-P1-M1-G12
 Seq. ID
                     BLASTX
Method
                     g4263711
NCBI GI
                     203
 BLAST score
                     2.0e-16
 E value
                     44
Match length
                      86
 % identity
                     (AC006223) putative CCR4-associated transcription factor
```

NCBI GI

E value

BLAST score

Match length

NCBI Description

% identity

## [Arabidopsis thaliana] 230317 Seq. No. LIB3196-055-P1-M1-G2 Seq. ID BLASTX Method g137578 NCBI GI 461 BLAST score 5.0e-58 E value 120 Match length 97 % identity VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) NCBI Description >gi\_81545\_pir\_\_S06398 alpha-globulin type A precursor -upland cotton >gi\_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi\_207906 (M18027) alpha globulin A [Artificial gene] >gi\_226119\_prf\_\_1410330A vicilin gene A [Saguinus oedipus] 230318 Seq. No. LIB3196-055-P1-M1-G6 Seq. ID BLASTX Method g2960216 NCBI GI 355 BLAST score 2.0e-36 E value 114 Match length 71 % identity (AJ223384) 26S proteasome regulatory ATPase subunit 10b NCBI Description (S10b) [Manduca sexta] 230319 Seq. No. LIB3196-055-P1-M1-H1 Seq. ID BLASTX Method q3869127 NCBI GI 282 BLAST score 3.0e-25 E value 81 Match length 63 % identity NCBI Description (AB019527) LDOC1 protein [Homo sapiens] 230320 Seq. No. LIB3196-055-P1-M1-H2 Seq. ID BLASTX Method g3869127 NCBI GI 170 BLAST score 5.0e-12 E value 77 Match length 47 % identity (AB019527) LDOC1 protein [Homo sapiens] NCBI Description 230321 Seq. No. LIB3196-055-P1-M1-H3 Seq. ID BLASTX Method

(U72725) retrofit [Oryza longistaminata]

g2586082

6.0e - 32

339

110

230322 Seq. No. LIB3196-056-P1-M1-A1 Seq. ID BLASTX Method g2583135 NCBI GI 436 BLAST score 3.0e-43E value 99 Match length 88 % identity (AC002387) hypothetical protein [Arabidopsis thaliana] NCBI Description >gi\_3822216 (AF074948) FIL [Arabidopsis thaliana] >gi 4322477 gb AAD16053 (AF087015) abnormal floral organs protein [Arabidopsis thaliana] Seq. No. 230323 LIB3196-056-P1-M1-A2 Seq. ID Method BLASTX NCBI GI q1170373 BLAST score 355 3.0e - 34E value 78 Match length 90 % identity HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi\_1072473\_pir\_\_S46302 NCBI Description heat shock cognate protein 70-1 - Arabidopsis thaliana >gi 397482 emb CAA52684 (X74604) heat shock protein 70 cognate [Arabidopsis thaliana] Seq. No. 230324 Seq. ID LIB3196-056-P1-M1-B7 Method BLASTX q3915742 NCBI GI 296 BLAST score 4.0e-27 E value 69 Match length 81 % identity LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi\_167319 NCBI Description (M69188) legumin A [Gossypium hirsutum] >gi 444320 prf\_\_1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum] Seq. No. 230325 LIB3196-056-P1-M1-C10 Seq. ID Method BLASTX g3915742 NCBI GI 259 BLAST score 1.0e-39 E value 90 Match length 93 % identity LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi\_167319 NCBI Description (M69188) legumin A [Gossypium hirsutum] >gi 444320 prf 1906369A legumin A:ISOTYPE=D alloallele [Gossypium hirsutum] Seq. No. 230326 LIB3196-056-P1-M1-C12 Seq. ID Method BLASTX NCBI GI g4539292

```
438
BLAST score
                  1.0e-43
E value
                  92
Match length
                  87
% identity
                  (ALO49480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                  thaliana]
                  230327
Seq. No.
                  LIB3196-056-P1-M1-C2
Seq. ID
                  BLASTX
Method
                  g1800317
NCBI GI
BLAST score
                  187
                  5.0e-17
E value
                  73
Match length
                  77
% identity
                   (U83896) Rat homologues of yeast sec7p [Rattus norvegicus]
NCBI Description
                  >gi_3660538_dbj_BAA33429_ (AB013466) cytohesin 2 [Mus
                  musculus] >qi 3885503 (AF079971) cytohesin-2 [Mus musculus]
                  230328
Seq. No.
                  LIB3196-056-P1-M1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1223922
BLAST score
                   486
                   4.0e-49
E value
                   113
Match length
% identity
                   74
                   (U49445) Vigna radiata vicilin peptidohydrolase [Vigna
NCBI Description
                   radiata]
                   230329
Seq. No.
                   LIB3196-056-P1-M1-C8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4538997
                   167
BLAST score
                   8.0e-12
E value
                   75
Match length
% identity
                   47
                   (ALO49481) AIG1-like protein [Arabidopsis thaliana]
NCBI Description
                   230330
Seq. No.
                   LIB3196-056-P1-M1-C9
Seq. ID
                   BLASTX
Method
                   g1107696
NCBI GI
                   457
BLAST score
                   6.0e-46
E value
                   94
Match length
                   90
% identity
                   (X86691) Mi-2 protein [Homo sapiens]
NCBI Description
                   >gi 4557453 ref NP 001264.1_pCHD4_ chromodomain helicase
                   DNA binding protein
                   230331
Seq. No.
                   LIB3196-056-P1-M1-D3
Seq. ID
Method
                   BLASTX
                   g3868758
NCBI GI
                   320
BLAST score
```

Seq. ID

Method

```
2.0e-32
E value
Match length
                  94
% identity
                  67
NCBI Description
                  (D89802) elongation factor 1B gamma [Oryza sativa]
                  230332
Seq. No.
                  LIB3196-056-P1-M1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2624326
BLAST score
                  338
                  6.0e-32
E value
Match length
                  93
% identity
                  74
NCBI Description
                  (AJ002893) OsGRP1 [Oryza sativa]
Seq. No.
                  230333
                  LIB3196-056-P1-M1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g137580
                  199
BLAST score
                  1.0e-15
E value
Match length
                  44
                  89
% identity
                  VICILIN PRECURSOR (ALPHA-GLOBULIN B) (CLONE C72)
NCBI Description
                  >gi_72286_pir__FWCNAB alpha-globulin B precursor (clone
                  C72) - upland cotton >gi_167375 (M16891) vicilin precursor
                  [Gossypium hirsutum]
                  230334
Seq. No.
                  LIB3196-056-P1-M1-E12
Seq. ID
Method
                  BLASTX
                  g3695408
NCBI GI
BLAST score
                  229
E value
                  5.0e-19
Match length
                  87
                  48
% identity
NCBI Description
                  (AF096373) contains similarity to Solanum lycopersicum
                   (tomato) wound-induced protein (GB:X59882) [Arabidopsis
                  thaliana] >gi_4538956_emb_CAB39780.1_ (AL049488) probable
                  wound-induced protein [Arabidopsis thaliana]
                  230335
Seq. No.
                  LIB3196-056-P1-M1-E9
Seq. ID
                  {\tt BLASTX}
Method
NCBI GI
                  g3915742
BLAST score
                  530
E value
                  2.0e-54
Match length
                  117
% identity
                  89
                  LEGUMIN A PRECURSOR (BETA-GLOBULIN) (LEGA-C94) >gi 167319
NCBI Description
                   (M69188) legumin A [Gossypium hirsutum]
                  >gi_444320_prf__1906369A legumin A:ISOTYPE=D alloallele
                  [Gossypium hirsutum]
                  230336
Seq. No.
```

33069

LIB3196-056-P1-M1-F12

BLASTX

```
NCBI GI
                   g113944
BLAST score
                   525
                   9.0e-54
E value
Match length
                   105
                   99
% identity
                   ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9)
NCBI Description
                   (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN)
                   >gi_71756_pir__LUHU annexin I - human
                   >gi_34388_emb_CAA29338_ (X05908) lipocortin (AA 1-346)
                   [Homo sapiens] >gi_224956_prf__1204261A lipocortin [Homo
                   sapiens] >gi 4502101 ref NP 000691.1 pANX1 annexin I
                   (lipocortin I)
                   230337
Seq. No.
                   LIB3196-056-P1-M1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q113944
                   434
BLAST score
                   5.0e-43
E value
Match length
                   100
% identity
                   88
                   ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9)
NCBI Description
                   (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN)
                   >gi_71756_pir__LUHU annexin I - human
                   >gi_34388_emb_CAA29338_ (X05908) lipocortin (AA 1-346)
                   [Homo sapiens] >gi_224956_prf__1204261A lipocortin [Homo
                   sapiens] >gi_45021\overline{0}1_ref_\overline{NP}_0\overline{000}691.1_pANX1_ annexin I
                   (lipocortin I)
                   230338
Seq. No.
Seq. ID
                   LIB3196-056-P1-M1-F3
Method
                   BLASTX
NCBI GI
                   q2832237
BLAST score
                   469
E value
                   4.0e-47
Match length
                   122
% identity
                   84
                   (AF022655) cep250 centrosome associated protein [Homo
NCBI Description
                   sapiens]
                   230339
Seq. No.
Seq. ID
                   LIB3196-056-P1-M1-F5
Method
                   BLASTX
NCBI GI
                   q130224
                   645
BLAST score
                   8.0e-68
E value
Match length
                   124 .
% identity
                   1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE
NCBI Description
                   GAMMA 1 (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II)
                   (PLC-148) >gi_89333_pir__S00666
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase
                    (EC 3.1.4.11) isozyme II - bovine >gi_639_emb_CAA68406_
                    (Y00301) phosphatidylinositol-specific phospholipase C.
                    [Bos taurus] >gi_225974_prf__1404383A phospholipase C [Bos
                   taurus]
```



```
Seq. No.
                   230340
Seq. ID
                   LIB3196-056-P1-M1-F6
Method
                   BLASTX
NCBI GI
                   q4193388
BLAST score
                   306
E value
                   3.0e-28
Match length
                   61
                   93
% identity
NCBI Description
                   (AF091455) translationally controlled tumor protein [Hevea
                   brasiliensis]
                   230341
Seq. No.
Seq. ID
                   LIB3196-056-P1-M1-F7
Method
                   BLASTX
NCBI GI
                   q137578
BLAST score
                   446
E value
                   7.0e-50
Match length
                   115
                   94
% identity
NCBI Description
                   VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
                   >gi_81545_pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                   [Artificial gene] >gi_226119_prf__1410330A vicilin gene A
                   [Saguinus oedipus]
Seq. No.
                   230342
Seq. ID
                   LIB3196-056-P1-M1-G10
Method
                   BLASTX
NCBI GI
                   q2088662.
BLAST score
                   211
E value
                   6.0e-17
Match length
                   102
% identity
                   48
NCBI Description
                  (AF002109) unknown protein [Arabidopsis thaliana]
Seq. No.
                   230343
Seq. ID
                   LIB3196-056-P1-M1-G12
Method
                   BLASTX
NCBI GI
                   g2507222
BLAST score
                   152
E value
                   5.0e-10
Match length
                   60
% identity
                   47
                   KINASE ASSOCIATED PROTEIN PHOSPHATASE >gi_1709236 (U09505)
NCBI Description
                   kinase associated protein phosphatase [Arabidopsis
                   thaliana]
Seq. No.
                   230344
Seq. ID
                   LIB3196-056-P1-M1-H1
Method
                  BLASTX
NCBI GI
                   g2213425
BLAST score
                   Ī50
E value
                   5.0e-10
                  76
Match length
% identity
```

NCBI Description (Z97064) hypothetical protein [Citrus x paradisi]

E value

1.0e-71

```
Seq. No.
                   230345
Seq. ID
                   LIB3196-057-P1-M1-A10
Method
                   BLASTX
NCBI GI
                   g113001
BLAST score
                   585
E value
                   9.0e-61
Match length
                   120
% identity
                   ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMUSCLE
NCBI Description
                   FILAMIN) (FILAMIN 1) >gi_106081_pir_A37098_9elation factor ABP-280, long form - human <math>>gi_28243_emb_CAA37495_(X53416)
                   actin-binding protein [Homo sapiens]
                   >gi_4503745_ref_NP 001447.1 pFLNA filamin 1 (actin-binding)
                   protein-280)
Seq. No.
                   230346
Seq. ID
                   LIB3196-057-P1-M1-A11
Method
                   BLASTX
NCBI GI
                   q137578
BLAST score
                   362
E value
                   3.0e-37
Match length
                   115
% identity
                   82
NCBI Description
                   VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
                   >gi_81545_pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                    [Artificial gene] >gi 226119 prf 1410330A vicilin gene A
                   [Saguinus oedipus]
Seq. No.
                   230347
Seq. ID
                   LIB3196-057-P1-M1-A2
Method
                   BLASTX
NCBI GI
                   q595768
BLAST score
                   160
E value
                   2.0e-11
Match length
                   51
% identity
NCBI Description (U13866) non-functional lacZ alpha peptide [Cloning vector]
Seq. No.
                   230348
Seq. ID
                   LIB3196-057-P1-M1-A5
Method
                   BLASTX
NCBI GI
                   g1864017
BLAST score
                   591
E value
                   2.0e-61
Match length
                   114
% identity
                   99
NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                   230349
Seq. ID
                   LIB3196-057-P1-M1-A6
Method
                   BLASTX
NCBI GI
                   g1070465
BLAST score
                   678
```

Seq. No.

230354

```
Match length
                   136
% identity
                   99
                   protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13),
NCBI Description
                   epidermal - human >gi_186790 (M55183) protein-glutamine
                   gamma-glutamyltransferase [Homo sapiens]
                   >gi_219632_dbj_BAA14329 (D90287) transglutaminase [Homo
                   sapiens] >gi_1256959 (M98447) keratinocyte transglutaminase
                   [Homo sapiens] >gi_3868760_dbj_BAA34203_ (D10353) transglutaminase 1 [Homo sapiens]
                   >gi_4507475_ref_NP_000350.1_pTGM1 transglutaminase 1 (K
                   polypeptide epidermal type I,
                   protein-glutamine-gamma-glutamyltransferase)
Seq. No.
                   230350
Seq. ID
                   LIB3196-057-P1-M1-B1
Method
                   BLASTX
NCBI GI
                   q3183031
BLAST score
                   238
E value
                   4.0e-20
Match length
                   122
% identity
                   48
NCBI Description
                   EUKARYOTIC TRANSLATION INITIATION FACTOR 4H (EIF-4H)
                   (KIAA0038) >gi_2914759 (AF045555) wbscr1 [Homo sapiens]
Seq. No.
                   230351
Seq. ID
                   LIB3196-057-P1-M1-B11
Method
                   BLASTX
NCBI GI
                   g2117743
BLAST score
                   525
E value
                   1.0e-53
Match length
                   121
% identity
NCBI Description
                   glutathione transferase (EC 2.5.1.18) A3 - human (fragment)
                   >gi_951352 (L13275) glutathione S-transferase A3 [Homo
                   sapiens]
Seq. No.
                   230352
Seq. ID
                   LIB3196-057-P1-M1-B12
Method
                   BLASTX
NCBI GI
                   g1769895
BLAST score
                   471
E value
                   2.0e-47
Match length
                   127
% identity
NCBI Description (X96598) CaLB protein [Arabidopsis thaliana]
Seq. No.
                   230353
Seq. ID
                   LIB3196-057-P1-M1-B4
Method
                   BLASTX
NCBI GI
                   q4191344
BLAST score
                   541
E value
                   1.0e-55
Match length
                   131
% identity
NCBI Description
                  (AF085199) golgin-84 [Homo sapiens]
```

BLASTX

LIB3196-057-P1-M1-B5

Seq. ID

Method

```
NCBI GI
                   q3319958
BLAST score
                   335
E value
                   2.0e-31
Match length
                   250
% identity
NCBI Description
                   (AJ228139) VAKTI precursor [Homo sapiens]
Seq. No.
                   230355
Seq. ID
                  LIB3196-057-P1-M1-B7
Method
                  BLASTX
NCBI GI
                   q3122072
BLAST score
                   531
E value
                   2.0e-54
Match length
                   105
% identity
                   96
                  ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION
NCBI Description
                  FACTOR TU) (EF-TU) >gi_2119922_pir__I50226 elongation
                   factor 1 alpha - chicken >gi_488468 (L00677) elongation
                  factor 1 alpha [Gallus gallus]
Seq. No.
                  230356
                  LIB3196-057-P1-M1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q485514
BLAST score
                  441
E value
                   7.0e-44
Match length
                  93
% identity
NCBI Description
                  ADR11-2 protein - soybean (fragment)
                  >gi_296443_emb_CAA49341 (X69640) auxin down regulated
                   [Glycine max]
Seq. No.
                  230357
Seq. ID
                  LIB3196-057-P1-M1-C2
Method
                  BLASTX
NCBI GI
                  q3876865
BLAST score
                  142
E value
                  7.0e-09
Match length
                  91
% identity
NCBI Description
                  (Z81534) predicted using Genefinder; cDNA EST EMBL:C08177
                  comes from this gene; cDNA EST EMBL: C09822 comes from this
                  gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST
                  yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co
Seq. No.
                  230358
Seq. ID
                  LIB3196-057-P1-M1-C3
Method
                  BLASTX
NCBI GI
                  g2979551
BLAST score
                  139
E value
                  7.0e-09
Match length
                  67
% identity
                  (AC003680) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thalianal
```

```
Seq. No.
                   230359
Seq. ID
                  LIB3196-057-P1-M1-D1
Method
                  BLASTX
NCBI GI
                  q167367
BLAST score
                  282
E value
                   1.0e-25
Match length
                  74
% identity
                  74
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                  230360
Seq. No.
Seq. ID
                  LIB3196-057-P1-M1-D12
Method
                  BLASTX
NCBI GI
                  a3758821
BLAST score
                  554
                  4.0e-57
E value
Match length
                  128
% identity
                  88
NCBI Description (AJ011896) Naf1 beta protein [Homo sapiens]
                  230361
Seq. No.
Seq. ID
                  LIB3196-057-P1-M1-D3
Method
                  BLASTX
NCBI GI
                  g2119533
BLAST score
                  584
E value
                  1.0e-60
Match length
                  116
% identity
                  98
NCBI Description giantin - human >gi 808869 dbj BAA05025 (D25542) human
                  gcp372 [Homo sapiens]
Seq. No.
                  230362
Seq. ID
                  LIB3196-057-P1-M1-D4
Method
                  BLASTX
NCBI GI
                  q1049084
BLAST score
                  282
E value
                  3.0e-25
Match length
                  54
% identity
                  89
NCBI Description (U30828) SRp55-2 [Homo sapiens]
Seq. No.
                  230363
Seq. ID
                  LIB3196-057-P1-M1-D5
Method
                  BLASTX
NCBI GI
                  g996057
BLAST score
                  505
E value
                  3.0e-51
                  97
Match length
                  97
% identity
NCBI Description (X90872) associated to Golgi apparatus [Homo sapiens]
Seq. No.
                  230364 --
Seq. ID
                  LIB3196-057-P1-M1-D6
Method
                  BLASTX
NCBI GI
                  g2951931
BLAST score
                  543
```

```
E value
                    9.0e-56
Match length
                   129
% identity
                   84
NCBI Description
                    (U55206) human gamma-glutamyl hydrolase [Homo sapiens]
                   >gi 4503987 ref NP 003869.1 pGGH UNKNOWN
Seq. No.
                   230365
Seq. ID
                   LIB3196-057-P1-M1-D7
Method
                   BLASTX
NCBI GI
                   g167367
BLAST score
                   384
E value
                   3.0e-37
Match length
                   88
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                   230366
Seq. ID
                   LIB3196-057-P1-M1-E11
Method
                   BLASTX
NCBI GI
                   q464986
BLAST score
                   526
E value
                   8.0e-54
Match length
                   99
% identity
                   97
NCBI Description
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
                   LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                   >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
6.3.2.19) UBC9 - Arabidopsis thaliana
                   >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                   enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                   ubiquitin conjugating enzyme [Arabidopsis thaliana]
                   >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating
enzyme E2 [Arabidopsis thaliana]
                   >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein
                   ligase UBC9 [Arabidopsis thaliana]
Seq. No.
                   230367
Seq. ID
                   LIB3196-057-P1-M1-E12
Method
                   BLASTX
NCBI GI
                   g2459928
BLAST score
                   285
E value
                   2.0e-25
Match length
                   71
% identity
NCBI Description
                   (AF007189) claudin 3 [Homo sapiens]
```

>gi\_2570129\_dbj\_BAA22986\_ (AB000714) RVP1 [Homo sapiens]
>gi\_4502875\_ref\_NP\_001297.1\_pCLDN3\_ Clostridium perfringens

enterotoxin receptor

Seq. No. 230368

Seq. ID LIB3196-057-P1-M1-E2

Method BLASTX NCBI GI g3023847 BLAST score 465 E value 1.0e-46 Match length 97 % identity 49



NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi\_2385376\_emb\_CAA69934\_ (Y08678) G protein beta subunit-like [Medicago sativa] 230369 Seq. No. LIB3196-057-P1-M1-E3 Seq. ID BLASTX Method g2652938 NCBI GI 567 BLAST score 1.0e-58 E value 116 Match length % identity 54

NCBI Description (Z47554) orf [Zea mays]

Seq. No. 230370 LIB3196-057-P1-M1-E7 Seq. ID BLASTX Method q4557067 329

NCBI GI BLAST score 1.0e-30 E value 127 Match length 47 % identity

NCBI Description (AC007045) putative pol polyprotein [Arabidopsis thaliana]

230371 Seq. No.

LIB3196-057-P1-M1-E8 Seq. ID

BLASTX Method NCBI GI g306926 190 BLAST score 1.0e-14 E value 57 Match length 61 % identity

(M69241) insulin-like growth factor binding protein 2 [Homo NCBI Description

sapiens]

230372 Seq. No.

Seq. ID LIB3196-057-P1-M1-E9

Method BLASTX NCBI GI q1083762 BLAST score 356 E value 7.0e - 34Match length 106 69 % identity

prolactin-induced T cell protein c15 - rat NCBI Description

>gi\_619907\_emb\_CAA57825\_ (X82445) RnudC [Rattus norvegicus]

Seq. No. 230373

Seq. ID LIB3196-057-P1-M1-F1

Method BLASTX NCBI GI q2605714 BLAST score 345 1.0e - 32E value Match length 87 % identity 79

(AF026275) beta-tonoplast intrinsic protein [Arabidopsis NCBI Description

thaliana]

Seq. ID Method

NCBI GI

BLAST score



```
Seq. No.
                  230374
                  LIB3196-057-P1-M1-F10
Seq. ID
Method
                  BLASTX
                  g136471
NCBI GI
                  249
BLAST score
                  2.0e-21
E value
Match length
                  112
                  53
% identity
                  TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36) (GROWTH
NCBI Description
                  FACTOR-INDUCIBLE NUCLEAR PROTEIN NUP475)
                  >gi 423132 pir S34427 tristetraproline protein - human
                  >gi 183443 (M92843) zinc finger transcriptional regulator
                  [Homo sapiens] >gi 183445 (M92844) zinc finger
                  transcriptional regulator [Homo sapiens] >gi 340013
                  (M63625) tristetraproline [Homo sapiens]
                  >gi 4507961 ref NP 003398.1 pZFP36 zinc finger protein
                  homologous to Zfp-36 in mouse
Seq. No.
                  230375
                  LIB3196-057-P1-M1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g266690
BLAST score
                  378
                  2.0e-36
E value
Match length
                  106
                  74
% identity
                  OLEOSIN 18.2 KD >gi 167363 (L00935) 18.2 kDa oleosin
NCBI Description
                  [Gossypium hirsutum] >gi 167365 (L00936) 18.2 kDa oleosin
                  [Gossypium hirsutum]
                  230376
Seq. No.
                  LIB3196-057-P1-M1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914962
                  600
BLAST score
                  2.0e-62
E value
Match length
                  130
% identity
                  88
                  SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 >gi 2232241
NCBI Description
                  (AF005038) secretory carrier membrane protein [Homo
                  sapiens]
Seq. No.
                  230377
                  LIB3196-057-P1-M1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3123515
BLAST score
                  608
E value
                  2.0e-63
Match length
                  125
% identity
                  94
NCBI Description (Y08761) Mago Nashi-like protein [Euphorbia lagascae]
Seq. No.
                  230378
```

33078

LIB3196-057-P1-M1-F6

BLASTX

207

q1083308

Method

NCBI GI

BLASTX

g1363944



```
E value
                  2.0e-16
Match length
                  42
                  95
% identity
                  enhancer-trap-locus-1 protein - mouse (fragment)
NCBI Description
                  >gi 50866 emb CAA49560 (X69942) enhancer-trap-locus-1 [Mus
                  musculus]
                  230379
Seq. No.
                  LIB3196-057-P1-M1-F7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g266691
BLAST score
                  201
                  7.0e-16
E value
                  80
Match length
% identity
                  56
                  OLEOSIN 16.4 KD >gi 167361 (L00934) 16.4 kDa oleosin
NCBI Description
                  [Gossypium hirsutum]
                  230380
Seq. No.
                  LIB3196-057-P1-M1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2114014
BLAST score
                  149
                  1.0e-09
E value
                  99
Match length
                  42
% identity
NCBI Description
                  (Z95558) hypothetical protein Rv0552 [Mycobacterium
                  tuberculosis]
                  230381
Seq. No.
                  LIB3196-057-P1-M1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g88052
BLAST score
                  190
                  2.0e-14
E value
Match length
                  99
% identity
                   45
                  keratin K5, 58K type II, epidermal (version 2) - human
NCBI Description
                   (fragment)
                   230382
Seq. No.
Seq. ID
                  LIB3196-057-P1-M1-G1
Method
                  BLASTX
NCBI GI
                  q3283166
BLAST score
                  287
                   9.0e-26
E value
Match length
                   110
% identity
                   54
NCBI Description
                  (AF057526) erythrocyte membrane protein Rh50 [Mus musculus]
                   >gi_3329467 (AF065395) Rh50-like protein [Mus musculus]
                       3445508_dbj_BAA32441_ (AB015192) 50 kD glycoprotein
                   (Rh50) [Mus musculus]
                   230383
Seq. No.
                  LIB3196-057-P1-M1-G11
Seq. ID
```



```
BLAST score
                  671
                  8.0e-71
E value
                  133
Match length
                  99
% identity
                  type I keratin 16 - human >gi_1195531_bbs_172338 (S79867)
NCBI Description
                  type I keratin 16, K16 [human, epidermal keratinocytes,
                  Peptide, 473 aa] [Homo sapiens]
                  230384
Seq. No.
                  LIB3196-057-P1-M1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g226120
BLAST score
                  557
                  2.0e-57
E value
                  108
Match length
% identity
                  100
NCBI Description vicilin gene B [Saguinus oedipus]
                  230385
Seq. No.
                  LIB3196-057-P1-M1-G3
Seq. ID
                  BLASTX
Method
                  g2623297
NCBI GI
BLAST score
                  229
                  5.0e-19
E value
                  99
Match length
% identity
                  43
NCBI Description
                  (AC002409) unknown protein [Arabidopsis thaliana]
                  >gi_3790583 (AF079180) RING-H2 finger protein RHC1a
                   [Arabidopsis thaliana]
                  230386
Seq. No.
                  LIB3196-057-P1-M1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2136462
                   698
BLAST score
E value
                   6.0e-74
Match length
                  136
                   99
% identity
                  ribosomal protein S3a - cat (fragment) >gi 950113 (U22231)
NCBI Description
                   ribosomal protein S3a [Felis catus]
Seq. No.
                   230387
                   LIB3196-057-P1-M1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2245077
BLAST score
                   358
E value
                   4.0e-34
Match length
                   118
% identity
NCBI Description (Z97343) glucanase homolog [Arabidopsis thaliana]
Seq. No.
                   230388
                   LIB3196-057-P1-M1-H11
Seq. ID
Method
                   BLASTX
```

33080

g1856971

1.0e-38

396

NCBI GI BLAST score

E value



83 Match length % identity 90 (D26058) This gene is specifically expressed at the S phase NCBI Description during the cell cycle in the synchronous culture of periwinkle cells. [Catharanthus roseus] 230389 Seq. No. Seq. ID LIB3196-057-P1-M1-H12 BLASTX Method g1171978 NCBI GI BLAST score 513 3.0e-52 E value Match length 129 % identity 24 POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) NCBI Description (PABP 2) >gi 304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >qi 2911051 emb CAA17561 (AL021961) poly(A)-binding protein [Arabidopsis thaliana] 230390 Seq. No. LIB3196-057-P1-M1-H5 Seq. ID BLASTX Method q3941736 NCBI GI BLAST score 165 E value 2.0e-11 77 Match length 48 % identity (AF109719) BAT3 [Mus musculus] NCBI Description Seq. No. 230391 LIB3196-057-P1-M1-H6 Seq. ID Method BLASTX g4104976 NCBI GI BLAST score 281 3.0e-25 E value Match length 55 % identity 100 (AF043117) ubiquitin-fusion degradation protein 2 [Homo NCBI Description sapiens] 230392 Seq. No. LIB3196-057-P1-M1-H9 Seq. ID BLASTX Method g2137308 NCBI GI BLAST score 529 4.0e-54E value 105 Match length 38 % identity G protein beta subuit like - mouse >gi\_475012\_dbj\_BAA06185\_ NCBI Description (D29802) G protein beta subuit like [Mus musculus] Seq. No. 230393

LIB3196-058-P1-M1-A1 Seq. ID

BLASTX Method g1350680 NCBI GI 185 BLAST score E value 8.0e-14

E value

Match length

% identity

1.0e-21

105 55



```
Match length
                       82
   % identity
   NCBI Description 60S RIBOSOMAL PROTEIN L1
                       230394
   Seq. No.
                       LIB3196-058-P1-M1-A10
   Seq. ID
   Method
                       BLASTX
                       q399940
   NCBI GI
   BLAST score
                       533
                        9.0e-55
   E value
   Match length
                       111
                        95
   % identity
                       MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR
   NCBI Description
                       >gi_100004_pir__ S25005 heat shock protein, 70K - kidney
bean >gi_22636_emb_CAA47345_ (X66874) 70 kDa heat shock
protein [Phaseolus vulgaris]
                       230395
   Seq. No.
                       LIB3196-058-P1-M1-A11
   Seq. ID
   Method
                       BLASTX
                        q2505876
   NCBI GI
   BLAST score
                        341
   E value
                        4.0e-32
   Match length
                        94
    % identity
                        72
   NCBI Description (Y12776) MYB-related protein [Arabidopsis thaliana]
                        230396
   Seq. No.
                       LIB3196-058-P1-M1-A12
   Seq. ID
                        BLASTX
   Method
   NCBI GI
                        q228316
                        189
    BLAST score
                        7.0e-15
    E value
   Match length
                        61
                        64
    % identity
    NCBI Description albumin [Theobroma cacao]
                        230397
    Seq. No.
                        LIB3196-058-P1-M1-A3
    Seq. ID
                        BLASTX
    Method
    NCBI GI
                        q1518540
    BLAST score
                        592
    E value
                        1.0e-61
    Match length
                        125
    % identity
                        89
    NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
    Seq. No.
                        230398
                        LIB3196-058-P1-M1-A7
    Seq. ID
    Method
                        BLASTX
    NCBI GI
                        g3650030
    BLAST score
                        252
```

33082

NCBI Description (AC005396) unknown protein [Arabidopsis thaliana]



```
230399
Seq. No.
                  LIB3196-058-P1-M1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q266691
                  314
BLAST score
                  5.0e-29
E value
                  100
Match length
                  67
% identity
                  OLEOSIN 16.4 KD >gi 167361 (L00934) 16.4 kDa oleosin
NCBI Description
                  [Gossypium hirsutum]
                  230400
Seq. No.
                  LIB3196-058-P1-M1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3273089
                  639
BLAST score
                  5.0e-67
E value
                  129
Match length
                  99
% identity
                  (Y16610) paraplegin [Homo sapiens]
NCBI Description
                  >gi 4507173 ref_NP_003110.1_pSPG7_ spastic paraplegia 7,
                  paraplegin (pure and complicated autosomal recessive)
                  230401
Seq. No.
                  LIB3196-058-P1-M1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2995405
BLAST score
                   459
                   6.0e-46
E value
                  127
Match length
                   66
% identity
NCBI Description (Y12432) polyprotein [Ananas comosus]
                   230402
Seq. No.
                   LIB3196-058-P1-M1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3885884
BLAST score
                   459
E value
                   5.0e-46
Match length
                   114
% identity
                   78
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]
                   230403
Seq. No.
                   LIB3196-058-P1-M1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1346347
BLAST score
                   606
E value
                   3.0e-63
Match length
                   123
                   98
% identity
                  KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D)
NCBI Description
                   (K6D KERATIN) >gi_2119225_pir__I61769 keratin type II -
                   human (fragment) >gi_914833 (L42610) keratin type II [Homo
```

Seq. No. 230404

sapiens]



```
LIB3196-058-P1-M1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2662343
BLAST score
                  553
                  4.0e-57
E value
                  105
Match length
% identity
                  100
                  (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                  230405
Seq. No.
Seq. ID
                  LIB3196-058-P1-M1-B3
Method
                  BLASTX
NCBI GI
                  q136479
                  217
BLAST score
E value
                  6.0e-18
                  48
Match length
                  88
% identity
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN (TCTP) (P23)
NCBI Description
                  >gi_88948_pir__S06590 IgE-dependent histamine-releasing
                  factor - human >gi_37496_emb_CAA34200_ (X16064) tumor
                  protein (AA 1 - 172) [Homo sapiens]
                  >gi_4507669_ref_NP_003286.1_pTPT1_ tumor protein,
                  translationally-controlled
Seq. No.
                  230406
                  LIB3196-058-P1-M1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1346349
                  318
BLAST score
                  1.0e-42
E value
Match length
                  114
% identity
                  KERATIN, TYPE II CYTOSKELETAL 6F (CYTOKERATIN 6F) (CK 6F)
NCBI Description
                   (K6F KERATIN) >gi_2119219_pir_161771 keratin type II -
                  human >gi 908805 (L42612) keratin type II [Homo sapiens]
Seq. No.
                  230407
                  LIB3196-058-P1-M1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3183316
BLAST score
                  190
E value
                  2.0e-14
Match length
                  88
                  44
% identity
                  HYPOTHETICAL 24.4 KD PROTEIN C16E8.14C IN CHROMOSOME I
NCBI Description
                  >qi 2330702 emb CAB11042 (Z98529) hypothetical protein
                   [Schizosaccharomyces pombe]
Seq. No.
                  230408
                  LIB3196-058-P1-M1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g207905
BLAST score
                  537
E value
                   4.0e-55
                  123
Match length
% identity
                  89
```

NCBI Description (M18027) alpha globulin B [Artificial gene]



```
Seq. No.
                    230409
Seq. ID
                    LIB3196-058-P1-M1-C6
Method
                    BLASTX
NCBI GI
                    g1351867
BLAST score
                    692
E value
                    3.0e-73
Match length
                    129
% identity
                    100
NCBI Description
                    ACTIN, CYTOPLASMIC 1 (BETA-ACTIN) >gi 761724 (U20114)
                    beta-actin [Cricetulus griseus]
Seq. No.
                    230410
Seq. ID
                    LIB3196-058-P1-M1-C7
Method
                    BLASTX
NCBI GI
                    g2244734
BLAST score
                    484
E value
                    6.0e-49
Match length
                    93
% identity
                    100
NCBI Description (D88414) actin [Gossypium hirsutum]
Seq. No.
                    230411
Seq. ID
                    LIB3196-058-P1-M1-D10
Method
                    BLASTX
NCBI GI
                    q126156
BLAST score
                    444
                    3.0e-44
E value
Match length
                    123
                    72
% identity
                    LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)
NCBI Description
                    >gi_72288_pir__FWCNBB beta-globulin B precursor (clone 134)
                    - upland cotton >gi_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi_1171335 (U43727) legumin B [Gossypium hirsutum] >gi_225582_prf__1306412C storage
                    protein C134 [Saguinus oedipus]
Seq. No.
                    230412
                    LIB3196-058-P1-M1-D11
Seq. ID
Method
                    BLASTX
NCBI GI
                    g225581
BLAST score
                    269
E value
                    1.0e-23
Match length
                    67
% identity
                    84
NCBI Description storage protein C94 [Saguinus oedipus]
                    230413
Seq. No.
Seq. ID
                    LIB3196-058-P1-M1-D3
Method
                    BLASTX
NCBI GI
                    g2118403
BLAST score
                    308
                    3.0e-28
E value
                    130
Match length
                    46
% identity
```

33085

(M36501) alpha-2-macroglobulin [Homo sapiens]

NCBI Description alpha-2-macroglobulin - human (fragment) >gi 177872



73

NCBI Description (L08199) peroxidase [Gossypium hirsutum]

% identity

```
230414
Seq. No.
                  LIB3196-058-P1-M1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g732207
                  159
BLAST score
                  7.0e-11
E value
                  87
Match length
% identity
                  37
                  HYPOTHETICAL 75.4 KD PROTEIN IN AUT1-CSE2 INTERGENIC REGION
NCBI Description
                  >gi_626466_pir__S45131 probable membrane protein YNR008w -
                  yeast (Saccharomyces cerevisiae) >gi_496725_emb_CAA54576_
                  (X77395) N2042 [Saccharomyces cerevisiae]
                  >qi 1302482 emb CAA96285_ (Z71623) ORF YNR008w
                  [Saccharomyces cerevisiae]
                  230415
Seq. No.
                  LIB3196-058-P1-M1-D6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3892051
                  504
BLAST score
                  3.0e-51
E value
                  110
Match length
                  84
% identity
                  (AC002330) predicted NADH dehydrogenase 24 kD subunit
NCBI Description
                  [Arabidopsis thaliana]
                  230416
Seq. No.
                  LIB3196-058-P1-M1-E1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2317905
                  178
BLAST score
                   5.0e-13
E value
                  115
Match length
% identity
NCBI Description (U89959) bZIP-like protein [Arabidopsis thaliana]
                   230417
Seq. No.
                   LIB3196-058-P1-M1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g225581
BLAST score
                   656
                   4.0e-69
E value
Match length
                   122
% identity
                   100
NCBI Description storage protein C94 [Saguinus oedipus]
                   230418
Seq. No.
                   LIB3196-058-P1-M1-E11
Seq. ID
                   BLASTX
Method
                   q167367
NCBI GI
BLAST score
                   395
                   2.0e-38
E value
                   106
'Match length
```



```
230419
Seq. No.
                  LIB3196-058-P1-M1-E6
Seq. ID
                  BLASTX
Method
                  q135098
NCBI GI
                  597
BLAST score
                  3.0e-62
E value
                  117
Match length
                  97
% identity
                  ASPARTYL-TRNA SYNTHETASE (ASPARTATE--TRNA LIGASE) (ASPRS)
NCBI Description
                  >gi_68530_pir__SYHUDT aspartate--tRNA ligase (EC 6.1.1.12)
                  - human >gi 179102 (J05032) aspartyl-tRNA synthetase [Homo
                  sapiens] >gi_4557513_ref_NP_001340.1_pDARS_ aspartyl-tRNA
                  synthetase
                  230420
Seq. No.
                  LIB3196-058-P1-M1-E7
Seq. ID
                  BLASTX
Method
                  g1373125
NCBI GI
                  285
BLAST score
                  1.0e-25
E value
                  103
Match length
                  59
% identity
                  (U43709) similar to the metB gene product of Escherichia
NCBI Description
                   coli; cloned by functional complementation of a metB mutant
                  strain of Escherichia coli LE392 [Arabidopsis thaliana]
                   230421
Seq. No.
                  LIB3196-058-P1-M1-E8
Seq. ID
                  BLASTX
Method
                  g1076389
NCBI GI
                   217
BLAST score
                   1.0e-17
E value
                   48
Match length
                   48
% identity
                  protein phosphatase 2A pDF1 - Arabidopsis thaliana
NCBI Description
                   >gi_683502_emb_CAA57528_ (X82002) protein phosphatase 2A 65
                   kDa regulatory subunit [Arabidopsis thaliana]
                   230422
Seq. No.
                   LIB3196-058-P1-M1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4510363
                   289
BLAST score
                   4.0e-26
E value
                   68
Match length
                   81
% identity
                   (AC007017) putative DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   230423
Seq. No.
                   LIB3196-058-P1-M1-F6
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g167359
BLAST score 161
E value 4.0e-11
Match length 100

% identity

BLAST score

E value

348

6.0e-33



```
(M86213) 2S albumin storage protein [Gossypium hirsutum]
NCBI Description
                   >gi 444334 prf 1906383A 2S albumin [Gossypium hirsutum]
Seq. No.
                   LIB3196-058-P1-M1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3746127
BLAST score
                   428
E value
                   2.0e-42
Match length
                   106
                   76
% identity
NCBI Description
                   (U76253) E25B protein [Mus musculus]
                   230425
Seq. No.
                   LIB3196-058-P1-M1-F9
Seq. ID
Method
                   BLASTX
                   q1703108
NCBI GI
BLAST score
                   586
                   7.0e-61
E value
                   120
Match length
                   95
% identity
                   ACTIN 2/7 >gi 2129525 pir S71210 actin 2 - Arabidopsis thaliana >gi 2129528 pir S68107 actin 7 - Arabidopsis
NCBI Description
                   thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis
                   thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis
                   thaliana]
                   230426
Seq. No.
                   LIB3196-058-P1-M1-G4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3063643
BLAST score
                   605
E value
                   4.0e-63
Match length
                   121
                   92
% identity
NCBI Description
                    (AF056622) putative Cu/Zn superoxide dismutase precursor
                    [Vitis vinifera]
                   230427
Seq. No.
Seq. ID
                   LIB3196-058-P1-M1-G7
Method
                   BLASTX
NCBI GI
                   q1169228
BLAST score
                   169
                    3.0e-12
E value
Match length
                    43
                   81
% identity
NCBI Description
                   RNA HELICASE-LIKE PROTEIN DB10 >gi 1084413 pir S42639
                   helicase-like protein - Wood tobacco
                   >gi_563986_dbj_BAA03763_ (D16247) RNA helicase like protein
                   DB10 [Nicotiana sylvestris]
Seq. No.
                   230428
                   LIB3196-058-P1-M1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g585922
```



```
Match length
                  85
                  78
% identity
NCBI Description DNA-DIRECTED RNA POLYMERASE BETA" CHAIN
Seq. No.
                  230429
                  LIB3196-058-P1-M1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q747900
BLAST score
                  180
E value
                  2.0e-13
                  48
Match length
                  58
% identity
NCBI Description
                 (Z48758) unknown [Saccharomyces cerevisiae]
                  230430
Seq. No.
Seq. ID
                  LIB3196-058-P1-M1-H10
                  BLASTX
Method
                  g3935151
NCBI GI
BLAST score
                  497
E value
                  2.0e-50
Match length
                  118
                  73
% identity
```

NCBI Description (AC005106) T25N20.15 [Arabidopsis thaliana]

230431 Seq. No. LIB3196-058-P1-M1-H2 Seq. ID Method BLASTX g137578 NCBI GI BLAST score 612 E value 6.0e-64

Match length 118 % identity

NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi\_81545\_pir\_\_S06398 alpha-globulin type A precursor -

upland cotton >gi\_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi\_207906 (M18027) alpha globulin A [Artificial gene] >gi\_226119\_prf\_\_1410330A vicilin gene A

[Saguinus oedipus]

Seq. No. 230432

Seq. ID LIB3196-058-P1-M1-H3

Method BLASTX NCBI GI g585966 BLAST score 529 E value 4.0e-54 Match length 106 % identity 92

NCBI Description AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED

SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH)

>gi 2135787 pir A49585 Na+ channel protein,

amiloride-sensitive - human >gi 452650 emb CAA53773 (X76180) Na+ channel protein [Homo sapiens] >qi 493605

(L29007) Na+ channel [Homo sapiens]

>gi\_2765702\_emb\_CAB07505\_ (Z92978) amiloride-sensitive epithelial sodium channel alpha subunit [Homo sapiens] >gi 744560 prf 2015190A amiloride-sensitive Na channel



[Homo sapiens] >gi\_4506815\_ref\_NP\_001029.1\_pSCNN1A\_ sodium channel, nonvoltage-gated 1 alpha >gi\_4507057\_ref\_NP\_003038.1\_pSLC9A1\_ solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na+/H+, amiloride sensitive)

Seq. No. LIB3196-058-P1-M1-H4 Seq. ID BLASTX Method g207905 NCBI GI 544 BLAST score E value 6.0e-56 Match length 127 % identity 86

230433

(M18027) alpha globulin B [Artificial gene] NCBI Description

Seq. No. 230434

LIB3196-059-P1-M1-A1 Seq. ID

BLASTX Method NCBI GI g3184184 BLAST score 261 5.0e-23E value 74 Match length 76 % identity

(AB002134) airway trypsin-like protease [Homo sapiens] NCBI Description

Seq. No. 230435

LIB3196-059-P1-M1-A10 Seq. ID

Method BLASTX q3063396 NCBI GI BLAST score 399 5.0e-39 E value 93 Match length % identity 81

NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 230436

Seq. ID LIB3196-059-P1-M1-A5

Method BLASTX NCBI GI q2506802 BLAST score 573 E value 2.0e-59 Match length 118 % identity

NCBI Description THYMIDYLATE KINASE (DTMP KINASE)

Seq. No. 230437

Seq. ID LIB3196-059-P1-M1-A6

Method BLASTX NCBI GI q4432846 BLAST score 306 E value 4.0e-28 Match length 115 % identity

(AC006283) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 230438

E value

Match length

6.0e-52

105



```
LIB3196-059-P1-M1-A8
Seq. ID
Method
                  BLASTX
                  g117759
NCBI GI
                  201
BLAST score
                  3.0e-16
E value
                  44
Match length
                  95
% identity
NCBI Description CYTOCHROME C1, HEME PROTEIN PRECURSOR >gi_181240 (J04444)
                  cytochrome c-1 [Homo sapiens]
                  230439
Seq. No.
                  LIB3196-059-P1-M1-A9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2443320
                  360
BLAST score
                  1.0e-34
E value
                  87
Match length
                  83
% identity
                 (D85597) polyprotein [Oryza australiensis]
NCBI Description
                  230440
Seq. No.
                  LIB3196-059-P1-M1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1843527
BLAST score
                  404
E value
                  1.0e-39
Match length
                  110
% identity
                  75
NCBI Description (U73747) annexin [Gossypium hirsutum]
                  230441
Seq. No.
                  LIB3196-059-P1-M1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g167367
BLAST score
                  445
                  2.0e-44
E value
Match length
                  116
% identity
                  75
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                  230442
Seq. No.
Seq. ID
                  LIB3196-059-P1-M1-B3
Method
                  BLASTX
NCBI GI
                  q2118384
                  584
BLAST score
                  1.0e-60
E value
Match length
                  127
% identity
NCBI Description squamous cell carcinoma antigen 2 - human
Seq. No.
                  230443
Seq. ID
                  LIB3196-059-P1-M1-B8
Method
                  BLASTX
NCBI GI
                  g2118965
BLAST score
                  510
```



31

% identity

NCBI Description

```
polyubiquitin [Bos taurus]
                  230444
Seq. No.
                  LIB3196-059-P1-M1-C10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2213867
BLAST score
                   517
                   7.0e-53
E value
Match length
                  111
                   89
% identity
                  (AF003124) fructose-biphosphate aldolase [Mesembryanthemum
NCBI Description
                   crystallinum]
Seq. No.
                   230445
                  LIB3196-059-P1-M1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g120668
BLAST score
                   351
                   2.0e-33
E value
Match length
                  84
                   83
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi 82399_pir__A24159 glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)
                   >gi 167044 (M36650) glyceraldehyde-3-phosphate
                   dehydrogenase [Hordeum vulgare] >gi_225347_prf__1301218A
                   dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var.
                   distichum]
Seq. No.
                   230446
                  LIB3196-059-P1-M1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3850816
                   352
BLAST score
E value
                   2.0e-33
Match length
                   69
                   91
% identity
                  (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza
NCBI Description
                   sativa]
Seq. No.
                   230447
                   LIB3196-059-P1-M1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2605714
BLAST score
                   382
E value
                   6.0e-37
Match length
                   99
                   77
% identity
                   (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
NCBI Description
                   thalianal
                   230448
Seq. No.
                   LIB3196-059-P1-M1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g602076
```

polyubiquitin - bovine (fragment) >gi\_163573 (M62428)



BLAST score 581 2.0e-60 E value 119 Match length 23 % identity NCBI Description (X77456) pentameric polyubiquitin [Nicotiana tabacum] 230449 Seq. No. LIB3196-059-P1-M1-C6 Seq. ID Method BLASTX NCBI GI q137578 230 BLAST score E value 1.0e-19 62 Match length 77 % identity VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) NCBI Description >gi\_81545\_pir\_\_S06398 alpha-globulin type A precursor -

upland cotton >gi\_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi\_207906 (M18027) alpha globulin A [Artificial gene] >gi 226119 prf 1410330A vicilin gene A [Saguinus oedipus]

Seq. No. 230450

LIB3196-059-P1-M1-C7 Seq. ID

Method BLASTX NCBI GI g1223926 BLAST score 144 E value 4.0e-09 Match length 110 % identity 34

(U49741) Vigna radiata carboxypeptidase II mRNA, partial NCBI Description

cds [Vigna radiata]

230451 Seq. No.

LIB3196-059-P1-M1-D1 Seq. ID

Method BLASTX NCBI GI g1263291 BLAST score 496 E value 2.0e-50 Match length 95 99 % identity

NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No. 230452

LIB3196-059-P1-M1-D10 Seq. ID

Method BLASTX NCBI GI q1346344 BLAST score 602 9.0e-63 E value Match length 123 % identity

KERATIN, TYPE II CYTOSKELETAL 6A (CYTOKERATIN 6A) (CK 6A) NCBI Description

> (K6A KERATIN) >gi\_2119221\_pir\_\_A57398 keratin type II human >gi 908779 (L42583) keratin type II [Homo sapiens]

Seq. No. 230453

LIB3196-059-P1-M1-D2 Seq. ID

Method BLASTX



```
g2129727
NCBI GI
BLAST score
                  163
                  2.0e-11
E value
Match length
                  97
                  42
% identity
                  RNA-binding protein 37 - Arabidopsis thaliana >gi 1174153
NCBI Description
                  (U44134) RNA-binding protein [Arabidopsis thaliana]
                  230454
Seq. No.
                  LIB3196-059-P1-M1-D4
Seq. ID
Method
                  BLASTX
                  g416922
NCBI GI
                  322
BLAST score
E value
                  6.0e-30
                  103
Match length
% identity
                  65
                  DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (DUTPASE)
NCBI Description
                  (DUTP PYROPHOSPHATASE) (P18) >gi 282947 pir_JQ1599 dUTP
                  pyrophosphatase (EC 3.6.1.23) - Tomato
                  >gi 251897 bbs 109276 (S40549) deoxyuridine triphosphatase,
                  dUTPase, P18 (EC 3.6.1.23) [tomatoes, Tint Tim cultivar
                  LA154, Peptide, 169 aa] [Lycopersicon esculentum]
                  230455
Seq. No.
                  LIB3196-059-P1-M1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2605714
BLAST score
                  309
                  2.0e-28
E value
                  79
Match length
                  78
% identity
NCBI Description
                  (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
                  thaliana]
                  230456
Seq. No.
Seq. ID
                  LIB3196-059-P1-M1-D6
Method
                  BLASTX
NCBI GI
                  q2578033
BLAST score
                  630
                   4.0e-66
E value
Match length
                  120
% identity
NCBI Description (X97016) omega-6 desaturase [Gossypium hirsutum]
                  230457
Seq. No.
Seq. ID
                  LIB3196-059-P1-M1-D8
Method
                  BLASTX
NCBI GI
                  g2781363
BLAST score
                  164
E value
                   2.0e-11
```

Match length 64 % identity

NCBI Description (AC003113) F2401.19 [Arabidopsis thaliana]

230458 Seq. No.

Seq. ID LIB3196-059-P1-M1-D9

Method BLASTX



```
q132659
NCBI GI
                  147
BLAST score
                  2.0e-09
E value
Match length
                  80
% identity
                  45
                  50S RIBOSOMAL PROTEIN L13, CHLOROPLAST PRECURSOR (CL13)
NCBI Description
                  >gi_81483_pir__A32033 ribosomal protein L13 precursor,
                  chloroplast - spinach >gi_170133 (J04461) ribosomal protein
                  L13 [Spinacia oleracea]
Seq. No.
                  230459
                  LIB3196-059-P1-M1-E1
Seq. ID
Method
                  BLASTX
                  g206440
NCBI GI
BLAST score
                  539
E value
                  2.0e-55
Match length
                  103
                  99
% identity
                  (M62752) statin-related protein [Rattus norvegicus]
NCBI Description
                  230460
Seq. No.
                  LIB3196-059-P1-M1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2982453
BLAST score
                  504
                  3.0e-51
E value
Match length
                  119
                  82
% identity
                  (AL022223) fructose-bisphosphate aldolase-like protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  230461
                  LIB3196-059-P1-M1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2498323
BLAST score
                  412
E value
                  2.0e-40
Match length
                  98
% identity
                  82
                  EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY
NCBI Description
                  COMPONENT P85) >gi 1488324 (U65932) extracellular matrix
                  protein 1 [Homo sapiens] >gi 1488332 (U65938) extracellular
                  matrix protein 1 [Homo sapiens] >gi 2654433 (U68186)
                  extracellular matrix protein 1 [Homo sapiens]
Seq. No.
                  230462
Seq. ID
                  LIB3196-059-P1-M1-E4
Method
                  BLASTX
NCBI GI
                  q542184
                  219
BLAST score
E value
                  7.0e-18
Match length
                  117
% identity
                  41
```

NCBI Description globulin-1S, GLB1S - maize

LIB3196-059-P1-M1-E6

230463

Seq. No.

Seq. ID



```
Method
                  BLASTX
                  g3915830
NCBI GI
                  626
BLAST score
                  1.0e-65
E value
                  127
Match length
                  95
% identity
                  REP-8 PROTEIN (D8S2298E) >gi 1913785 dbj BAA18958 (D83767)
NCBI Description
                  Rep-8 [Homo sapiens]
                  230464
Seq. No.
                  LIB3196-059-P1-M1-E8
Seq. ID
Method
                  BLASTX
                  g2497938
NCBI GI
                  571
BLAST score
                  8.0e-60
E value
Match length
                  123
                  97
% identity
                  AQUAPORIN 3 >qi 1854374 dbj BAA19237 (AB001325) aquaporin
NCBI Description
                  3 [Homo sapiens]
                  230465
Seq. No.
                  LIB3196-059-P1-M1-E9
Seq. ID
Method
                  BLASTX
                  g283971
NCBI GI
BLAST score
                  648
                  4.0e-68
E value
                  126
Match length
% identity
                  97
                  aldehyde dehydrogenase (NAD(P)+) (EC 1.2.1.5) 3 - human
NCBI Description
                  >qi 178375 (M77477) aldehyde dehydrogenase [Homo sapiens]
                  >gi_300402 bbs_132241 (S61044) aldehyde dehydrogenase
                  isozyme 3, ALDH3 {EC 1.2.1.3} [human, stomach, Peptide, 453
                  aa] [Homo sapiens]
                  230466
Seq. No.
                  LIB3196-059-P1-M1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1199772
BLAST score
                  218
                   9.0e-18
E value
Match length
                   45
% identity
                   87
                  (D83226) extensin like protein [Populus nigra]
NCBI Description
                   >gi_1199774_dbj_BAA11855_ (D83227) extensin like protein
                   [Populus nigra]
                   230467
Seq. No.
Seq. ID
                  LIB3196-059-P1-M1-F12
Method
                  BLASTX
                   q4454026
NCBI GI
BLAST score
                   326
                   2.0e-30
E value
Match length
                   94
% identity
                   69
```

Seq. No. 230468

NCBI Description

(AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No.

230473



```
LIB3196-059-P1-M1-F2
  Seq. ID
Method
                     BLASTX
  NCBI GI
                     q137578
  BLAST score
                     509
  E value
                     7.0e-52
  Match length
                     100
                     96
  % identity
                     VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
  NCBI Description
                     >gi_81545_pir__S06398 alpha-globulin type A precursor -
                     upland cotton >gi_167371 (M19378) vicilin precursor
                     [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                     [Artificial gene] >gi_226119_prf__1410330A vicilin gene A
                     [Saguinus oedipus]
                     230469
  Seq. No.
                     LIB3196-059-P1-M1-F3
  Seq. ID
  Method
                     BLASTX
                     g804996
  NCBI GI
  BLAST score
                     297
                     6.0e-27
  E value
  Match length
                     61
                     90
  % identity
                     (Z49216) mitoxantrone-resistance associated gene [Homo
  NCBI Description
                     sapiens]
                     230470
  Seq. No.
  Seq. ID
                     LIB3196-059-P1-M1-F5
  Method
                     BLASTX
                     g346219
  NCBI GI
  BLAST score
                     214
                     3.0e-17
  E value
                     77
  Match length
                     62
  % identity
  NCBI Description keratin K4a - human (fragment)
  Seq. No.
                     230471
  Seq. ID
                     LIB3196-059-P1-M1-F6
  Method
                     BLASTX
  NCBI GI
                     q3599491
  BLAST score
                     234
  E value
                     1.0e-19
  Match length
                     55
   % identity
                     78
  NCBI Description
                    (AF085149) putative aminotransferase [Capsicum chinense]
  Seq. No.
                     230472
  Seq. ID
                     LIB3196-059-P1-M1-F7
  Method
                     BLASTX
  NCBI GI
                     g3445210
  BLAST score
                     342
  E value
                     3.0e-32
  Match length
                     108
                     57
   % identity
                     (AC004786) putative flavonol 3-o-glucosyltransferase
  NCBI Description
                     [Arabidopsis thaliana]
```

NCBI Description



```
Seq. ID
                   LIB3196-059-P1-M1-F9
Method
                   BLASTX
                   g1083762
NCBI GI
BLAST score
                   293
E value
                   2.0e-26
                   57
Match length
                   98
% identity
                   prolactin-induced T cell protein c15 - rat
NCBI Description
                   >gi_619907_emb_CAA57825_ (X82445) RnudC [Rattus norvegicus]
Seq. No.
                   230474
Seq. ID
                   LIB3196-059-P1-M1-G1
Method
                   BLASTX
NCBI GI
                   g477138
                   365
BLAST score
E value
                   6.0e-35
                   71
Match length
                   94
% identity
                   carcinoma-associated antigen GA733-1 precursor - human
NCBI Description
                   >gi 31591 emb CAA31781 (X13425) GA733-1 protein (AA 1-323)
                   [Homo sapiens]
                   230475
Seq. No.
                   LIB3196-059-P1-M1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4455287
BLAST score
                   284
                   2.0e-25
E value
Match length
                   97
                   56
% identity
NCBI Description
                  (AL035527) putative protein [Arabidopsis thaliana]
Seq. No.
                   230476
                   LIB3196-059-P1-M1-G12
Seq. ID
Method
                   BLASTX
                   g137578
NCBI GI
BLAST score
                   273
E value
                   2.0e-42
Match length
                   95
% identity
NCBI Description
                   VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
                   >gi_81545_pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                    [Artificial gene] >gi_226119_prf__1410330A vicilin gene A
                    [Saguinus oedipus]
Seq. No.
                   230477
Seq. ID
                   LIB3196-059-P1-M1-G4
Method
                   BLASTX
NCBI GI
                   g3122072
BLAST score
                   522
E value
                   2.0e-53
Match length
                   104
% identity
                   96
```

ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION

FACTOR TU) (EF-TU) >gi\_2119922\_pir\_\_I50226 elongation



factor 1 alpha - chicken >gi 488468 (L00677) elongation factor 1 alpha [Gallus gallus]

230478 Seq. No. Seq. ID LIB3196-059-P1-M1-G6 Method BLASTX NCBI GI g126156 308 BLAST score 2.0e-28 E value Match length 110 64 % identity

NCBI Description LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134)

>gi\_72288\_pir\_\_FWCNBB beta-globulin B precursor (clone 134)

- upland cotton >gi\_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi\_1171335 (U43727) legumin B [Gossypium hirsutum] >gi 225582 prf 1306412C storage

protein C134 [Saguinus oedipus]

230479 Seq. No.

LIB3196-059-P1-M1-G7 Seq. ID

Method BLASTX NCBI GI g88044 589 BLAST score E value 3.0e-61 Match length 125 96 % identity

NCBI Description keratin 4, type II, cytoskeletal - human (fragment)

>gi 34073 emb CAA30534 (X07695) cytokeratin 4 (408 AA)

[Homo sapiens]

230480 Seq. No.

Seq. ID LIB3196-059-P1-M1-G9

Method BLASTX g3158376 NCBI GI BLAST score 234 E value 1.0e-19 Match length 90

% identity 53

NCBI Description (AF035385) unknown [Arabidopsis thaliana]

230481 Seq. No.

Seq. ID LIB3196-059-P1-M1-H1

Method BLASTX NCBI GI q1702983 BLAST score 356 E value 6.0e - 34Match length 111 % identity

AUXIN-REPRESSED 12.5 KD PROTEIN >gi\_99855\_pir\_\_S11850 NCBI Description

hypothetical protein - garden strawberry >gi\_22573\_emb\_CAA36676\_ (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi\_927034 (L44142) auxin-repressed protein

[Fragaria ananassa]

Seq. No. 230482

Seq. ID LIB3196-059-P1-M1-H12

Method BLASTX



```
NCBI GI
                  g207905
                  543
BLAST score
                  7.0e-56
E value
Match length
                  121
% identity
                  89
                  (M18027) alpha globulin B [Artificial gene]
NCBI Description
Seq. No.
                  230483
Seq. ID
                  LIB3196-059-P1-M1-H2
                  BLASTX
Method
NCBI GI
                  q547753
BLAST score
                  452
                   4.0e-45
E value
                  94
Match length
                   96
% identity
                  KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)
NCBI Description
                   230484
Seq. No.
                  LIB3196-059-P1-M1-H3
Seq. ID
                  BLASTX
Method
                   q137578
NCBI GI
BLAST score
                   494
                   4.0e-50
E value
Match length
                   116
                   84
% identity
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                   >gi 81545 pir__S06398 alpha-globulin type A precursor -
                   upland cotton >gi_167371 (M19378) vicilin precursor
                   [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                   [Artificial gene] >gi_226119_prf__1410330A vicilin gene A
                   [Saguinus oedipus]
                   230485
Seq. No.
                   LIB3196-059-P1-M1-H4
Seq. ID
                   BLASTX
Method
                   g133041
NCBI GI
                   519
BLAST score
                   5.0e-53
E value
Match length
                   101
                   99
% identity
                   60S ACIDIC RIBOSOMAL PROTEIN PO (L10E)
NCBI Description
                   >gi 71137_pir__R5HUPO acidic ribosomal protein P0 - human
                   >qi 190232 (M17885) acidic ribosomal phosphoprotein (P0)
                   [Homo sapiens] >gi_2935618_gb_AAC05176_ (AC004263) 60S
                   ACIDIC RIBOSOMAL PROTEIN; match to P05388 (PID:g133041)
                   [Homo sapiens] >gi_4506667_ref_NP_000993.1_pRPLP0_
                   ribosomal protein, large, PO
                   230486
Seq. No.
                   LIB3196-059-P1-M1-H9
Seq. ID
Method
                   BLASTX
                   g3851636
NCBI GI
                   451
BLAST score
                   4.0e-45
E value
                   103
Match length
% identity
```

NCBI Description (AF098519) unknown [Avicennia marina] >gi 4128206



## (AF056316) 40S ribosome protein S7 [Avicennia marina]

```
Seq. No.
                  230487
                  LIB3196-064-P1-M1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1800147
BLAST score
                  174
E value
                  1.0e-12
                  100
Match length
                  43
% identity
                  (U83655) membrane associated protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  230488
                  LIB3196-064-P1-M1-A3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4235430
BLAST score
                  361
                  1.0e-34
E value
Match length
                  115
% identity
                  (AF098458) latex-abundant protein [Hevea brasiliensis]
NCBI Description
                  230489
Seq. No.
                  LIB3196-064-P1-M1-A7
Seq. ID
                  BLASTX
Method
                  q3913961
NCBI GI
BLAST score
                   650
                   2.0e-68
E value
Match length
                  125
% identity
                   99
                  KINESIN-LIKE PROTEIN KIF1C >gi 2738149 (U91329)
NCBI Description
                  kinesin-like motor protein KIFIC [Homo sapiens]
Seq. No.
                   230490
                  LIB3196-064-P1-M1-A9
Seq. ID
                  BLASTX
Method
                   g115492
NCBI GI
                   296
BLAST score
E value
                   6.0e-27
Match length
                  80
                   39
% identity
NCBI Description CALMODULIN-RELATED PROTEIN >gi_169205 (M80831)
                   calmodulin-related protein [Petunia hybrida]
                   230491
Seq. No.
                   LIB3196-064-P1-M1-B1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1346347
                   517
BLAST score
                   9.0e-53
E value
Match length
                   109
                   96
% identity
                  KERATIN, TYPE II CYTOSKELETAL 6D (CYTOKERATIN 6D) (CK 6D)
NCBI Description
                   (K6D KERATIN) >gi_2119225_pir__I61769 keratin type II -
```

sapiens]

human (fragment) >gi\_914833 (L42610) keratin type II [Homo



```
Seq. No.
                  230492
                  LIB3196-064-P1-M1-B10
Seq. ID
Method
                  BLASTX
                  g461994
NCBI GI
                  379
BLAST score
                  1.0e-36
E value
Match length
                  84
                  88
% identity
                  ELONGATION FACTOR 1-DELTA (EF-1-DELTA)
NCBI Description
                  >gi 1085404 pir S34626 translation elongation factor eEF-1
                  delta chain - human >gi_38522_emb_CAA79716_ (Z21507) human
                  elongation factor-1-delta [Homo sapiens]
                  >gi 4503479 ref NP 001951.1_pEEF1D_ eukaryotic translation
                  elongation factor 1 delta (guanine nucleotide exchange
                  protein)
                  230493
Seq. No.
Seq. ID
                  LIB3196-064-P1-M1-B11
Method
                  BLASTX
                  g3395758
NCBI GI
BLAST score
                  172
                  2.0e-12
E value
Match length
                  79
% identity
                  41
                  (U76300) unknown [Arabidopsis thaliana]
NCBI Description
                  230494
Seq. No.
Seq. ID
                  LIB3196-064-P1-M1-B3
Method
                  BLASTX
NCBI GI
                  g2832617
BLAST score
                  178
                  2.0e-13
E value
                  42
Match length
% identity
                  76
                  (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
                  230495
Seq. No.
                  LIB3196-064-P1-M1-B4
Seq. ID
Method
                  BLASTX
                  g3335226
NCBI GI
                   371
BLAST score
                  1.0e-35
E value
                  77
Match length
                   29
% identity
                  (AF077374) small proline-rich protein [Homo sapiens]
NCBI Description
                   230496
Seq. No.
                  LIB3196-064-P1-M1-B8
Seq. ID
Method
                  BLASTX
                   g224877
NCBI GI
                   448
BLAST score
                   9.0e-45
E value
                   87
Match length
                   97
% identity
```

Seq. No. 230497

NCBI Description deaminase a, adenosine [Homo sapiens]

Seq. No.

Seq. ID

230502

LIB3196-064-P1-M1-D3



```
LIB3196-064-P1-M1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3724114
BLAST score
                  647
                  5.0e-68
E value
Match length
                  128
                  97
% identity
                  (Y16792) keratin, type I [Homo sapiens]
NCBI Description
                  >gi 4504927 ref NP 003762.1 pKRTHA6 UNKNOWN
                  230498
Seq. No.
                  LIB3196-064-P1-M1-C7
Seq. ID
                  BLASTX
Method
                  g2119924
NCBI GI
BLAST score
                  509
                  5.0e-52
E value
                  99
Match length
                  97
% identity
                  oncogene PTI-1 - human >gi 927065 gb AAC09385.1 (L41490)
NCBI Description
                  eukaryotic translation elongation factor 1 alpha 1-like 14
                  [Homo sapiens] >qi 927067 (L41498) longation factor 1-alpha
                  1 [Homo sapiens] >gi 4503473 ref NP 001394.1 pEEF1A1L14
                  eukaryotic translation elongation factor 1 alpha 1-like
                  230499
Seq. No.
                  LIB3196-064-P1-M1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245136
BLAST score
                  403
                  1.0e-39
E value
Match length
                  103
                  67
% identity
NCBI Description
                  (Z97344) trehalose-6-phosphate synthase homolog
                   [Arabidopsis thaliana]
                  230500
Seq. No.
                  LIB3196-064-P1-M1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2804273
BLAST score
                  617
E value
                  2.0e-64
Match length
                  123
                  98
% identity
                  (D89980) alpha actinin 4 [Homo sapiens]
NCBI Description
                  230501
Seq. No.
                  LIB3196-064-P1-M1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1001309
BLAST score
                  177
E value
                  6.0e-13
Match length
                  103
% identity
                  36
                  (D64006) aspartate aminotransferase [Synechocystis sp.]
NCBI Description
```



```
Method
                  BLASTX
NCBI GI
                  g137578
                  524
BLAST score
                  1.0e-53
E value
Match length
                  102
                  100
% identity
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                  >gi_81545_pir__S06398 alpha-globulin type A precursor -
                  upland cotton >gi 167371 (M19378) vicilin precursor
                  [Gossypium hirsutum] >gi_207906 (M18027) alpha globulin A
                  [Artificial gene] >gi 226119 prf 1410330A vicilin gene A
                  [Saguinus oedipus]
                  230503
Seq. No.
Seq. ID
                  LIB3196-064-P1-M1-D5
Method
                  BLASTX
                  q1504008
NCBI GI
BLAST score
                  315
                  4.0e-29
E value
                  94
Match length
                  64
% identity
                  (D86967) Containing ATP/GTP-binding site motif A(P-loop):
NCBI Description
                  Similar to C.elegans protein(P1:CEC47E128); Similar to Mouse
                  alpha-mannosidase(P1:B54407) [Homo sapiens]
                  230504
Seq. No.
                  LIB3196-064-P1-M1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q266690
BLAST score
                  335
                  2.0e-31
E value
                  96
Match length
                  72
% identity
                  OLEOSIN 18.2 KD >gi_167363 (L00935) 18.2 kDa oleosin
NCBI Description
                   [Gossypium hirsutum] >gi 167365 (L00936) 18.2 kDa oleosin
                   [Gossypium hirsutum]
Seq. No.
                  230505
                  LIB3196-064-P1-M1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q81546
BLAST score
                  541
E value
                  1.0e-55
Match length
                  114
                  94
% identity
                  alpha-globulin type B precursor (tandem 1) - upland cotton
NCBI Description
                   (fragment)
Seq. No.
                  230506
                  LIB3196-064-P1-M1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1223922
BLAST score
                  465
```

NCBI GI g1223922 BLAST score 465 E value 1.0e-46 Match length 104 % identity 77

NCBI Description (U49445) Vigna radiata vicilin peptidohydrolase [Vigna



## radiata]

```
230507
Seq. No.
                  LIB3196-064-P1-M1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2522228
                  455
BLAST score
E value
                  1.0e-45
                  115
Match length
% identity
                  (AB007466) reverse transcriptase-like protein [Vicia faba]
NCBI Description
Seq. No.
                  230508
                  LIB3196-064-P1-M1-E6
Seq. ID
                  BLASTX
Method
                  q3415119
NCBI GI
BLAST score
                  560
                  8.0e-58
E value
Match length
                  116
% identity
                  (AF081672) calmodulin [Gallus gallus]
NCBI Description
                   230509
Seq. No.
Seq. ID
                  LIB3196-064-P1-M1-E8
Method
                  BLASTX
                  g547683
NCBI GI
                   608
BLAST score
                   2.0e-63
E value
Match length
                   119
% identity
                   97
                  HEAT SHOCK COGNATE PROTEIN 80 >gi_170456 (M96549) heat
NCBI Description
                   shock cognate protein 80 [Solanum lycopersicum]
                   >gi 445601 prf_ 1909348A heat shock protein hsp80
                   [Lycopersicon esculentum]
                   230510
Seq. No.
                   LIB3196-064-P1-M1-F1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3123271
BLAST score
                   340
                   1.0e-32
E value
                   70
Match length
                   90
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052)
                   ribosomal protein S6 [Arabidopsis thaliana]
                   230511
Seq. No.
                   LIB3196-064-P1-M1-F10
Seq. ID
                   BLASTX
Method
                   g3023180
NCBI GI
                   375
BLAST score
                   3.0e-36
E value
                   89
Match length
                   85
% identity
NCBI Description 14-3-3-LIKE PROTEIN 10 >gi_1771166_emb_CAA67374.1_ (X98866)
```

14-3-3 protein [Lycopersicon esculentum]



```
230512
Seq. No.
                   LIB3196-064-P1-M1-F11
Seq. ID
                   BLASTX
Method
                   q940395
NCBI GI
                   539
BLAST score
                   2.0e-55
E value
                   109
Match length
                   12
% identity
                  (D63782) polyubiquitin [Cricetulus sp.]
NCBI Description
                   230513
Seq. No.
                   LIB3196-064-P1-M1-F3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g167367
                   598
BLAST score
                   2.0e-62
E value
Match length
                   112
% identity
                   98
                  (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                   230514
Seq. No.
                   LIB3196-064-P1-M1-F4
Seq. ID
Method
                   BLASTX
                   g627584
NCBI GI
                   613
BLAST score
                   5.0e-64
E value
                   129
Match length
% identity
                   89
NCBI Description protein p84 - human >gi_550058 (L36529) protein p84 [Homo
                   sapiens]
                   230515
Seq. No.
                   LIB3196-064-P1-M1-G1
Seq. ID
                   BLASTX
Method
                   g136452
NCBI GI
                   342
BLAST score
                   3.0e - 32
E value
Match length
                   105
                   62
% identity
                   STEM-SPECIFIC PROTEIN TSJT1 >qi 100383 pir S13551
NCBI Description
                   stem-specific protein - common tobacco
>gi_20037_emb_CAA36525_ (X52283) stem specific, weakly
                   expressed in other organs [Nicotiana tabacum]
                   230516
Seq. No.
                   LIB3196-064-P1-M1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g70753
BLAST score
                   408
                   5.0e-40
E value
                   99
Match length
% identity
NCBI Description histone H3 - garden pea >gi_82610 pir_ S00373 histone H3 -
                   wheat
```

230517

LIB3196-064-P1-M1-G2

Seq. No.

Seq. ID

Method

NCBI GI

BLASTX

g1346345



```
Method
                   BLASTX
                   g1931647
NCBI GI
BLAST score
                   434
                   4.0e-43
E value
Match length
                   117
                   68
% identity
NCBI Description
                   (U95973) endomembrane protein EMP70 precusor isolog
                   [Arabidopsis thaliana]
Seq. No.
                   230518
                   LIB3196-064-P1-M1-G4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3341695
BLAST score
                   306
                   5.0e-28
E value
Match length
                   88
% identity
                   67
                   (AC003672) putative thiamin pyrophosphokinase [Arabidopsis
NCBI Description
                   thaliana]
                   230519
Seq. No.
                   LIB3196-064-P1-M1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g224877
BLAST score
                   493
                   6.0e-50
E value
Match length
                   97
                   96
% identity
NCBI Description deaminase a, adenosine [Homo sapiens]
                   230520
Seq. No.
                   LIB3196-064-P1-M1-G6
Seq. ID
                   BLASTX
Method
                   g3548818
NCBI GI
                   260
BLAST score
                   1.0e-22
E value
                   128
Match length
                   45
% identity
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
                   230521
Seq. No.
                   LIB3196-064-P1-M1-G8
Seq. ID
Method
                   BLASTX
                   g1707889
NCBI GI
                   531
BLAST score
                   2.0e-54
E value
                   103
Match length
                   100
% identity
                  RAB GDP DISSOCIATION INHIBITOR BETA (RAB GDI BETA) (GDI-2)
NCBI Description
                   >gi_285975_dbj_BAA03095_ (D13988) human rab GDI [Homo
sapiens] >gi_4503973_ref_NP_001485.1_pGDI2_ GDP
                   dissociation inhibitor
Seq. No.
                   230522
                   LIB3196-064-P1-M1-H11
Seq. ID
```

BLAST score

E value Match length 652 1.0e-68

128



```
BLAST score
                  617
E value
                  2.0e-64
Match length
                  124
% identity
                  98
                  KERATIN, TYPE II CYTOSKELETAL 6B (CYTOKERATIN 6B) (CK 6B)
NCBI Description
                  (K6B KERATIN) >qi 2119220 pir I61767 keratin type II -
                  human >gi 908790 (L42592) keratin type II [Homo sapiens]
                  230523
Seq. No.
                  LIB3196-064-P1-M1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2880051
BLAST score
                  272
                  4.0e-24
E value
Match length
                  64
                  81
% identity
                  (AC002340) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  230524
Seq. ID
                  LIB3196-064-P1-M1-H5
                  BLASTX
Method
                  g2244979
NCBI GI
BLAST score
                  501
E value
                  6.0e-51
                  118
Match length
% identity
                  (Z97340) similarity to enoyl-CoA hydratase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  230525
Seq. ID
                  LIB3196-064-P1-M1-H9
                  BLASTX
Method
NCBI GI
                  q2605714
BLAST score
                  285
                  1.0e-25
E value
Match length
                  75
                  77
% identity
                  (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
NCBI Description
                  thaliana]
                   230526
Seq. No.
                  LIB3196-065-P1-M1-A1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q809561
BLAST score
                   213
                  1.0e-17
E value
                  61
Match length
                   72
% identity
NCBI Description
                  (X13055) gamma-actin [Mus musculus]
Seq. No.
                   230527
                  LIB3196-065-P1-M1-A11
Seq. ID
Method
                  BLASTX
                   q2497938
NCBI GI
```



% identity NCBI Description AQUAPORIN 3 >gi 1854374 dbj BAA19237 (AB001325) aquaporin 3 [Homo sapiens] 230528 Seq. No. LIB3196-065-P1-M1-A2 Seq. ID Method BLASTX NCBI GI g2144098 403 BLAST score 2.0e-39 E value Match length 115 % identity 74 SC2 - rat >gi 256994 bbs 115268 (S45663) SC2=synaptic NCBI Description glycoprotein [rats, brain, Peptide, 308 aa] [Rattus sp.] Seq. No. 230529 LIB3196-065-P1-M1-A7 Seq. ID Method BLASTX NCBI GI g1346344 BLAST score 539 E value 2.0e-55 Match length 108 100 % identity NCBI Description KERATIN, TYPE II CYTOSKELETAL 6A (CYTOKERATIN 6A) (CK 6A) (K6A KERATIN) >gi 2119221 pir A57398 keratin type II human >gi 908779 (L42583) keratin type II [Homo sapiens] Seq. No. 230530 Seq. ID LIB3196-065-P1-M1-B10 Method BLASTX NCBI GI q126156 BLAST score 369 2.0e-40 E value Match length 117 79 % identity LEGUMIN B PRECURSOR (BETA-GLOBULIN B) (LEGB-C134) NCBI Description >gi\_72288\_pir\_\_FWCNBB beta-globulin B precursor (clone 134) - upland cotton >gi\_167373 (M16936) vicilin precursor [Gossypium hirsutum] >gi\_1171335 (U43727) legumin B [Gossypium hirsutum] >gi 225582 prf 1306412C storage protein C134 [Saguinus oedipus] Seq. No. 230531 LIB3196-065-P1-M1-B12 Seq. ID Method BLASTX NCBI GI g1076316 BLAST score 342 E value 3.0e-32 Match length 90 % identity 61 NCBI Description drought-induced protein Di19 - Arabidopsis thaliana

>gi\_469110\_emb\_CAA55321 (X78584) Di19 [Arabidopsis

thaliana]

230532 Seq. No.

LIB3196-065-P1-M1-B3 Seq. ID

Method BLASTX



```
g3901014
NCBI GI
                  214
BLAST score
                  3.0e-17
E value
                  55
Match length
                  71
% identity
                  (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                  sylvatica]
                  230533
Seq. No.
                  LIB3196-065-P1-M1-B5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g167367
                  480
BLAST score
                  2.0e-48
E value
Match length
                  122
                  76
% identity
                  (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                  230534
Seq. No.
                  LIB3196-065-P1-M1-B7
Seq. ID
Method
                  BLASTX
                   g3122380
NCBI GI
BLAST score
                   647
                   5.0e-68
E value
Match length
                   131
% identity
                   95
                  ALPHA-MANNOSIDASE II (MANNOSYL-OLIGOSACCHARIDE
NCBI Description
                   1,3-1,6-ALPHA-MANNOSIDASE) (MAN II) (GOLGI
                  ALPHA-MANNOSIDASE II) >gi 1117827 (U31520) alpha
                  mannosidase II [Homo sapiens]
                   230535
Seq. No.
                   LIB3196-065-P1-M1-B8
Seq. ID
                   BLASTX
Method
                   g266690
NCBI GI
                   364
BLAST score
                   8.0e-35
E value
Match length
                   105
                   72
% identity
                   OLEOSIN 18.2 KD >gi_167363 (L00935) 18.2 kDa oleosin
NCBI Description
                   [Gossypium hirsutum] >gi_167365 (L00936) 18.2 kDa oleosin
                   [Gossypium hirsutum]
                   230536
Seq. No.
                   LIB3196-065-P1-M1-B9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2827715
BLAST score
                   244
E value
                   9.0e-21
                   102
Match length
                   43
% identity
                   (AL021684) receptor protein kinase - like protein
```

NCBI Description

[Arabidopsis thaliana]

230537 Seq. No.

LIB3196-065-P1-M1-C10 Seq. ID

Method BLASTX



```
NCBI GI
                  g3687237
                  198
BLAST score
                  2.0e-15
E value
Match length
                  99
                  53
% identity
                  (AC005169) putative Cys3His zinc-finger protein
NCBI Description
                   [Arabidopsis thaliana]
                  230538
Seq. No.
                  LIB3196-065-P1-M1-C11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2262172
BLAST score
                  151
                  7.0e-10
E value
Match length
                  98
% identity
                   40
                  (AC002329) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                  230539
Seq. No.
                  LIB3196-065-P1-M1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g494415
BLAST score
                   326
                   2.0e-30
E value
Match length
                  66
                   100
% identity
NCBI Description Homo sapiens >gi 494416_pdb_1NRC_B Homo sapiens
                   230540
Seq. No.
                  LIB3196-065-P1-M1-C2
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4105683
                   547
BLAST score
                   3.0e-56
E value
                   126
Match length
                   76
% identity
                  (AF049892) unknown [Oryza sativa] >gi_4105692 (AF050155)
NCBI Description
                   embryo-specific protein [Oryza sativa subsp. indica]
                   230541
Seq. No.
                   LIB3196-065-P1-M1-C3
Seq. ID
Method
                   BLASTX
                   g72223
NCBI GI
                   524
BLAST score
                   1.0e-53
E value
                   131
Match length
                   82
% identity
NCBI Description heat shock protein 84 - mouse
Seq. No.
                   230542
                   LIB3196-065-P1-M1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2134794
```

33111

695

133

1.0e-73

BLAST score

E value Match length



```
% identity
                  autoantigen - human >gi 533202 (L26339) autoantigen [Homo
NCBI Description
                  sapiens]
                  230543
Seq. No.
                  LIB3196-065-P1-M1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1917019
BLAST score
                  548
                  2.0e-56
E value
Match length
                  127
% identity
                  83
                  (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
NCBI Description
                  230544
Seq. No.
                  LIB3196-065-P1-M1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1565223
BLAST score
                  409
E value
                  4.0e-40
Match length
                  128
                  64
% identity
                  (Y08301) MCM2-related protein [Arabidopsis thaliana]
NCBI Description
                  230545
Seq. No.
                  LIB3196-065-P1-M1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4529893
                  373
BLAST score
                  8.0e-36
E value
Match length
                  121
                   69
% identity
NCBI Description (AF134726) HSP70-1 [Homo sapiens]
                   230546
Seq. No.
Seq. ID
                  LIB3196-065-P1-M1-C8
Method
                  BLASTX
NCBI GI
                   q88044
BLAST score
                   637
E value
                   8.0e-67
Match length
                   132
% identity
                   98
                   keratin 4, type II, cytoskeletal - human (fragment)
NCBI Description
                   >gi 34073 emb CAA30534 (X07695) cytokeratin 4 (408 AA)
                   [Homo sapiens]
Seq. No.
                   230547
                   LIB3196-065-P1-M1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g137578
BLAST score
                   611
E value
                   8.0e-64
                   123
Match length
% identity
                   95
                  VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)
NCBI Description
                   >gi 81545 pir S06398 alpha-globulin type A precursor -
```

33112

upland cotton >gi 167371 (M19378) vicilin precursor



[Gossypium hirsutum] >gi\_207906 (M18027) alpha globulin A [Artificial gene] >gi\_226119\_prf\_\_1410330A vicilin gene A [Saguinus oedipus]

Seq. No. 230548

Seq. ID LIB3196-065-P1-M1-D1

Method BLASTX
NCBI GI g2293575
BLAST score 606
E value 3.0e-63
Match length 131
% identity 91

NCBI Description (AF013213) elongation factor 1 alpha [Bos taurus]

Seq. No. 230549

Seq. ID LIB3196-065-P1-M1-D10

Method BLASTX
NCBI GI g137578
BLAST score 531
E value 2.0e-54
Match length 125
% identity 86

NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A)

>gi\_81545\_pir\_\_S06398 alpha-globulin type A precursor upland cotton >gi\_167371 (M19378) vicilin precursor
[Gossypium hirsutum] >gi\_207906 (M18027) alpha globulin A
[Artificial gene] >gi\_226119\_prf\_\_1410330A vicilin gene A

[Saguinus oedipus]

Seq. No. 230550

Seq. ID LIB3196-065-P1-M1-D11

Method BLASTX
NCBI GI g1330343
BLAST score 327
E value 2.0e-30
Match length 104
% identity 60

•NCBI Description (U58755) C34D4.12 gene product [Caenorhabditis elegans]

Seq. No. 230551

Seq. ID LIB3196-065-P1-M1-D2

Method BLASTX
NCBI GI 94529892
BLAST score 659
E value 2.0e-69
Match length 132
% identity 100

NCBI Description (AF134726) HSP70-2 [Homo sapiens]

Seq. No. 230552

Seq. ID LIB3196-065-P1-M1-D3

Method BLASTX
NCBI GI g2842648
BLAST score 256
E value 4.0e-22
Match length 120
% identity 42



NCBI Description U2 SMALL NUCLEAR RIBONUCLEOPROTEIN AUXILIARY FACTOR 35 KD SUBUNIT RELATED-PROTEIN 2 >gi\_2137782\_pir\_\_A57120 small nuclear ribonucleoprotein auxiliary factor U2 - mouse >gi 927659 dbj BAA08143 (D45205) U2af1-rs2 [Mus musculus] Seq. No. 230553 LIB3196-065-P1-M1-D4 Seq. ID Method BLASTX NCBI GI g2662415 BLAST score 214 E value 3.0e-17 Match length 53 % identity NCBI Description (U97494) metallothionein-like protein [Prunus armeniaca] Seq. No. 230554 LIB3196-065-P1-M1-D6 Seq. ID Method BLASTX g2129538 NCBI GI BLAST score 644 E value 1.0e-67 Match length 128 98 % identity NCBI Description AT103 protein - Arabidopsis thaliana >gi 1033195 (U38232) AT103 [Arabidopsis thaliana] Seq. No. 230555 LIB3196-065-P1-M1-D9 Seq. ID Method BLASTX g2464914 NCBI GI BLAST score 155 E value 2.0e-10 Match length 59 % identity 54 NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana] Seq. No. 230556 Seq. ID LIB3196-065-P1-M1-E1 Method BLASTX NCBI GI g113950 BLAST score 661 1.0e-69 E value Match length 133 % identity NCBI Description ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN) (CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL ANTICOAGULANT PROTEIN IV) (PAP-IV) >gi 71761\_pir LUHU36 annexin II -

human >gi\_219910\_dbj\_BAA00013\_ (D00017) lipocortin II [Homo

sapiens]

Seq. No. 230557

Seq. ID LIB3196-065-P1-M1-E10

Method BLASTX NCBI GI g2735010 BLAST score 195 E value 5.0e-15 76 Match length

33114



```
% identity
                  (U82166) CD99 type II-COS7 [Cercopithecus aethiops]
NCBI Description
                  230558
Seq. No.
                  LIB3196-065-P1-M1-E2
Seq. ID
                  BLASTX
Method
                  g1843527
NCBI GI
                  301
BLAST score
                  5.0e-33
E value
Match length
                  106
                  75
% identity
                  (U73747) annexin [Gossypium hirsutum]
NCBI Description
                  230559
Seq. No.
                  LIB3196-065-P1-M1-E3
Seq. ID
                  BLASTX
Method
                  g3184283
NCBI GI
                  270
BLAST score
                  8.0e-24
E value
                  77
Match length
                  70
% identity
                  (AC004136) putative TBP-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                   230560
Seq. No.
                  LIB3196-065-P1-M1-E5
Seq. ID
Method
                  BLASTX
                   q1890152
NCBI GI
                   480
BLAST score
                   2.0e-48
E value
                   128
Match length
                   69
% identity
                  (X92510) allene oxide synthase [Arabidopsis thaliana]
NCBI Description
                   230561
Seq. No.
                   LIB3196-065-P1-M1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2062167
                   410
BLAST score
                   3.0e-40
E value
                   85
Match length
                   89
% identity
                  (AC001645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                   thaliana]
                   230562
Seq. No.
Seq. ID
                   LIB3196-065-P1-M1-F1
Method
                   BLASTX
NCBI GI
                   q1854035
                   697
BLAST score
                   8.0e-74
E value
Match length
                   134
% identity
                   99
                  (U86753) pombe Cdc5-related protein [Homo sapiens]
NCBI Description
```

Seq. ID LIB3196-065-P1-M1-F4

NCBI GI BLAST score

E value

461

3.0e-46



```
BLASTX
Method
                  g3738283
NCBI GI
                  402
BLAST score
                  3.0e-39
E value
                  82
Match length
                  85
% identity
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                  230564
Seq. No.
                  LIB3196-065-P1-M1-G10
Seq. ID
                  BLASTX
Method
                  g2894599
NCBI GI
                   290
BLAST score
                   3.0e-26
E value
                   72
Match length
                   69
% identity
                  (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
                   230565
Seq. No.
                   LIB3196-065-P1-M1-G11
Seq. ID
                   BLASTX
Method
                   g1351867
NCBI GI
BLAST score
                   670
                   1.0e-70
E value
                   131
Match length
                   99
% identity
                  ACTIN, CYTOPLASMIC 1 (BETA-ACTIN) >gi 761724 (U20114)
NCBI Description
                   beta-actin [Cricetulus griseus]
                   230566
Seq. No.
                   LIB3196-065-P1-M1-G12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g167367
                   438
BLAST score
                   1.0e-43
E value
                   117
Match length
% identity
                   74
                  (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                   230567
Seq. No.
                   LIB3196-065-P1-M1-G3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1363944
BLAST score
                   669
                   1.0e-70
E value
                   133
Match length
                   99
% identity
NCBI Description
                   type I keratin 16 - human >gi_1195531_bbs_172338 (S79867)
                   type I keratin 16, K16 [human, epidermal keratinocytes,
                   Peptide, 473 aa] [Homo sapiens]
                   230568
Seq. No.
Seq. ID
                   LIB3196-065-P1-M1-H1
                   BLASTX
Method
                   g2134996
```

33116



```
Match length
                  131
% identity
                  74
NCBI Description desmoplakin I - human
Seq. No.
                  230569
                  LIB3196-065-P1-M1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885884
BLAST score
                  613
                  5.0e-64
E value
Match length
                  121
                  94
% identity
                 (AF093630) 60S ribosomal protein L21 [Oryza sativa]
NCBI Description
Seq. No.
                  230570
                  LIB3196-065-P1-M1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q72287
BLAST score
                  601
                  1.0e-62
E value
Match length
                  116
                  100
% identity
NCBI Description
                 beta-globulin A precursor (clone 94) - upland cotton
                  (fragment) >gi 167377 (M16905) legumin precursor [Gossypium
                  hirsutum]
                  230571
Seq. No.
Seq. ID
                  LIB3196-065-P1-M1-H3
Method
                  BLASTX
NCBI GI
                  q119350
BLAST score
                  472
                  2.0e-47
E value
Match length
                  103
% identity
                  89
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187
                  phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                  thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
                  [Arabidopsis thaliana]
Seq. No.
                  230572
Seq. ID
                  LIB3196-065-P1-M1-H4
Method
                  BLASTX
                  g732893
NCBI GI
BLAST score
                  548
E value
                  2.0e-56
Match length
                  130
% identity
NCBI Description (X85382) tobacco calretulin [Nicotiana tabacum]
```

Seq. ID LIB3196-065-P1-M1-H6

Method BLASTX
NCBI GI g3128168
BLAST score 388
E value 1.0e-37
Match length 114



55 % identity (AC004521) putative carboxyl-terminal peptidase NCBI Description [Arabidopsis thaliana] 230574 Seq. No. LIB3196-065-P1-M1-H7 Seq. ID Method BLASTX g1345132 NCBI GI 533 BLAST score 1.0e-54E value 123 Match length % identity 83 (U47029) ERECTA [Arabidopsis thaliana] NCBI Description

>gi 1389566 dbj BAA11869 (D83257) receptor protein kinase [Arabidopsis thaliana] >gi 3075386 (AC004484) receptor

protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No. 230575

LIB3196-065-P1-M1-H8 Seq. ID

Method BLASTX NCBI GI g126719 BLAST score 397 E value 2.0e-50 Match length 106 94 % identity

T-LYMPHOCYTE MATURATION-ASSOCIATED PROTEIN NCBI Description

>gi\_88813\_pir\_\_A29472 T-cell surface glycoprotein MAL, splice form a - human >gi 307157 (M15800) MAL protein [Homo sapiens] >gi\_435478\_emb\_CAA54100\_ (X76678) MAL-a [Homo sapiens] >gi\_2654296\_emb\_CAA53809\_ (X76220) MAL [Homo sapiens] >gi 4505091 ref NP 002362.1 pMAL mal, T-cell

differentiation protein

230576 Seq. No.

LIB3196-065-P1-M1-H9 Seq. ID

BLASTX Method g407942 NCBI GI BLAST score 221 4.0e-18 E value Match length 63 60 % identity

NCBI Description (U02496) epoxide hydrolase [Solanum tuberosum]

230577 Seq. No.

LIB3197-001-P1-M1-D12 Seq. ID

BLASTX Method g1351202 NCBI GI BLAST score 665 5.0e-70 E value Match length 142 89 % identity

TUBULIN BETA CHAIN >gi 312989 emb CAA42777 (X60216) NCBI Description

beta-tubulin [Glycine max]

230578 Seq. No.

LIB3197-001-P1-M1-D7 Seq. ID

Method BLASTX



NCBI GI g1172977 BLAST score 561 8.0e-58 E value 126 Match length 83 % identity NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana] 230579 LIB3197-001-P1-M1-D8 Seq. ID

Seq. No.

BLASTX Method NCBI GI g549597 201 BLAST score 9.0e-16 E value Match length 91 % identity 44

ATP-DEPENDENT RNA HELICASE DBP7 >gi 539330 pir S38093 NCBI Description

probable purine nucleotide-binding protein YKR024c - yeast

(Saccharomyces cerevisiae) >qi 486449 emb CAA82096 (Z28249) ORF YKR024c [Saccharomyces cerevisiae]

230580 Seq. No.

Seq. ID LIB3197-001-P1-M1-D9

Method BLASTX NCBI GI g1931647 BLAST score 375 5.0e-36 E value Match length 102 % identity 65

NCBI Description (U95973) endomembrane protein EMP70 precusor isolog

[Arabidopsis thaliana]

Seq. No. 230581

LIB3197-001-P1-M1-E1 Seq. ID

Method BLASTX NCBI GI g1403522 BLAST score 417 E value 6.0e-41132 Match length % identity 62

NCBI Description (X57187) chitinase [Phaseolus vulgaris]

Seq. No. 230582

LIB3197-001-P1-M1-E10 Seq. ID

BLASTX Method NCBI GI g2811278 BLAST score 567 E value 1.0e-58 Match length 135 % identity 77

NCBI Description (AF043284) expansin [Gossypium hirsutum]

Seq. No. 230583

LIB3197-001-P1-M1-E11 Seq. ID

Method BLASTX g1890281 NCBI GI BLAST score 356



1.0e-33 E value Match length 123 21 % identity (U89984) transformation-sensitive protein homolog NCBI Description [Acanthamoeba castellanii] 230584 Seq. No. LIB3197-001-P1-M1-E12 Seq. ID BLASTX Method g133940 NCBI GI BLAST score 565 4.0e-58 E value 136 Match length 82 % identity 40S RIBOSOMAL PROTEIN S3A (S1A) >gi 70851\_pir\_\_R3XL3A NCBI Description ribosomal protein S3a - African clawed frog >gi 65091 emb CAA40592 (X57322) ribosomal protein Sla [Xenopus laevis] 230585 Seq. No. LIB3197-001-P1-M1-E6 Seq. ID BLASTX Method g2979559 NCBI GI 335 BLAST score 3.0e-31 E value 81 Match length 77 % identity (AC003680) putative DNA binding protein [Arabidopsis NCBI Description thaliana] 230586 Seq. No. LIB3197-001-P1-M1-E7 Seq. ID BLASTX Method NCBI GI g1743354 BLAST score 287 8.0e-26 E value Match length 62 % identity 82 NCBI Description (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum] 230587 Seq. No. Seq. ID LIB3197-001-P1-M1-F5 Method BLASTX NCBI GI q3947719 180 BLAST score 3.0e-13E value 44

Match length % identity 82

(AJ012653) ribosomal protein S28 [Prunus persica] NCBI Description

>gi\_3947721\_emb\_CAA10102 (AJ012654) ribosomal protein S28
[Prunus persica] >gi\_3947723\_emb\_CAA10103\_ (AJ012655)

ribosomal protein S28 [Prunus persica]

230588 Seq. No.

LIB3197-001-P1-M1-F6 Seq. ID

Method BLASTX NCBI GI g1710587



```
BLAST score
                  277
                   2.0e-24
E value
Match length
                  95
                  60
% identity
                  60S ACIDIC RIBOSOMAL PROTEIN PO >gi 1196897 (L46848) acidic
NCBI Description
                  ribosomal protein PO [Glycine max]
                  230589
Seq. No.
                  LIB3197-001-P1-M1-F8
Seq. ID
                  BLASTX
Method
                  g3721856
NCBI GI
BLAST score
                   492
                   8.0e-50
E value
Match length
                  133
% identity
                   64
                  (AB014057) beta-Amyrin Synthase [Panax ginseng]
NCBI Description
Seq. No.
                   230590
                  LIB3197-001-P1-M1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g437327
BLAST score
                   352
                   2.0e-33
E value
                   136
Match length
                   53
% identity
                  (L04497) MYB A; putative [Gossypium hirsutum]
NCBI Description
Seq. No.
                   230591
                   LIB3197-001-P1-M1-G11
Seq. ID
                   BLASTX
Method
                   g4574320
NCBI GI
                   192
BLAST score
                   1.0e-14
E value
                   62
Match length
                   66
% identity
                  (AF117224) wound-induced protein WI12 [Mesembryanthemum
NCBI Description
                   crystallinum]
                   230592
Seq. No.
                   LIB3197-001-P1-M1-G12
Seq. ID
                   BLASTX
Method
                   g4322563
NCBI GI
BLAST score
                   149
                   2.0e-09
E value
                   111
Match length
                   31
% identity
                  (AF089838) phosphatidylglycerol/phosphatidylinositol
NCBI Description
                   transfer protein [Aspergillus oryzae]
Seq. No.
                   230593
                   LIB3197-001-P1-M1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4210948
```

555

147 77

5.0e-57

BLAST score

% identity

E value Match length

BLAST score

E value

534

9.0e-55





```
(AF085275) DnaJ protein [Hevea brasiliensis]
NCBI Description
                  230594
Seq. No.
                  LIB3197-001-P1-M1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2911060
                  237
BLAST score
                  6.0e-20
E value
                  96
Match length
                  36
% identity
                  (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3297826_emb_CAA19884.1_ (AL031032) putative protein
                   [Arabidopsis thaliana]
                  230595
Seq. No.
                  LIB3197-001-P1-M1-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1172874
                  217
BLAST score
                  1.0e-17
E value
                  84
Match length
                   54
% identity
                  DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
NCBI Description
                   >gi_479589_pir__S34823 dehydration-induced protein RD22 -
                  Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22
                   [Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene
                   [Arabidopsis thaliana]
                   230596
Seq. No.
                  LIB3197-001-P1-M1-G8
Seq. ID
                   BLASTX
Method
                   g1174592
NCBI GI
                   586
BLAST score
                   8.0e-61
E value
                   111
Match length
                   97
% identity
                  TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin
NCBI Description
                   - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
                   sativum]
                   230597
Seq. No.
                   LIB3197-001-P1-M1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2191150
BLAST score
                   227
                   1.0e-18
E value
Match length
                   67
                   81
% identity
                  (AF007269) similar to mitochondrial carrier family
NCBI Description
                   [Arabidopsis thaliana]
                   230598
Seq. No.
Seq. ID
                   LIB3197-001-P1-M1-H8
                   BLASTX
Method
                   g120673
NCBI GI
```

BLAST score

% identity

E value Match length 138 1.0e-08

76

38



```
Match length
                  126
                  81
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 66013 pir DEPJG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - garden petunia
                  >gi 20551 emb CAA42904 (X60346) glyceraldehyde
                  3-phosphate dehydrogenase [Petunia x hybrida]
                  230599
Seq. No.
                  LIB3197-001-P1-M1-H9
Seq. ID
                  BLASTX
Method
                  g2231312
NCBI GI
                  196
BLAST score
E value
                  3.0e-15
                  47
Match length
                  81
% identity
                  (U75603) AtRab18 [Arabidopsis thaliana]
NCBI Description
                  230600
Seq. No.
                  LIB3197-002-P1-M1-A2
Seq. ID
Method
                  BLASTX
                  g3641252
NCBI GI
BLAST score
                  156
                  2.0e-10
E value
                  104
Match length
% identity
                  (AF053127) leucine-rich receptor-like protein kinase [Malus
NCBI Description
                  domestica]
                  230601
Seq. No.
                  LIB3197-002-P1-M1-A5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3869088
                  535
BLAST score
                  6.0e-55
E value
                  102
Match length
                  99
% identity
NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
                  230602
Seq. No.
                  LIB3197-002-P1-M1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3925703
BLAST score
                  454
                  2.0e-45
E value
                  127
Match length
                  73
% identity
NCBI Description (X95905) 14-3-3 protein [Lycopersicon esculentum]
Seq. No.
                  230603
                  LIB3197-002-P1-M1-A9
Seq. ID
Method
                  BLASTX'
NCBI GI
                  q3377831
```

33123

(AF075598) similar to maize transposon MuDR mudrA NCBI Description (GB:M76978) [Arabidopsis thaliana] 230604 Seq. No. LIB3197-002-P1-M1-B12 Seq. ID Method BLASTX q495725 NCBI GI 406 BLAST score 4.0e-40E value 82 Match length % identity 94 (L25042) acetyl-CoA carboxylase [Medicago sativa] NCBI Description Seq. No. 230605 LIB3197-002-P1-M1-B2 Seq. ID Method BLASTX NCBI GI g4455209 BLAST score 347 7.0e-33 E value 98 Match length 76 % identity NCBI Description (AL035440) putative Proline synthetase associated protein [Arabidopsis thaliana] 230606 Seq. No. LIB3197-002-P1-M1-B3 Seq. ID Method BLASTX NCBI GI g2832625 360 BLAST score 2.0e-34 E value 86 Match length 79 % identity (AL021711) putative protein [Arabidopsis thaliana] NCBI Description 230607 Seq. No. LIB3197-002-P1-M1-B8 Seq. ID Method BLASTX

Method BLASTX
NCBI GI g3695406
BLAST score 381
E value 5.0e-37
Match length 111
% identity 71

NCBI Description (AF096373) similar to isoleucyl-tRNA synthetases

[Arabidopsis thaliana]

Seq. No. 230608

Seq. ID LIB3197-002-P1-M1-C10

Method BLASTX
NCBI GI 94240116
BLAST score 349
E value 5.0e-33
Match length 105
% identity 67

NCBI Description (AB007799) NADH-cytochrome b5 reductase [Arabidopsis

thaliana] >gi\_4240118\_dbj\_BAA74838\_ (AB007800)

NADH-cytochrome b5 reductase [Arabidopsis thaliana]

% identity

NCBI Description

91



```
230609
Seq. No.
Seq. ID
                  LIB3197-002-P1-M1-C12
                  BLASTX
Method
                  g3914394
NCBI GI
BLAST score
                  349
                  4.0e-33
E value
                  78
Match length
                  82
% identity
                  2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
NCBI Description
                  (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
                  >gi_2118335_pir__S60473 phosphoglycerate mutase (EC
                  5.4.2.1) - common ice plant >gi 602426 (U16021)
                  phosphoglyceromutase [Mesembryanthemum crystallinum]
                  230610
Seq. No.
                  LIB3197-002-P1-M1-C2
Seq. ID
Method
                  BLASTX
                  g3318611
NCBI GI
                  205
BLAST score
                  4.0e-16
E value
                  94
Match length
                  50
% identity
                  (AB016063) mitochondrial phosphate transporter [Glycine
NCBI Description
                  max]
Seq. No.
                  230611
                  LIB3197-002-P1-M1-C3
Seq. ID
Method
                  BLASTX
                  g1705678
NCBI GI
BLAST score
                  325
E value
                  3.0e - 30
Match length
                  137
                  39
% identity
NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
                  PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213)
                  valosin-containing protein [Glycine max]
Seq. No.
                  230612
                  LIB3197-002-P1-M1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3335370
BLAST score
                  152
                  6.0e-10
E value
Match length
                  72
% identity
                  43
NCBI Description (AC003028) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  230613
Seq. ID
                  LIB3197-002-P1-M1-C8
Method
                  BLASTX
NCBI GI
                  g2129499
BLAST score
                  521
E value
                  3.0e-53
Match length
                  109
```

33125

>gi 1000086 (U30506) E6 [Gossypium hirsutum]

fiber protein E6 (clone CKE6-4A) - upland cotton



```
230614
Seq. No.
                  LIB3197-002-P1-M1-C9
Seq. ID
Method
                  BLASTX
                  g4455299
NCBI GI
                  239
BLAST score
                  4.0e-20
E value
                  143
Match length
                  43
% identity
                  (AL035528) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  230615
                  LIB3197-002-P1-M1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2286153
BLAST score
                   513
                   3.0e-52
E value
Match length
                  110
                   95
% identity
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
                   230616
Seq. No.
Seq. ID
                   LIB3197-002-P1-M1-D6
Method
                   BLASTX
NCBI GI
                   g4567311
BLAST score
                   287
                   6.0e-26
E value
Match length
                   69
                   70
% identity
                  (AC005956) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   230617
Seq. No.
                   LIB3197-002-P1-M1-D7
Seq. ID
Method
                   BLASTX
                   g3236476
NCBI GI
                   422
BLAST score
                 -1.0e-41
E value
Match length
                   87
                   99
% identity
                  (AF071195) 26S protease regulatory subunit [Gossypium
NCBI Description
                   hirsutum]
                   230618
Seq. No.
                   LIB3197-002-P1-M1-D8
Seq. ID
                   BLASTX
Method
                   g2465434
NCBI GI
                   332
BLAST score
E value
                   3.0e-31
                   75
Match lèngth
                   85
% identity
                  (AF022142) flavanone 3beta-hydroxylase [Petunia x hybrida]
NCBI Description
                   230619
Seq. No.
                   LIB3197-002-P1-M1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3193301
```

285

BLAST score



```
1.0e-25
  E value
                    124
  Match length
                    53
  % identity
                     (AF069298) Arabidopsis putative chloroplast outer envelope
  NCBI Description
                    86-like protein T10P11.19 (GB: AC002330) [Arabidopsis
                    thaliana]
                    230620
  Seq. No.
                    LIB3197-002-P1-M1-E3
  Seq. ID
                    BLASTX
  Method
                    g2425066
  NCBI GI
                    231
  BLAST score
                    9.0e-20
  E value
                    53
  Match length
  % identity
                    83
                    (AF019147) cysteine proteinase Mir3 [Zea mays]
  NCBI Description
  Seq. No.
                    230621
                    LIB3197-002-P1-M1-E4
  Seq. ID
                    BLASTX
  Method
                     g3309575
  NCBI GI
                     227
  BLAST score
                     1.0e-18
  E value
                     67
  Match length
                     75
  % identity
                     (AF060553) calcium sensor homolog [Arabidopsis thaliana]
  NCBI Description
                     >gi_4538989_emb_CAB39731.1_ (Y18870) CBL4 protein
                     [Arabidopsis thaliana]
                     230622
  Seq. No.
                     LIB3197-002-P1-M1-E5
  Seq. ID
                     BLASTX
  Method
                     g70753
  NCBI GI
                     357
  BLAST score
                     2.0e-34
  E value
                     77
  Match length
                     94
  % identity
                    histone H3 - garden pea >gi 82610_pir S00373 histone H3 -
  NCBI Description
                     wheat
                     230623
  Seq. No.
                     LIB3197-002-P1-M1-E7
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     q2738248
                     391
  BLAST score
                     3.0e-38
  E value
  Match length
                     95
% identity
                     (U97200) cobalamin-independent methionine synthase
  NCBI Description
                     [Arabidopsis thaliana]
```

Seq. ID LIB3197-002-P1-M1-F11

Method BLASTX
NCBI GI g4006893
BLAST score 336
E value 1.0e-31

230630



```
Match length
                  78
                  86
% identity
NCBI Description (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]
                  230625
Seq. No.
                  LIB3197-002-P1-M1-F2
Seq. ID
Method
                  BLASTX
                  g1888485
NCBI GI
BLAST score
                  226
                  2.0e-23
E value
                  72
Match length
                  73
% identity
                 (Y11749) dihydroflavonol 4-reductase [Vitis vinifera]
NCBI Description
                  230626
Seq. No.
                  LIB3197-002-P1-M1-F6
Seq. ID
                  BLASTX
Method
                  g444791
NCBI GI
                  106
BLAST score
                  8.0e-10
E value
                  70
Match length
                  16
% identity
NCBI Description ubiquitin [Bos taurus]
                  230627
Seq. No.
                  LIB3197-002-P1-M1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1703375
BLAST score
                  649
                  3.0e-68
E value
                  133
Match length
                  96
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420)
                  DcARF1 [Daucus carota]
                  230628
Seq. No.
Seq. ID
                  LIB3197-002-P1-M1-H11
Method
                  BLASTX
NCBI GI
                  a3334144
                  206
BLAST score
                  1.0e-16
E value
Match length
                  62
% identity
                   66
NCBI Description G1/S-SPECIFIC CYCLIN C-TYPE >gi 1695698 dbj_BAA13181
                   (D86925) C-type cyclin [Oryza sativa]
Seq. No.
                  230629
Seq. ID
                  LIB3197-002-P1-M1-H4
Method
                  BLASTX
NCBI GI
                  g1399450
BLAST score
                  105
E value
                   2.0e-12
Match length
                  54
                   74
% identity
NCBI Description (U47660) beta-tubulin 2 [Lupinus albus]
```

33128



```
LIB3197-002-P1-M1-H5
 Seq. ID
 Method
                   BLASTX
                    g3334144
 NCBI GI
 BLAST score
                    203
 E value
                    1.0e-17
                    67
 Match length
                    71
 % identity
                   G1/S-SPECIFIC CYCLIN C-TYPE >gi 1695698 dbj BAA13181
 NCBI Description
                    (D86925) C-type cyclin [Oryza sativa]
                    230631
 Seq. No.
                   LIB3197-002-P1-M1-H6
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2493046
                    273
 BLAST score
                    3.0e-24
 E value
                    83
 Match length
                    66
 % identity
                   ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR
 NCBI Description
                    >qi 82297 pir A41740 H+-transporting ATP synthase (EC
                    3.6.1.34) delta' chain precursor - sweet potato
                    >gi_217938_dbj_BAA01511_ (D10660) mitochondrial F1-ATPase
                    delta subunit [Ipomoea batatas]
                    230632
 Seq. No.
                    LIB3197-002-P1-M1-H7
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2811278
                    478
 BLAST score
 E value
                    3.0e-48
                    104
 Match length
                    85
 % identity
 NCBI Description (AF043284) expansin [Gossypium hirsutum]
                    230633
Seq. No.
                    LIB3197-002-P1-M1-H9
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q136739
                    287
 BLAST score
                    6.0e-26
 E value
                    68
 Match length
                    81
 % identity
 NCBI Description UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
                    PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU
                    UTP--glucose-1-phosphate uridy Tyltransferase (EC 2.7.7.9) -
                    potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose
                    pyrophosphorylase precursor [Solanum tuberosum]
 Seq. No.
                    230634
                    LIB3197-003-P1-M1-A1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q232024
 BLAST score
                    247
 E value
                    1.0e-21
                    50
 Match length
 % identity
                    98
```

NCBI Description PROTEIN E6 >gi\_421806\_pir\_\_A46130 fiber protein - upland



cotton >gi\_2129498\_pir\_\_S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi 167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi\_1000084 (U30505) E6 [Gossypium hirsutum]

230635 Seq. No. LIB3197-003-P1-M1-A2 Seq. ID BLASTX Method g2497753 NCBI GI BLAST score 370 E value 2.0e-35 123 Match length 54 % identity

NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) NCBI Description

>gi\_1321915\_emb\_CAA65477\_ (X96716) lipid transfer protein

[Prunus dulcis]

230636 Seq. No.

LIB3197-003-P1-M1-B1 Seq. ID

Method BLASTX NCBI GI g3387808 BLAST score 160 7.0e-11 E value Match length 134 27 % identity

NCBI Description (AF035251) tripeptidyl peptidase II; dTPP II;

subtilisin-like serine protease [Drosophila melanogaster]

230637 Seq. No.

LIB3197-003-P1-M1-B9 Seq. ID

Method BLASTX NCBI GI g585204 BLAST score 397 9.0e-39 E value 81 Match length 91 % identity

NCBI Description GLUTAMINE SYNTHETASE ROOT ISOZYME 4 (GLUTAMATE--AMMONIA

LIGASE) (GS107) >gi\_481809\_pir\_\_S39480 glutamate--ammonia ligase (EC 6.3.1.2) 1-4, cytosolic - maize

>gi\_434330\_emb\_CAA46722\_ (X65929) glutamine synthetase [Zea

mays]

230638 Seq. No.

LIB3197-003-P1-M1-C3 Seq. ID

Method BLASTX NCBI GI q3056595 BLAST score 340 E∵value 5.0e - 32Match length 121 % identity

NCBI Description (AC004255) T1F9.16 [Arabidopsis thaliana]

Seq. No. 230639

LIB3197-003-P1-M1-D1 Seq. ID

Method BLASTX NCBI GI g3687250 BLAST score 168

Method

NCBI GI

BLASTX

g267069



```
E value
                  7.0e-12
Match length
                  45
                  69
% identity
                  (AC005169) putative arginine n-methyltransferase
NCBI Description
                  [Arabidopsis thaliana]
                  230640
Seq. No.
                  LIB3197-003-P1-M1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267069
BLAST score
                  497
E value
                  2.0e-50
Match length
                  91
                  99
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  230641
Seq. No.
                  LIB3197-003-P1-M1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131770
BLAST score
                  355
E value
                  8.0e-34
                  100
Match length
% identity
                  64
                  40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
NCBI Description
                   (VEGETATIVE SPECIFIC PROTEIN V12) >gi 70880 pir R3D024
                  ribosomal protein S9.e - slime mold (Dictyostelium
                  discoideum) >gi 7353 emb CAA29844 (X06636) rp1024 protein
                  [Dictyostelium discoideum]
Seq. No.
                  230642
                  LIB3197-003-P1-M1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3901268
BLAST score
                  221
                  5.0e-18
E value
Match length
                  132
% identity
NCBI Description (AF060173) SV2 related protein [Rattus norvegicus]
Seq. No.
                  230643
Seq. ID
                  LIB3197-003-P1-M1-E11
Method
                  BLASTX
NCBI GI
                  q4580389
BLAST score
                  405
E value
                  9.0e-40
Match length
                  104
% identity
                  71
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]
Seq. No.
                  230644
                  LIB3197-003-P1-M1-E2
Seq. ID
```

NCBI GI

E value

BLAST score

g1483218

6.0e-24

271



```
BLAST score
                  676
E value
                  2.0e-71
Match length
                  126
                  99
% identity
NCBI Description
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  230645
Seq. No.
                  LIB3197-003-P1-M1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455202
BLAST score
                  219
                  7.0e-18
E value
                  75
Match length
                  57
% identity
NCBI Description
                  (AL035440) putative APG protein [Arabidopsis thaliana]
                  230646
Seq. No.
                  LIB3197-003-P1-M1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334320
BLAST score
                  518
                  8.0e-53
E value
Match length
                  114
                  93
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
                  ribosome-associated protein p40 [Glycine max]
                  230647
Seq. No.
                  LIB3197-003-P1-M1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2706450
BLAST score
                  275
E value
                  2.0e-24
Match length
                  71
% identity
                  77
NCBI Description
                  (AJ225172) magnesium dependent soluble inorganic
                  pyrophosphatase [Solanum tuberosum]
Seq. No.
                  230648
Seq. ID
                  LIB3197-003-P1-M1-F1
Method
                  BLASTX
NCBI GI
                  g1694621
BLAST score
                  415
E value
                  1.0e-40
Match length
                  118
% identity
                  71
NCBI Description
                  (D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]
Seq. No.
                  230649
Seq. ID
                  LIB3197-003-P1-M1-F2
Method
                  BLASTX
```

33132



```
63
Match length
                  79
% identity
                  (X99793) induced upon wounding stress [Arabidopsis
NCBI Description
                  thaliana]
                  230650
Seq. No.
                  LIB3197-003-P1-M1-F5
Seq. ID
                  BLASTX
Method
                  g729470
NCBI GI
                  182
BLAST score
                  1.0e-13
E value
                  75
Match length
                  56
% identity
NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
                  (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
                  >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2)
                  precursor, mitochondrial - potato >gi 297798 emb CAA79702_
                  (Z21493) mitochondrial formate dehydrogenase precursor
                  [Solanum tuberosum]
                  230651
Seq. No.
                  LIB3197-003-P1-M1-G10
Seq. ID
Method
                  BLASTX
                  g4467153
NCBI GI
                  439
BLAST score
                  2.0e-43
E value
Match length
                  104
% identity
                  81
                  (AL035540) putative thaumatin-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  230652
Seq. No.
                  LIB3197-003-P1-M1-G3
Seq. ID
Method
                  BLASTX
                  g3080426
NCBI GI
BLAST score
                  288
                  6.0e-26
E value
                  99
Match length
                  55
% identity
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
                  230653
Seq. No.
                  LIB3197-003-P1-M1-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3298555
                  247
BLAST score
E value
                   5.0e-21
Match length
                  54
                   83
% identity
```

NCBI Description (AC004681) putative homeobox protein, 3' partial [Arabidopsis thaliana]

Seq. No. 230654

Seq. ID LIB3197-003-P1-M1-G8

Method BLASTX NCBI GI g232031 BLAST score 188



```
3.0e-14
E value
                   65
Match length
                   52
% identity
                   ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224 translation elongation factor eEF-1 beta' chain - rice
NCBI Description
                   >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta'
                   [Oryza sativa]
                   230655
Seq. No.
                   LIB3197-003-P1-M1-H4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2781433
                   729
BLAST score
                   1.0e-77
E value
Match length
                   142
% identity
                   94
                   (AF030052) RSW1-like cellulose synthase catalytic subunit
NCBI Description
                   [Oryza sativa subsp. japonica]
                   230656
Seq. No.
                  LIB3197-003-P1-M1-H5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2281115
                   599
BLAST score
                   3.0e-62
È value
Match length
                   123
                   89
% identity
                   (AC002330) putative cullin-like 1 protein [Arabidopsis
NCBI Description
                   thaliana]
                   230657
Seq. No.
                   LIB3197-004-P1-M1-A10
Seq. ID
                   BLASTX
Method
                   g4309698
NCBI GI
                   166
BLAST score
                   1.0e-11
E value
                   56
Match length
                    66
% identity
                   (AC006266) putative glucosyltransferase [Arabidopsis
NCBI Description
                    thaliana]
                    230658
Seq. No.
                   LIB3197-004-P1-M1-B1
Seq. ID
                   BLASTX
Method
NCBI GI
                    q2832625
                    215
BLAST score
                    6.0e-35
E value
Match length
                    95
                    79
% identity
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
                    230659
Seq. No.
Seq. ID
                    LIB3197-004-P1-M1-B2
```

BLASTX

Method g2736147 NCBI GI 403 BLAST score E value 2.0e-39



```
Match length
                     101
                     71
 % identity
                     (AF021804) fatty acid hydroxylase Fahlp [Arabidopsis
 NCBI Description
                     thaliana] >gi_3132481 (AC003096) fatty acid hydroxylase,
                     FAH1 [Arabidopsis thaliana]
                     230660
 Seq. No.
                    LIB3197-004-P1-M1-B4
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                     g2463666
 BLAST score
                     450
                     5.0e-45
 E value
                     85
 Match length
                     100
 % identity
                     (AF006490) adenine nucleotide translocator 2 [Gossypium
 NCBI Description
                     hirsutum]
                     230661
 Seq. No.
                    LIB3197-004-P1-M1-B5
 Seq. ID
                     BLASTX
 Method
                     g3046700
 NCBI GI
                     196
 BLAST score
                     2.0e-15
 E value
                     62
 Match length
                     66
 % identity
                     (AJ005261) cytidine deaminase [Arabidopsis thaliana]
 NCBI Description
                     >gi_3093276_emb_CAA06671_ (AJ005687) cytidine deaminase
[Arabidopsis thaliana] >gi_4191787 (AC005917) putative
                     cytidine deaminase [Arabidopsis thaliana]
 Seq. No.
                     230662
                     LIB3197-004-P1-M1-B6
 Seq. ID
                     BLASTX
 Method
 NCBI GI
                     g1587206
 BLAST score
                     521
                     3.0e-53
 E value
 Match length
                     110
* % identity
                     95
 NCBI Description T complex protein [Cucumis sativus]
                     230663
 Seq. No.
 Seq. ID
                     LIB3197-004-P1-M1-B9
 Method
                     BLASTX
 NCBI GI
                     q87765
 BLAST score
                     146
                     1.0e-09
 E value
 Match length
                     56
  % identity
 NCBI Description
                     hypothetical L1 protein (third intron of gene TS) - human
                     >gi 364964 prf__1510254A L1 repetitive element ORF [Homo
                     sapiens]
```

Seq. ID LIB3197-004-P1-M1-C12

Method BLASTX
NCBI GI g2462746
BLAST score 629



```
8.0e-66
E value
                  136
Match length
                  85
% identity
                  (AC002292) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                  thaliana]
                  230665
Seq. No.
                  LIB3197-004-P1-M1-C4
Seq. ID
                  BLASTX
Method
                  g4580523
NCBI GI
                  275
BLAST score
                  2.0e-24
E value
                  113
Match length
                  51
% identity
                  (AF036305) scarecrow-like 8 [Arabidopsis thaliana]
NCBI Description
                  230666
Seq. No.
                  LIB3197-004-P1-M1-C7
Seq. ID
                  BLASTX
Method
                  g4510383
NCBI GI
                  199
BLAST score
                  7.0e-16
E value
                  78
Match length
                  58
% identity
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
                  230667
Seq. No.
                  LIB3197-004-P1-M1-C8
Seq. ID
Method
                  BLASTX
                   g3236237
NCBI GI
                   425
BLAST score
                   6.0e-42
E value
                  130
Match length
                   60
% identity
                  (AC004684) putative ribotol dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   230668
                   LIB3197-004-P1-M1-D1
Seq. ID
                   BLASTX
Method
                   q2832680
NCBI GI
                   443
BLAST score
                   4.0e-44
E value
                   131
Match length
                   39
% identity
NCBI Description (AL021712) putative protein [Arabidopsis thaliana]
                   230669
Seq. No.
                   LIB3197-004-P1-M1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3128176
                   347
BLAST score
                   9.0e-33
E value
                   116
Match length
                   57
% identity
```

NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                  230670
                  LIB3197-004-P1-M1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2506139
                  336
BLAST score
                  1.0e-31
E value
Match length
                  76
                  87
% identity
                  COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
NCBI Description
                  (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962)
                  archain/delta-COP [Oryza sativa]
Seq. No.
                  230671
                  LIB3197-004-P1-M1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885329
BLAST score
                  203
                  6.0e-25
E value
Match length
                  74
                  84
% identity
                  (AC005623) alien-like protein [Arabidopsis thaliana]
NCBI Description
                  230672
Seq. No.
                  LIB3197-004-P1-M1-E1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3097321
BLAST score
                  187
                  5.0e-14
E value
Match length
                  88
                  43
% identity
                  (AB013289) Bd 30K [Glycine max]
NCBI Description
                  230673
Seq. No.
                  LIB3197-004-P1-M1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1408471
BLAST score
                  455
E value
                  2.0e-45
Match length
                  102
                   79
% identity
                  (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                   thaliana] >gi 3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
                   230674
Seq. No.
Seq. ID
                  LIB3197-004-P1-M1-E3
Method
                  BLASTX
                  q862640
NCBI GI
BLAST score
                   393
                   2.0e-38
E value
```

Match length 82 % identity 91

(U20182) MADS-box protein AGL11 [Arabidopsis thaliana] NCBI Description

>gi 4538999 emb CAB39620.1 (AL049481) MADS-box protein

AGL11 [Arabidopsis thaliana]

Seq. No. 230675

Method NCBI GI

BLAST score



```
LIB3197-004-P1-M1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2832682
BLAST score
                  156
                  8.0e-11
E value
                  66
Match length
                  61
% identity
                  (AL021712) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  230676
Seq. No.
                  LIB3197-004-P1-M1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1170898
BLAST score
                  588
                  5.0e-61
E value
Match length
                  139
                  85
% identity
                  MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi_629659_pir__S44167 malate dehydrogenase, mitochondrial
                  - cider tree >gi 473206 emb_CAA55383_ (X78800)
                  mitochondrial malate dehydrogenase [Eucalyptus gunnii]
Seq. No.
                  230677
                  LIB3197-004-P1-M1-F11
Seq. ID
Method
                  BLASTX
                  g2982456
NCBI GI
BLAST score
                  504
                  3.0e-51
E value
Match length
                  125
                  76
% identity
NCBI Description
                  (AL022223) putative protein [Arabidopsis thaliana]
Seq. No.
                  230678
                  LIB3197-004-P1-M1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982456
BLAST score
                  165
E value
                   7.0e-12
Match length
                  62
% identity
                   50
NCBI Description
                  (AL022223) putative protein [Arabidopsis thaliana]
Seq. No.
                   230679
                  LIB3197-004-P1-M1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2791834
BLAST score
                  606
                   4.0e-63
E value
                  120
Match length
                   97
% identity
                  (AF041463) elongation factor 1-alpha [Manihot esculenta]
NCBI Description
Seq. No.
                   230680
Seq. ID
                  LIB3197-004-P1-M1-F8
                  BLASTX
```

33138

g401011

454



```
2.0e-45
E value
                  119
Match length
                  82
% identity
                  DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 2)
NCBI Description
                  >gi_279535_pir__JDMU2 DNA-directed RNA polymerase (EC
                  2.7.7.6) II largest chain (version 2) - Arabidopsis
                  thaliana >gi 16494 emb CAA36735 (X52494) DNA-directed RNA
                  polymerase [Arabidopsis thaliana]
                  230681
Seq. No.
                  LIB3197-004-P1-M1-F9
Seq. ID
Method
                  BLASTX
                  g401011
NCBI GI
BLAST score
                  144
                  6.0e-11
E value
                  85
Match length
                  53
% identity
                  DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 2)
NCBI Description
                  >gi_279535_pir__JDMU2 DNA-directed RNA polymerase (EC
                  2.7.7.6) II largest chain (version 2) - Arabidopsis
                  thaliana >gi 16494_emb_CAA36735_ (X52494) DNA-directed RNA
                  polymerase [Arabidopsis thaliana]
                  230682
Seq. No.
                  LIB3197-004-P1-M1-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1220196
                  400
BLAST score
E value
                  5.0e-43
                  111
Match length
                  79
% identity
                 (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
NCBI Description
                  230683
Seq. No.
                  LIB3197-004-P1-M1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q417060
BLAST score
                  589
                  4.0e-61
E value
Match length
                  119
                  92
% identity
                  GLUTAMINE SYNTHETASE NODULE ISOZYME (GLUTAMATE--AMMONIA
NCBI Description
                  LIGASE) (GS) >gi 170637 (M94765) glutamine synthetase
                  [Vigna aconitifolia] >gi_1094850 prf 2106409A Gln
                  synthetase [Vigna aconitifolia]
```

Seq. ID LIB3197-004-P1-M1-G7

Method BLASTX NCBI GI q2642429 BLAST score 306 E value 6.0e-28 Match length 134 % identity

(AC002391) putative poly(A)-binding protein [Arabidopsis NCBI Description

thaliana]

Seq. ID

230690

LIB3197-004-P1-M1-H9



```
Seq. No.
                  230685
                  LIB3197-004-P1-M1-G8
Seq. ID
Method
                  BLASTX
                  g462253
NCBI GI
                  289
BLAST score
                   3.0e-26
E value
                  89
Match length
                   67
% identity
                  TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP
NCBI Description
                   >gi_284975_pir__S26660 HCNGP protein - mouse
                   >gi_57912_emb_CAA48198_ (X68061) HCNGP [Mus musculus]
                   230686
Seq. No.
                  LIB3197-004-P1-M1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q401322
                   625
BLAST score
                   2.0e-65
E value
                   127
Match length
                   96
% identity
                  VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
NCBI Description
                   SUBUNIT) >gi 167313 (L03186) vacuolar H+-ATPase catalytic
                   subunit [Gossypium hirsutum]
                   230687
Seq. No.
                   LIB3197-004-P1-M1-H10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4539543
                   363
BLAST score
                   6.0e-35
E value
                   94
Match length
                   74
% identity
                  (AJ133422) glyceraldehyde-3-phosphate dehydrogenase
NCBI Description
                   [Nicotiana tabacum]
                   230688
Seq. No.
Seq. ID
                   LIB3197-004-P1-M1-H2
Method
                   BLASTX
NCBI GI
                   a1518540
BLAST score
                   416
E value
                   5.0e-41
Match length
                   92
% identity
                   87
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
                   230689
Seq. No.
                   LIB3197-004-P1-M1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3869088
BLAST score
                   536
                   5.0e-55
E value
Match length
                   103
% identity
                   99
                  (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
NCBI Description
```



```
BLASTX
Method
NCBI GI
                  q4454012
                  180
BLAST score
E value
                  2.0e-13
                  49
Match length
                  69
% identity
                  (AL035396) Pollen-specific protein precursor like
NCBI Description
                  [Arabidopsis thaliana]
                  230691
Seq. No.
                  LIB3197-005-P1-M1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455293
BLAST score
                  387
E value
                  2.0e-37
Match length
                  89
                  91
% identity
NCBI Description
                  (AL035528) putative protein [Arabidopsis thaliana]
                  230692
Seq. No.
                  LIB3197-005-P1-M1-A10
Seq. ID
                  BLASTX
Method
                  g2760334
NCBI GI
BLAST score
                  241
E value
                  2.0e-20
Match length
                  86
% identity
                  55
                 (AC002130) F1N21.5 [Arabidopsis thaliana]
NCBI Description
                  230693
Seq. No.
                  LIB3197-005-P1-M1-A11
Seq. ID
Method
                  BLASTX
                  g1076627
NCBI GI
BLAST score
                  219
                  7.0e-18
E value
Match length
                  78
% identity
                  62
NCBI Description inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco
                  >gi_790479_emb_CAA58701_ (X83730) inorganic pyrophosphatase
                  [Nicotiana tabacum]
Seq. No.
                  230694
Seq. ID
                  LIB3197-005-P1-M1-A2
Method
                  BLASTX
NCBI GI
                  g1351856
BLAST score
                  454
E value
                  2.0e-45
Match length
                  108
% identity
                  84
                  ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
NCBI Description
                   (ACONITASE) >gi 868003 dbj BAA06108 (D29629) aconitase
                  [Cucurbita sp.]
```

Seq. ID LIB3197-005-P1-M1-A4

Method BLASTX NCBI GI g1346180



BLAST score 386 E value 2.0e-37 Match length 86 % identity 85

NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN GRP1A >gi\_496233 (L31374) homology with RNA-binding proteins in meristematic tissue

[Sinapis alba]

Seq. No. 230696

Seq. ID LIB3197-005-P1-M1-A5

Method BLASTX
NCBI GI g464840
BLAST score 441
E value 7.0e-46
Match length 105
% identity 87

NCBI Description TUBULIN ALPHA-1 CHAIN >gi\_421781\_pir\_\_S32666 tubulin

alpha-1 chain - fern (Anemia phyllitidis)

>gi 296494 emb CAA48927 (X69183) alpha tubulin [Anemia

phyllitidis]

Seq. No. 230697

Seq. ID LIB3197-005-P1-M1-A8

Method BLASTX
NCBI GI g3377797
BLAST score 471
E value 2.0e-47
Match length 110
% identity 84

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No. 230698

Seq. ID LIB3197-005-P1-M1-A9

Method BLASTX
NCBI GI g2501565
BLAST score 223
E value 3.0e-18
Match length 83
% identity 49

NCBI Description HYPOTHETICAL 40.2 KD PROTEIN IN CTF13-YPK2 INTERGENIC

REGION >gi\_1078518\_pir\_\_S55087 hypothetical protein YMR101c - yeast (Saccharomyces cerevisiae) >gi\_854438\_emb\_CAA89902\_

(Z49807) unknown [Saccharomyces cerevisiae]

>gi\_4126459\_dbj\_BAA36578\_ (AB013498) cis-prenyltransferase

homologue [Saccharomyces cerevisiae]

Seq. No. 230699

Seq. ID LIB3197-005-P1-M1-B1

Method BLASTX
NCBI GI g623586
BLAST score 237
E value 3.0e-20
Match length 47

230705



```
100
% identity
                  (L29273) putative [Nicotiana tabacum]
NCBI Description
                  230700
Seq. No.
                  LIB3197-005-P1-M1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4371285
BLAST score
                  234
E value
                  2.0e-19
Match length
                  122
% identity
                  43
                  (AC006260) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  230701
                  LIB3197-005-P1-M1-B12
Seq. ID
                  BLASTX
Method
                  g1658193
NCBI GI
BLAST score
                  690
                  6.0e-73
E value
                  156
Match length
% identity
                  79
                  (U74319) obtusifoliol 14-alpha demethylase CYP51 [Sorghum
NCBI Description
                  bicolor]
                  230702
Seq. No.
                  LIB3197-005-P1-M1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3128168
                  461
BLAST score
                  3.0e-46
E value
Match length
                  131
% identity
                  59
NCBI Description
                  (AC004521) putative carboxyl-terminal peptidase
                   [Arabidopsis thaliana]
Seq. No.
                  230703
Seq. ID
                  LIB3197-005-P1-M1-B3
Method
                  BLASTX
NCBI GI
                  q4580394
BLAST score
                  231
E value
                  3.0e-19
Match length
                  101
% identity
                  45
                  (AC007171) putative fatty acid elongase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  230704
Seq. ID
                  LIB3197-005-P1-M1-B4
Method
                  BLASTX
NCBI GI
                  q2347199
BLAST score
                  241
E value
                   6.0e-21
Match length
                  56
% identity
                  (AC002338) protein kinase isolog [Arabidopsis thaliana]
NCBI Description
```

33143

Seq. ID

230710

LIB3197-005-P1-M1-D1



```
LIB3197-005-P1-M1-B5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g125077
                  675
BLAST score
                  3.0e-71
E value
Match length
                  136
                  99
% identity
                  KERATIN, TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13) (CK
NCBI Description
                  13) >gi_71526_pir__KRHU3 keratin 13, type I, cytoskeletal,
                  long form - human >gi_34033_emb_CAA32786_ (X14640) keratin
                  13 [Homo sapiens]
                  230706
Seq. No.
                  LIB3197-005-P1-M1-B6
Seq. ID
                  BLASTX
Method
                  g4455246
NCBI GI
BLAST score
                  311
                  2.0e-28
E value
                  89
Match length
                  66
% identity
                 (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
                  230707
Seq. No.
                  LIB3197-005-P1-M1-B9
Seq. ID
                  BLASTX
Method
                  g2500521
NCBI GI
                  226
BLAST score
E value
                  1.0e-18
Match length
                  51
                  84
% identity
                  EUKARYOTIC INITIATION FACTOR 4A-15 (EIF-4A-15)
NCBI Description
                  >gi 485945 emb CAA55739 (X79138) NeIF-4A15 [Nicotiana
                  tabacum]
                  230708
Seq. No.
                  LIB3197-005-P1-M1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3869088
                  552
BLAST score
                  7.0e-57
E value
                  105
Match length
                  100
% identity
NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
                  230709
Seq. No.
                  LIB3197-005-P1-M1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4538923
BLAST score
                  287
                   3.0e-46
E value
                  148
Match length
% identity
                  (AL049483) predicted protein destination factor
NCBI Description
                   [Arabidopsis thaliana]
```



```
Method
                  BLASTX
NCBI GI
                  g99992
BLAST score
                  231
                  8.0e-20
E value
Match length
                  67
                  63
% identity
                  protein disulfide-isomerase (EC 5.3.4.1) precursor -
NCBI Description
                  alfalfa (clone B2) >gi_166418 (M82973) putative
                  endomembrane protein; putative [Medicago sativa]
                  230711
Seq. No.
                  LIB3197-005-P1-M1-D11
Seq. ID
Method
                  BLASTX
                  g2292917
NCBI GI
BLAST score
                  682
                  5.0e-72
E value
Match length
                  155
                  83
% identity
                  (X99851) galactokinase [Arabidopsis thaliana]
NCBI Description
                  230712
Seq. No.
                  LIB3197-005-P1-M1-D12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2292917
                  208
BLAST score
                   8.0e-21
E value
                   93
Match length
% identity
                  (X99851) galactokinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   230713
                   LIB3197-005-P1-M1-E10
Seq. ID
Method
                   BLASTX
                   g4467144
NCBI GI
BLAST score
                   442
                   7.0e-44
E value
                   101
Match length
                   79
% identity
                  (AL035540) putative phosphatidylinositol synthase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   230714
                   LIB3197-005-P1-M1-E4
Seq. ID
                   BLASTX
Method
                   g4454472
NCBI GI
                   188
BLAST score
                   4.0e-14
E value
Match length
                   104
% identity
                   43
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                   230715
Seq. No.
                   LIB3197-005-P1-M1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4454472
```

177

9.0e-13

BLAST score

E value



```
Match length
                  106
% identity
                  42
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                  230716
Seq. No.
                  LIB3197-005-P1-M1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2613143
                  262
BLAST score
                  5.0e-23
E value
                  72
Match length
% identity
                  72
                  (AF030548) tubulin [Oryza sativa]
NCBI Description
Seq. No.
                  230717
                  LIB3197-005-P1-M1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2465434
                  272
BLAST score
                  3.0e-24
E value
Match length
                  65
% identity
                  82
                  (AF022142) flavanone 3beta-hydroxylase [Petunia x hybrida]
NCBI Description
                  230718
Seq. No.
                  LIB3197-005-P1-M1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3360289
                  209
BLAST score
                  1.0e-16
E value
                   66
Match length
                   55
% identity
                  (AF023164) leucine-rich repeat transmembrane protein kinase
NCBI Description
                  1 [Zea mays]
                   230719
Seq. No.
                  LIB3197-005-P1-M1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                   q232024
BLAST score
                   618
                   1.0e-64
E value
                   116
Match length
                   100
% identity
                  PROTEIN E6 >gi 421806 pir_A46130 fiber protein - upland
NCBI Description
                   cotton >gi_2129498_pir__S65061 fiber protein E6 (clone
                   CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site
                   is putative; putative [Gossypium hirsutum] >gi_1000084
                   (U30505) E6 [Gossypium hirsutum]
Seq. No.
                   230720
                   LIB3197-005-P1-M1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3702368
                   589
BLAST score
```

4.0e-61

150 73

E value Match length

% identity



```
NCBI Description (AJ001855) alpha subunit of F-actin capping protein
                  [Arabidopsis thaliana]
                  230721
Seq. No.
                  LIB3197-005-P1-M1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q167324
                  245
BLAST score
                  8.0e-21
E value
                  46
Match length
                  96
% identity
                 (M92051) 5' start site is putative; putative [Gossypium
NCBI Description
                  hirsutum]
                  230722
Seq. No.
                  LIB3197-005-P1-M1-G6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q548774
                  310
BLAST score
                  2.0e-28
E value
                  83
Match length
                  72
% identity
                 60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal
NCBI Description
                  protein L7a - rice >gi_303855_dbj_BAA02156 (D12631)
                  ribosomal protein L7A [Oryza sativa]
                  230723
Seq. No.
Seq. ID
                  LIB3197-005-P1-M1-G9
Method
                  BLASTX
NCBI GI
                  q3805847
BLAST score
                  141
                  3.0e-09
E value
Match length
                  40
                  68
% identity
NCBI Description (AL031986) putative protein [Arabidopsis thaliana]
                  230724
Seq. No.
                  LIB3197-005-P1-M1-H1
Seq. ID
                  BLASTX
Method
                  g1350680
NCBI GI
BLAST score
                  265
                  1.0e-23
E value
Match length
                  72
                  65
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L1
                  230725
Seq. No.
Seq. ID
                  LIB3197-005-P1-M1-H10
Method
                  BLASTX
NCBI GI
                  g3914191
BLAST score
                  262
                  8.0e-23
E value
Match length
                  133
% identity
                  42
NCBI Description UDP-N-ACETYLGLUCOSAMINE--PEPTIDE
```

N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (O-GLCNAC TRANSFERASE P110 SUBUNIT) >gi 1931579 (U76557) O-GlcNAc



# transferase, p110 subunit [Rattus norvegicus]

```
Seq. No.
                  230726
                  LIB3197-005-P1-M1-H6
Seq. ID
Method
                  BLASTX
                  g2811278
NCBI GI
BLAST score
                  381
                  8.0e-37
E value
                  115
Match length
                  64
% identity
                  (AF043284) expansin [Gossypium hirsutum]
NCBI Description
Seq. No.
                  230727
                  LIB3197-005-P1-M1-H7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3212869
BLAST score
                  333
                  2.0e-32
E value
Match length
                   94
                   77
% identity
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                   230728
Seq. No.
                  LIB3197-006-P1-M1-A12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1020315
BLAST score
                   227
                   1.0e-18
E value
Match length
                   143
                   38
% identity
                   (U36310) glycerol-3-phosphate dehydrogenase [Homo sapiens]
NCBI Description
                   >qi 1389721 (U40367) glycerol-3-phosphate dehydrogenase
                   [Homo sapiens]
                   230729
Seq. No.
                   LIB3197-006-P1-M1-A2
Seq. ID
                   BLASTX
Method
                   g1666234
NCBI GI
BLAST score
                   433
                   6.0e-43
E value
                   82
Match length
                   99
% identity
                  (U76193) actin [Pisum sativum] >gi 1724143 (U81049) actin
NCBI Description
                   [Pisum sativum]
                   230730
Seq. No.
                   LIB3197-006-P1-M1-A3
Seq. ID
                   BLASTX
Method
                   g2924520
NCBI GI
                   451
BLAST score
                   4.0e-45
E value
                   109
Match length
                   81
% identity
                   (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 230731



```
Seq. ID
                  LIB3197-006-P1-M1-A4
Method
                  BLASTX
NCBI GI
                  g2245128
BLAST score
                  420
                  3.0e-41
E value
Match length
                  133
                  62
% identity
                  (Z97344) peroxidase [Arabidopsis thaliana]
NCBI Description
                  230732
Seq. No.
                  LIB3197-006-P1-M1-A5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4098129
BLAST score
                  370
                  2.0e-35
E value
Match length
                  70
% identity
                  100
                  (U73588) sucrose synthase [Gossypium hirsutum]
NCBI Description
                  230733
Seq. No.
Seq. ID
                  LIB3197-006-P1-M1-A6
                  BLASTX
Method
                  g2245128
NCBI GI
BLAST score
                  409
                  5.0e-40
E value
Match length
                  112
                  67
% identity
NCBI Description
                  (Z97344) peroxidase [Arabidopsis thaliana]
Seq. No.
                  230734
                  LIB3197-006-P1-M1-B1
Seq. ID
Method
                  BLASTX
                  g4097579
NCBI GI
BLAST score
                  413
                  1.0e-40
E value
                  89
Match length
                  84
% identity
NCBI Description (U64922) NTGP1 [Nicotiana tabacum]
                   230735
Seq. No.
                  LIB3197-006-P1-M1-B10
Seq. ID
                  BLASTX
Method
                   g4572679
NCBI GI
                   458
BLAST score
                   9.0e-46
E value
                   121
Match length
                   71
% identity
                  (AC006954) RSZp22 splicing factor; contains RNA recognition
NCBI Description
                   motif [Arabidopsis thaliana]
                   230736
Seq. No.
                   LIB3197-006-P1-M1-B11
Seq. ID
                   BLASTX
Method
                   g2662343
NCBI GI
BLAST score
                   639
```

5.0e-67

125

E value Match length



```
% identity
                  (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                  230737
Seq. No.
                  LIB3197-006-P1-M1-B12
Seq. ID
                  BLASTX
Method
                  g2829206
NCBI GI
                  147
BLAST score
                  3.0e-09
E value
                  31
Match length
                  90
% identity
                  (AF044205) proline-rich protein precursor [Gossypium
NCBI Description
                  hirsutum]
                  230738
Seq. No.
                  LIB3197-006-P1-M1-B3
Seq. ID
                  BLASTX
Method
                  q2895576
NCBI GI
                  158
BLAST score
                  1.0e-10
E value
                  118
Match length
% identity
                  26
                  (AF041337) vacuolar proton pump subunit SFD beta isoform
NCBI Description
                   [Bos taurus]
                  230739
Seq. No.
                  LIB3197-006-P1-M1-B4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2342727
BLAST score
                  175
                   1.0e-12
E value
Match length
                   47
                   64
% identity
NCBI Description (AC002341) hypothetical protein [Arabidopsis thaliana]
                   230740
Seq. No.
Seq. ID
                   LIB3197-006-P1-M1-B6
                   BLASTX
Method -
NCBI GI
                   q2623310
BLAST score
                   296
                   8.0e-27
E value
Match length
                   77
                   74
% identity
                   (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3402721 (AC004261) unknown protein [Arabidopsis
                   thaliana]
Seq. No.
                   230741
                   LIB3197-006-P1-M1-B7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3860308
BLAST score
                   158
E value
                   1.0e-10
Match length
                   41
                   76
% identity
NCBI Description (AJ012681) hypothetical protein [Cicer arietinum]
```



```
230742
Seq. No.
                  LIB3197-006-P1-M1-C1
Seq. ID
                  BLASTX
Method
                  q3024703
NCBI GI
BLAST score
                  289
                  4.0e-26
E value
                  77
Match length
                  74
% identity
                  PROBABLE T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA)
NCBI Description
                  (CCT-ETA) >gi_2104461_emb_CAB08778_ (Z95397) Cct7p
                  [Schizosaccharomyces pombe]
                  230743
Seq. No.
                  LIB3197-006-P1-M1-C10
Seq. ID
Method
                  BLASTX
                  q1718097
NCBI GI
BLAST score
                  520
                  5.0e-53
E value
Match length
                  143
% identity
                  66
                  VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
NCBI Description
                   (41 KD ACCESSORY PROTEIN) (DVA41) >gi 626048_pir__A55016
                  lysosomal membrane protein DVA41 - slime mold
                   (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar
                  ATPase subunit DVA41 [Dictyostelium discoideum]
                  230744
Seq. No.
Seq. ID
                  LIB3197-006-P1-M1-C11
                  BLASTX
Method
NCBI GI
                  q3881780
BLAST score
                  152
                   5.0e-10
E value
Match length
                  103
                   38
% identity
                  (Z48638) similar to lipid transfer protein [Caenorhabditis
NCBI Description
                   elegans]
                   230745
Seq. No.
Seq. ID
                   LIB3197-006-P1-M1-C12
Method
                   BLASTX
                   g3269288
NCBI GI
                   490
BLAST score
                   2.0e-49
E value
                   133
Match length
% identity
                   74
                  (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                   230746
Seq. No.
                   LIB3197-006-P1-M1-C2
Seq. ID
                   BLASTX
Method
                   g3873872
NCBI GI
BLAST score
                   156
                   6.0e-11
E value
Match length
                   36
                   69
% identity
                  (Z81030) cDNA EST CEMSC45R comes from this gene; cDNA EST
NCBI Description
```

yk436a5.3 comes from this gene; cDNA EST yk436a5.5 comes



## from this gene [Caenorhabditis elegans]

```
230747
Seq. No.
                   LIB3197-006-P1-M1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3776009
BLAST score
                   607
E value
                   3.0e-63
                   150
Match length
% identity
                   74
                  (AJ010468) RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   230748
                   LIB3197-006-P1-M1-C5
Seq. ID
                   BLASTX
Method
                   q4539404
NCBI GI
BLAST score
                   205
                   4.0e-16
E value
Match length
                   107
% identity
                   45
                  (AL049524) putative protein [Arabidopsis thaliana]
NCBI Description
                   230749
Seq. No.
Seq. ID
                   LIB3197-006-P1-M1-D10
                   BLASTX
Method
                   g3885329
NCBI GI
                   480
BLAST score
                   3.0e-50
E value
Match length
                   126
 % identity
                  (AC005623) alien-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   230750
                   LIB3197-006-P1-M1-D11
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g120673
 BLAST score
                   635
                   2.0e-66
E value
Match length
                   146
 % identity
                   83
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
 NCBI Description
                   >gi_66013_pir__DEPJG glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) - garden petunia
                   >gi_20551_emb_CAA42904_ (X60346) glyceraldehyde
                   3-phosphate dehydrogenase [Petunia x hybrida]
                   230751
Seq. No.
                   LIB3197-006-P1-M1-D12
Seq. ID
 Method
                   BLASTX
                   g2443878
 NCBI GI
                   177
 BLAST score
                   8.0e-13
 E value
                   77
 Match length
                   60
 % identity
 NCBI Description (AC002294) Unknown protein [Arabidopsis thaliana]
```

33152

230752

Seq. No.



LIB3197-006-P1-M1-D2 ~Seq. ID BLASTX Method NCBI GI g3915031 BLAST score 765 9.0e-82 E value Match length 149 99 % identity ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR NCBI Description (STEAROYL-ACP DESATURASE) >gi\_1217628\_emb CAA65232 (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase [Gossypium hirsutum] 230753 Seq. No. LIB3197-006-P1-M1-D3 Seq. ID Method BLASTX NCBI GI q3914394 355 BLAST score 9.0e-34 E value 79 Match length 82 % identity 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE NCBI Description (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi 2118335 pir S60473 phosphoglycerate mutase (EC 5.4.2.1) - common ice plant >gi\_602426 (U16021) phosphoglyceromutase [Mesembryanthemum crystallinum] Seq. No. 230754 Seq. ID LIB3197-006-P1-M1-D4 Method BLASTX NCBI GI g1724100 579 BLAST score 6.0e-60 E value 131 Match length % identity NCBI Description (U79765) porin [Mesembryanthemum crystallinum] Seq. No. 230755 LIB3197-006-P1-M1-D5 Seq. ID Method BLASTX NCBI GI a4468979 BLAST score 453 E value 4.0e-45Match length 112 % identity NCBI Description (AL035605) putative protein [Arabidopsis thaliana] Seq. No. 230756 Seq. ID LIB3197-006-P1-M1-D8 Method BLASTX NCBI GI q2245378 BLAST score 336 E value 2.0e-31 Match length 83

Seq. No. 230757

72

% identity

NCBI Description (U83245) auxin response factor 1 [Arabidopsis thaliana]



```
LIB3197-006-P1-M1-E1
Seq. ID
Method
                  BLASTX
                  a992706
NCBI GI
BLAST score
                  552
                  9.0e-57
E value
                  119
Match length
                  82
% identity
                 (U33758) UBC13 [Arabidopsis thaliana]
NCBI Description
                  230758
Seq. No.
                  LIB3197-006-P1-M1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827709
BLAST score
                   317
                   3.0e-29
E value
                  99
Match length
                   59
% identity
NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]
                  230759
Seq. No.
                  LIB3197-006-P1-M1-E2
Seq. ID
                  BLASTX
Method
                  g2129499
NCBI GI
                   679
BLAST score
E value
                  1.0e-71
Match length
                   149
% identity
                   85
NCBI Description fiber protein E6 (clone CKE6-4A) - upland cotton
                   >gi 1000086 (U30506) E6 [Gossypium hirsutum]
                   230760
Seq. No.
                   LIB3197-006-P1-M1-E3
Seq. ID
Method
                   BLASTX
                   q2827709
NCBI GI
BLAST score
                   307
E value
                   4.0e-28
Match length
                   93
% identity
NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]
                   230761
Seq. No.
                   LIB3197-006-P1-M1-E7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3688600
BLAST score
                   275
                   2.0e-24
E value
Match length
                   101
% identity
NCBI Description (AB009030) beta-Amyrin Synthase [Panax ginseng]
                   230762
Seq. No.
Seq. ID
                   LIB3197-006-P1-M1-E9
Method
                   BLASTX
NCBI GI
                   g2827709
```

33154

321

97

1.0e-29

BLAST score

E value Match length



```
% identity
                  (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
                  230763
Seq. No.
                  LIB3197-006-P1-M1-F1
Seq. ID
Method
                  BLASTX
                  g3892056
NCBI GI
                   400
BLAST score
                   6.0e-39
E value
                  94
Match length
                  83
% identity
                  (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]
NCBI Description
                  230764
Seq. No.
                  LIB3197-006-P1-M1-F2
Seq. ID
Method
                  BLASTX
                  q2832625
NCBI GI
BLAST score
                   384
                   3.0e-37
E value
                   91
Match length
                   80
% identity
                  (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  230765
                  LIB3197-006-P1-M1-F3
Seq. ID
Method
                  BLASTX
                  g120669
NCBI GI
BLAST score
                   529
                   4.0e-54
E value
Match length
                   123
                   82
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                   230766
                   LIB3197-006-P1-M1-F7
Seq. ID
                   BLASTX
Method
                   g3892056
NCBI GI
BLAST score
                   316
E value
                   4.0e-29
                   84
Match length
                   75
% identity
NCBI Description (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]
                   230767
Seq. No.
                   LIB3197-006-P1-M1-F8
Seq. ID
Method
                   BLASTX
                   g3097056
NCBI GI
BLAST score
                   295
```

E value 1.0e-26 Match length 86 67 % identity

(AJ003139) dihydrofolate reductase-thymidylate synthetase NCBI Description

[Daucus carota]



```
230768
Seq. No.
                   LIB3197-006-P1-M1-G1
Seq. ID
                   BLASTX
Method
                   g2058282
NCBI GI
                   504
BLAST score
                   4.0e-51
E value
                   140
Match length
                   67
% identity
                   (X97377) atranbpla [Arabidopsis thaliana]
NCBI Description
                   230769
Seq. No.
                   LIB3197-006-P1-M1-G2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2921512
BLAST score
                   395
                   2.0e-38
E value
                   98
Match length
                   83
% identity
                  (AF037460) GF14 protein [Fritillaria agrestis]
NCBI Description
                   230770
Seq. No.
                   LIB3197-006-P1-M1-G7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2995990
                   322
BLAST score
E value
                   8.0e-30
                   102
Match length
                    62
% identity
                   (AF053746) dormancy-associated protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2995992 (AF053747) dormancy-associated
                   protein [Arabidopsis thaliana]
                   230771
Seq. No.
                   LIB3197-006-P1-M1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                    g116923
BLAST score
                    500
                    1.0e-50
E value
Match length
                   137
                    69
% identity
                   COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
NCBI Description
                   >gi_111414_pir__S13520 beta-COP protein - rat
>gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus
                    norvegicus]
Seq. No.
                    230772
                    LIB3197-006-P1-M1-G9
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2119278
BLAST score
                    636
E value
                    1.0e-66
                   118
Match length
                    97
% identity
```

NCBI Description tubulin beta-1 chain - rice

230773

Seq. No.



LIB3197-006-P1-M1-H2 Seq. ID BLASTX Method g4379025 NCBI GI 175 BLAST score 2.0e-15 E value 106 Match length 49 % identity (X03145) pot. ORF VI [Homo sapiens] NCBI Description 230774 Seq. No. LIB3197-007-P1-M1-A2 Seq. ID Method BLASTX g1707955 NCBI GI 550 BLAST score 1.0e-56 E value Match length 110 92 % identity GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME 1 NCBI Description (GLUTAMATE--AMMONIA LIGASE) >gi\_1134896\_emb\_CAA63981\_ (X94320) glutamine synthetase [Vitis vinifera] 230775 Seq. No. LIB3197-007-P1-M1-A9 Seq. ID Method BLASTX q1708236 NCBI GI BLAST score 309 8.0e-29 E value Match length 78 % identity 78 HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) NCBI Description (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi\_2129617\_pir\_\_JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana >gi\_1143390\_emb\_CAA58763\_ (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi\_1586548\_prf\_\_2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana] 230776 Seq. No. LIB3197-007-P1-M1-B11 Seq. ID BLASTX Method g3047108 NCBI GI 218 BLAST score 1.0e-17 E value 112 Match length % identity NCBI Description (AF058919) No definition line found [Arabidopsis thaliana] 230777 Seq. No. LIB3197-007-P1-M1-B12 Seq. ID BLASTX Method NCBI GI q4538929

Method BLASTX
NCBI GI 94538929
BLAST score 165
E value 2.0e-11
Match length 58
% identity 59

NCBI Description (AL049483) putative nucleic acid binding protein



## [Arabidopsis thaliana]

```
230778
Seq. No.
                  LIB3197-007-P1-M1-B4
Seq. ID
                   BLASTX
Method
                   g267069
NCBI GI
                   339
BLAST score
                   4.0e-32
E value
                   72
Match length
                   85
% identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                   230779
                   LIB3197-007-P1-M1-C10
Seq. ID
Method
                   BLASTX
                   q1708236
NCBI GI
                   295
BLAST score
                   2.0e-27
E value
                   111
Match length
% identity
                   62
                   HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE)
NCBI Description
                   (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)
                   >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase
                   (EC 4.1.3.5) - Arabidopsis thaliana
                   >gi_1143390_emb_CAA58763_ (X83882)
hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]
                   >qi 1586548 prf 2204245A hydroxy methylglutaryl CoA
                   synthase [Arabidopsis thaliana]
                   230780
Seq. No.
                   LIB3197-007-P1-M1-C2
Seq. ID
Method
                   BLASTX
                   g464621
NCBI GI
BLAST score
                   164
E value
                   2.0e-11
                   47
Match length
                   68
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374_pir__S28586
                   ribosomal protein ML16 - common ice plant
                   >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
                   230781
Seq. No.
                   LIB3197-007-P1-M1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q416731
BLAST score
                   143
E value
                   3.0e-09
                   67
Match length
% identity
                   46
NCBI Description POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi 82655 pir JQ1107
                   18.3K protein precursor, pollen - maize
                   >gi_255569_bbs_113677 (S44171) pollen specific protein [Zea
```

mays=corn, Peptide, 170 aa] [Zea mays]





## >gi\_1588669\_prf\_\_2209273A Zm13 [Zea mays]

230782 Seq. No. LIB3197-007-P1-M1-E1 Seq. ID BLASTX Method NCBI GI g1778370 416 BLAST score 7.0e-43 E value 102 Match length 85 % identity NCBI Description (U77678) asparagine synthetase 2 [Glycine max] 230783 Seq. No. LIB3197-007-P1-M1-E2 Seq. ID Method BLASTX NCBI GI g100203 BLAST score 331 6.0e-31 E value Match length 108 63 % identity cysteine proteinase (EC 3.4.22.-) precursor - tomato NCBI Description >gi 19195\_emb\_CAA78403\_ (Z14028) pre-pro-cysteine proteinase [Lycopersicon esculentum] 230784 Seq. No. LIB3197-007-P1-M1-E6 Seq. ID Method BLASTX NCBI GI g1587206 BLAST score 161 4.0e-11 E value 35 Match length 94 % identity T complex protein [Cucumis sativus] NCBI Description 230785 Seq. No. LIB3197-007-P1-M1-F4 Seq. ID Method BLASTX NCBI GI g3873710 BLAST score 272 1.0e-27 E value 110 Match length 56 % identity (Z73102) predicted using Genefinder; similar to Zinc NCBI Description finger, C2H2 type; cDNA EST EMBL:M89161 comes from this gene; cDNA EST EMBL:T01394 comes from this gene; cDNA EST EMBL:T02192 comes from this gene; cDNA EST EMBL:D71409 comes 230786 Seq. No. Seq. ID LIB3197-007-P1-M1-F5 Method BLASTX NCBI GI q267069 BLAST score 583 2.0e-60 E value Match length 108

% identity 98
NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594



tubulin alpha chain - Arabidopsis thaliana >gi\_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

 Seq. No.
 230787

 Seq. ID
 LIB3197-007-P1-M1-F6

 Method
 BLASTX

 NCBI GI
 g2760830

 BLAST score
 220

 E value
 7.0e-18

 Match length
 70

% identity 57 NCBI Description (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana]

Seq. No. 230788

Seq. ID LIB3197-007-P1-M1-G8

Method BLASTX
NCBI GI g2811278
BLAST score 137
E value 1.0e-08
Match length 70
% identity 44

NCBI Description (AF043284) expansin [Gossypium hirsutum]

Seq. No. 230789

Seq. ID LIB3197-007-P1-M1-H5

Method BLASTX
NCBI GI g3851001
BLAST score 303
E value 1.0e-27
Match length 83
% identity 76

NCBI Description (AF069909) pyruvate dehydrogenase E1 beta subunit isoform 2

[Zea mays]

Seq. No. 230790

Seq. ID LIB3197-007-P1-M1-H7

Method BLASTX
NCBI GI g3415117
BLAST score 438
E value 2.0e-43
Match length 109
% identity 42

NCBI Description (AF081203) villin 3 [Arabidopsis thaliana]

Seq. No. 230791

Seq. ID LIB3197-007-P1-M1-H9

Method BLASTX
NCBI GI g267069
BLAST score 322
E value 1.0e-54
Match length 110
% identity 92

NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi\_166914

(M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916

Seq. No.

230797



#### (M84697) alpha-4 tubulin [Arabidopsis thaliana]

```
230792
Seq. No.
                  LIB3197-008-P1-M1-A12
Seq. ID
                  BLASTX
Method
                  g2146727
NCBI GI
                  374
BLAST score
                  3.0e-36
E value
                  90
Match length
                  74
% identity
                  cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) CAD1 -
NCBI Description
                  Arabidopsis thaliana (fragment) >gi_598069 (L37884)
                  cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]
                  230793
Seq. No.
                  LIB3197-008-P1-M1-A5
Seq. ID
                  BLASTX
Method
                  g1766046
NCBI GI
                  469
BLAST score
                  4.0e-47
E value
                  101
Match length
                  85
% identity
                  (U81993) NAD+ dependent isocitrate dehydrogenase subunit 1
NCBI Description
                   [Arabidopsis thaliana]
                  230794
Seq. No.
                  LIB3197-008-P1-M1-A6
Seq. ID
Method
                  BLASTX
                  g3641836
NCBI GI
                  168
BLAST score
                   1.0e-11
E value
                   103
Match length
                   41
% identity
                  (AL023094) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   230795
                   LIB3197-008-P1-M1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244765
BLAST score
                   312
                   1.0e-28
E value
                   93
Match length
                   55
% identity
NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   230796
                   LIB3197-008-P1-M1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3252806
BLAST score
                   158
                   1.0e-10
E value
                   97
Match length
% identity
NCBI Description (AC004705) hypothetical protein [Arabidopsis thaliana]
```



```
LIB3197-008-P1-M1-B12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3983665
BLAST score
                  339
                  8.0e-32
E value
                  88
Match length
                  77
% identity
                  (AB011271) importin-beta2 [Oryza sativa]
NCBI Description
                  230798
Seq. No.
                  LIB3197-008-P1-M1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760326
BLAST score
                  232
                  2.0e-19
E value
Match length
                  112
% identity
                  46
                  (AC002130) F1N21.11 [Arabidopsis thaliana]
NCBI Description
                  230799
Seq. No.
                  LIB3197-008-P1-M1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832625
BLAST score
                  466
                  1.0e-46
E value
Match length
                  114
% identity
                  78
                  (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
                  230800
Seq. No.
                  LIB3197-008-P1-M1-B7
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3892051
BLAST score
                   313
                   6.0e-29
E value
                   86
Match length
                   72
% identity
                  (AC002330) predicted NADH dehydrogenase 24 kD subunit
NCBI Description
                   [Arabidopsis thaliana]
                   230801
Seq. No.
                   LIB3197-008-P1-M1-B9
Seq. ID
Method
                   BLASTX
                   g3269284
NCBI GI
                   245
BLAST score
                   6.0e-21
E value
                   98
Match length
                   55
% identity
                  (AL030978) histone H2A- like protein [Arabidopsis thaliana]
NCBI Description
                   230802
Seq. No.
                   LIB3197-008-P1-M1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3269284
                   369
BLAST score
```

33162

2.0e-35

112

E value Match length

% identity

NCBI Description



% identity (AL030978) histone H2A- like protein [Arabidopsis thaliana] NCBI Description 230803 Seq. No. LIB3197-008-P1-M1-C11 Seq. ID Method BLASTX g3377820 NCBI GI BLAST score 172 2.0e-12 E value 75 Match length 48 % identity (AF076275) contains similarity to coatomer zeta chains NCBI Description [Arabidopsis thaliana] 230804 Seq. No. LIB3197-008-P1-M1-C3 Seq. ID Method BLASTX g1076668 NCBI GI 732 BLAST score 7.0e-78 E value 145 Match length 92 % identity NADH dehydrogenase (EC 1.6.99.3) - potato NCBI Description >gi 639834 emb CAA58823 (X83999) NADH dehydrogenase [Solanum tuberosum] Seq. No. 230805 LIB3197-008-P1-M1-C4 Seq. ID BLASTX Method NCBI GI q4432846 BLAST score 173 E value 2.0e-12 Match length 99 54 % identity (AC006283) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 230806 LIB3197-008-P1-M1-C5 Seq. ID Method BLASTX g2970051 NCBI GI 269 BLAST score E value 9.0e-24Match length 83 63 % identity (AB012110) ARG10 [Vigna radiata] NCBI Description Seq. No. 230807 Seq. ID LIB3197-008-P1-M1-C6 Method BLASTX NCBI GI q3377820 BLAST score 136 1.0e-08 E value Match length 35

22.

[Arabidopsis thaliana]

(AF076275) contains similarity to coatomer zeta chains



```
230808
Seq. No.
                   LIB3197-008-P1-M1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g464849
BLAST score
                   693
                   2.0e-73
E value
                   129
Match length
                   100
% identity
                   TUBULIN ALPHA CHAIN >gi 486847 pir_S36232 tubulin alpha
NCBI Description
                   chain - almond >gi_2041\overline{3}_{emb}C\overline{A}A47\overline{635}_{cm}(X67162)
                   alpha-tubulin [Prunus dulcis]
                   230809
Seq. No.
                   LIB3197-008-P1-M1-D1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2344894
BLAST score
                   358
                   3.0e-34
E value
Match length
                   114
% identity
                   60
                  (AC002388) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   230810
Seq. No.
                   LIB3197-008-P1-M1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1354849
                   394
BLAST score
                   3.0e - 38
E value
                   119
Match length
                   65
% identity
NCBI Description (U57350) epoxide hydrolase [Nicotiana tabacum]
                   230811
Seq. No.
                   LIB3197-008-P1-M1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3337356
BLAST score
                   504
                   4.0e-51
E value
Match length
                   102
                   96
% identity
                  (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
                   230812
Seq. No.
                   LIB3197-008-P1-M1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3023195
BLAST score
                   525
E value
                   1.0e-53
Match length
                   127
% identity
                   80
NCBI Description 14-3-3-LIKE PROTEIN B (SGF14B) >gi 1575727 (U70534) SGF14B
                   [Glycine max]
```

Seq. No. 230813

Seq. ID LIB3197-008-P1-M1-D5

Method BLASTX

Match length

% identity

137



```
g4376650
 NCBI GI
                    145
 BLAST score
                    5.0e-09
 E value
                    69
 Match length
                    48
 % identity
                    (AE001621) GcpE Protein [Chlamydia pneumoniae]
 NCBI Description
                    230814
 Seq. No.
                    LIB3197-008-P1-M1-D7
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g3695388
                    209
 BLAST score
                    1.0e-16
 E value
                    62
 Match length
                    60
 % identity
                   (AF096371) No definition line found [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    230815
                    LIB3197-008-P1-M1-E3
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g3402279
 BLAST score
                    574
                    2.0e-59
 E value
 Match length
                    127
                    83
 % identity
                    (AJ000999) putative beta-subunit of K+ channels [Solanum
 NCBI Description
                    tuberosum]
 Seq. No.
                    230816
                    LIB3197-008-P1-M1-E4
 Seq. ID
                    BLASTX
 Method
                    g4539301
 NCBI GI
 BLAST score
                    166
                    1.0e-11
 E value
                    67
 Match length
                    51
 % identity
 NCBI Description
                    (AL049480) putative mitochondrial protein [Arabidopsis
                    thaliana]
                    230817
 Seq. No.
                    LIB3197-008-P1-M1-E5
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1332579
                    236
 BLAST score
 E value
                    9.0e-20
                    73
 Match length
 % identity
                   (X98063) polyubiquitin [Pinus sylvestris]
* NCBI Description
 Seq. No.
                    230818
 Seq. ID
                    LIB3197-008-P1-M1-E8
 Method
                    BLASTX
 NCBI GI
                    q4099611
 BLAST score
                    243
                    1.0e-20
 E value
```



```
(U88873) BUB2-like protein 1 [Mus musculus]
NCBI Description
                  230819
Seq. No.
                  LIB3197-008-P1-M1-F1
Seq. ID
Method
                  BLASTX
                  q2689631
NCBI GI
BLAST score
                  702
                  2.0e-74
E value
                  140
Match length
% identity
                  99
                  (AF022389) ADP-ribosylation factor [Vigna unguiculata]
NCBI Description
                  230820
Seq. No.
                  LIB3197-008-P1-M1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q70644
BLAST score
                  649
E value
                  4.0e-68
                  131
Match length
% identity
                  19
                  ubiquitin precursor - common sunflower (fragment)
NCBI Description
Seq. No.
                  230821
                  LIB3197-008-P1-M1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1255951
BLAST score
                  513
                  3.0e-52
E value
Match length
                  128
% identity
                  73
                  (X96932) PS60 [Nicotiana tabacum]
NCBI Description
                  230822
Seq. No.
                  LIB3197-008-P1-M1-F6
Seq. ID
                  BLASTX
Method
                  g1708313
NCBI GI
                   390
BLAST score
                  8.0e-38
E value
                  85
Match length
                   92
% identity
                 HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi 999396 bbs 163637
NCBI Description
                   (S77849) heat-shock Protein=HSP81-3 [Arabidopsis
                   thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis
                  thaliana]
                   230823
Seq. No.
                  LIB3197-008-P1-M1-F8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3914424
```

Method BLASTX
NCBI GI g3914424
BLAST score 486
E value 4.0e-49
Match length 112
% identity 81

NCBI Description PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8)

(MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8)

>gi 2511592 emb CAA74027.1 (Y13693) multicatalytic

endopeptidase complex, proteasome component, alpha subunit

Match length

% identity

130 38



#### [Arabidopsis thaliana]

```
Seq. No.
                  230824
                  LIB3197-008-P1-M1-G1
Seq. ID
                  BLASTX
Method
                  q3881189
NCBI GI
BLAST score
                  448
                  1.0e-44
E value
                  110
Match length
% identity
                  73
                  (Z99281) similar to ADP-ribosylation factor; cDNA EST
NCBI Description
                  EMBL: C08179 comes from this gene; cDNA EST EMBL: C08337
                  comes from this gene; cDNA EST EMBL: C09829 comes from this
                  gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4
Seq. No.
                  230825
                  LIB3197-008-P1-M1-G4
Seq. ID
Method
                  BLASTX
                  q2266992
NCBI GI
BLAST score
                  307
                  4.0e-28
E value
Match length
                  137
% identity
                  7
                  (U77412) O-linked GlcNAc transferase [Caenorhabditis
NCBI Description
                  elegans]
                  230826
Seq. No.
Seq. ID
                  LIB3197-008-P1-M1-G7
Method
                  BLASTX
                  q1703375
NCBI GI
                  543
BLAST score
                  1.0e-55
E value
Match length
                  112
                  96
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420)
                  DcARF1 [Daucus carota]
Seq. No.
                  230827
                  LIB3197-008-P1-M1-H1
Seq. ID
Method
                  BLASTX
                  g1706652
NCBI GI
BLAST score
                   294
                   2.0e-26
E value
                  90
Match length
                   61
% identity
NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_498862 (U09736)
                   enolase [Entamoeba histolytica]
Seq. No.
                   230828
Seq. ID
                  LIB3197-008-P1-M1-H2
Method
                  BLASTX
NCBI GI
                   q3176098
                   430
BLAST score
E value
                   1.0e-42
```



NCBI Description (Y15036) annexin [Medicago truncatula] 230829 Seq. No. LIB3197-008-P1-M1-H5 Seq. ID BLASTX Method q3757521 NCBI GI 300 BLAST score 3.0e-27E value 130 Match length 45 % identity (AC005167) unknown protein [Arabidopsis thaliana] NCBI Description 230830 Seq. No. LIB3197-008-P1-M1-H7 Seq. ID BLASTX Method NCBI GI g400650 BLAST score 187 5.0e-14E value 98 Match length 42 % identity NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (COMPLEX NCBI Description I-13KD-B) (CI-13KD-B) (B13) >gi\_346535\_pir\_\_S28244 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B13 bovine >gi\_238\_emb\_CAA44903\_ (X63218) NADH dehydrogenase [Bos taurus] Seq. No. 230831 LIB3197-008-P1-M1-H8 Seq. ID Method BLASTX NCBI GI g4455351 293 BLAST score E value 2.0e-26 72 Match length 76 % identity NCBI Description (AL035524) putative protein [Arabidopsis thaliana] Seq. No. 230832 LIB3197-010-P1-M1-A1 Seq. ID Method BLASTX NCBI GI q113217 BLAST score 247 E value 3.0e-21Match length 54 % identity NCBI Description ACTIN 1 >gi 100149 pir S07002 actin 1 - carrot Seq. No. 230833 LIB3197-010-P1-M1-A12 Seq. ID Method BLASTX NCBI GI

g1220196 BLAST score 618 E value 2.0e-64Match length 134 % identity 87

(U49061) alcohol dehydrogenase 2a [Gossypium hirsutum] NCBI Description

Seq. No. 230834

NCBI GI

E value

BLAST score

g4417271

2.0e-09

143



```
Seq. ID
                  LIB3197-010-P1-M1-A3
Method
                  BLASTX
NCBI GI
                  g2879811
BLAST score
                  411
E value
                  2.0e-40
                  92
Match length
                  85
% identity
                 (AJ223316) ribosomal protein L30 [Lupinus luteus]
NCBI Description
                  230835
Seq. No.
                  LIB3197-010-P1-M1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455158
BLAST score
                  439
                  3.0e-52
E value
Match length
                  117
% identity
                  85
                 (AL021687) kinase-like protein [Arabidopsis thaliana]
NCBI Description
                  230836
Seq. No.
                  LIB3197-010-P1-M1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3169287
BLAST score
                  261
                  9.0e-24
E value
Match length
                  66
% identity
                  91
NCBI Description
                  (AF050673) vacuolar H+-ATPase catalytic subunit [Gossypium
                  hirsutum]
                  230837
Seq. No.
                  LIB3197-010-P1-M1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245100
BLAST score
                  149
E value
                  9.0e-10
Match length
                  91
% identity
                  44
NCBI Description
                 (Z97343) DNA-binding protein homolog [Arabidopsis thaliana]
Seq. No.
                  230838
Seq. ID
                  LIB3197-010-P1-M1-B1
Method
                  BLASTX
                  g3800951
NCBI GI
BLAST score
                  176
E value
                  7.0e-13
Match length
                  68
% identity
                  49
NCBI Description
                  (AF100657) No definition line found [Caenorhabditis
                  elegans]
Seq. No.
                  230839
Seq. ID
                  LIB3197-010-P1-M1-B6
Method
                  BLASTX
```



43 Match length 70 % identity NCBI Description Seq. No. Seq. ID

(AC007019) putative cellulose synthase catalytic subunit [Arabidopsis thaliana]

230840

LIB3197-010-P1-M1-C11 BLASTX Method g832876 NCBI GI BLAST score 169 2.0e-12 E value 36 Match length

92 % identity NCBI Description (L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi\_1097368\_prf\_\_2113407A ascorbate free

radical reductase [Lycopersicon esculentum]

Seq. No. 230841

LIB3197-010-P1-M1-C2 Seq. ID

BLASTX Method NCBI GI g862640 BLAST score 337 3.0e-33 E value 82 Match length 87 % identity

(U20182) MADS-box protein AGL11 [Arabidopsis thaliana] NCBI Description

>gi\_4538999\_emb\_CAB39620.1\_ (AL049481) MADS-box protein

AGL11 [Arabidopsis thaliana]

230842 Seq. No.

LIB3197-010-P1-M1-C3 Seq. ID

Method BLASTX g4105798 NCBI GI BLAST score 392 4.0e-38 E value Match length 94

% identity 67

(AF049930) PGP237-11 [Petunia x hybrida] NCBI Description

230843 Seq. No.

LIB3197-010-P1-M1-C5 Seq. ID

Method BLASTX NCBI GI g1362086 334 BLAST score 2.0e-31 E value 99 Match length 68 % identity

NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi\_2129919\_pir\_\_S65957

5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi\_886471\_emb\_CAA58474\_ (X83499) methionine synthase

[Catharanthus roseus]

Seq. No. 230844

Seq. ID LIB3197-010-P1-M1-C7



```
Method
                  BLASTX
NCBI GI
                  q832876
BLAST score
                  410
                  4.0e-40
E value
Match length
                  100
                  81
% identity
NCBI Description
                  (L41345) ascorbate free radical reductase [Solanum
                  lycopersicum] >gi 1097368 prf 2113407A ascorbate free
                  radical reductase [Lycopersicon esculentum]
                  230845
Seq. No.
Seq. ID
                  LIB3197-010-P1-M1-D1
Method
                  BLASTX
                  g1076738
NCBI GI
BLAST score
                  431
                  7.0e-43
E value
Match length
                  84
                  95
% identity
NCBI Description beta-tubulin R2242 - rice
                  230846
Seq. No.
Seq. ID
                  LIB3197-010-P1-M1-D12
                  BLASTX
Method
NCBI GI
                  g3176874
BLAST score
                  338
                  6.0e - 32
E value
Match length
                  102
                  65
% identity
NCBI Description
                  (AF065639) cucumisin-like serine protease [Arabidopsis
                  thaliana]
                  230847
Seq. No.
                  LIB3197-010-P1-M1-D3
Seq. ID
Method
                  BLASTX
                  g4056432
NCBI GI
BLAST score
                  145
                   5.0e-09
E value
Match length
                  38
% identity
                  71
                  (AC005990) Similar to gi_2245014 glucosyltransferase
NCBI Description
                  homolog from Arabidopsis thaliana chromosome 4 contig
                  gb Z97341. ESTs gb T20778 and gb AA586281 come from this
                  gene. [Arabidopsis thaliana]
                   230848
Seq. No.
                  LIB3197-010-P1-M1-D8
Seq. ID
Method
                  BLASTX
                  g629806
NCBI GI
BLAST score
                   455
                   2.0e-47
E value
                  108
Match length
% identity
                   85
NCBI Description tubulin beta chain - rice >gi_493725_emb_CAA55912_ (X79367)
```

Seq. No. 230849

Seq. ID LIB3197-010-P1-M1-E3

beta tubulin [Oryza sativa]

E value

3.0e-25



```
BLASTX
Method
                  q4098128
NCBI GI
                  223
BLAST score
E value
                  2.0e-18
                  52
Match length
                  85
% identity
                 (U73588) sucrose synthase [Gossypium hirsutum]
NCBI Description
                  230850
Seq. No.
                  LIB3197-010-P1-M1-E4
Seq. ID
Method
                  BLASTX
                  g3273200
NCBI GI
                  174
BLAST score
                  1.0e-12
E value
Match length
                  50
                  70
% identity
                  (AB010917) responce reactor3 [Arabidopsis thaliana]
NCBI Description
                  >gi 3894192 (AC005662) response regulator 3 [Arabidopsis
                  thaliana]
Seq. No.
                  230851
                  LIB3197-010-P1-M1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2832700
BLAST score
                  139
E value
                  1.0e-08
                  80
Match length
                   46
% identity
NCBI Description (AL021713) unknown protein [Arabidopsis thaliana]
Seq. No.
                   230852
                  LIB3197-010-P1-M1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q100484
BLAST score
                   190
E value
                   1.0e-14
                   98
Match length
                   40
% identity
NCBI Description hypothetical protein - garden snapdragon
Seq. No.
                   230853
                   LIB3197-010-P1-M1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3395938
BLAST score
                   340
E value
                   4.0e-32
Match length
                   91
                   70
% identity
                   (AF076924) polypyrimidine tract-binding protein homolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   230854
                   LIB3197-010-P1-M1-F11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g121631
BLAST score
                   281
```

·\_ ',.



Match length 70 % identity 74

NCBI Description GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR

>gi 72323 pir KNNT2S glycine-rich protein 2 - wood tobacco

>gi 19743 emb CAA42622 (X60007) nsGRP-2 [Nicotiana

sylvestris]

Seq. No. 230855

Seq. ID LIB3197-010-P1-M1-F12

Method BLASTX
NCBI GI g1346802
BLAST score 281
E value 3.0e-25
Match length 93
% identity 59

NCBI Description PROFILIN 1 >gi 1076516 pir S49351 profilin - kidney bean

>gi 556836 emb CAA57508 (X81982) profilin [Phaseolus

vulgaris]

Seq. No. 230856

Seq. ID LIB3197-010-P1-M1-F3

Method BLASTX
NCBI GI g1706319
BLAST score 158
E value 4.0e-11
Match length 72
% identity 47

NCBI Description HISTIDINE DECARBOXYLASE (HDC) (TOM92)

>gi\_481829\_pir\_\_S39554 histidine decarboxylase (EC
4.1.1.22) - tomato >gi\_416534\_emb\_CAA50719\_(X71900)
histidine decarboxylase [Lycopersicon esculentum]

Seq. No. 230857

Seq. ID LIB3197-010-P1-M1-G1

Method BLASTX
NCBI GI g2661840
BLAST score 166
E value 6.0e-12
Match length 51
% identity 67

NCBI Description (Y15430) adenosine kinase [Physcomitrella patens]

Seq. No. 230858

Seq. ID LIB3197-010-P1-M1-G12

Method BLASTX
NCBI GI g3426039
BLAST score 140
E value 6.0e-18
Match length 76
% identity 57

NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 230859

Seq. ID LIB3197-010-P1-M1-G3

Method BLASTX NCBI GI g2842490 BLAST score 206

BLAST score

Match length

E value

221

74

5.0e-18



```
E value
                   1.0e-16
Match length
                   61
% identity
                   64
                  (AL021749) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                  230860
Seq. No.
Seq. ID
                  LIB3197-010-P1-M1-G7
Method
                  BLASTX
NCBI GI
                  q2347098
BLAST score
                  334
E value
                  2.0e-31
Match length
                  72
% identity
                  94
NCBI Description
                  (U76845) ubiquitin-specific protease [Arabidopsis thaliana]
                  >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific
                  protease (AtUBP3) [Arabidopsis thaliana]
                  230861
Seq. No.
Seq. ID
                  LIB3197-010-P1-M1-H1
Method
                  BLASTX
NCBI GI
                  g421876
BLAST score
                  173
E value
                  5.0e-13
Match length
                  59
                  63
% identity
NCBI Description
                  probable ATP synthase chain - soybean
                  >gi_396230_emb_CAA52349_ (X74296) putative ATP synthase
                  subunit [Glycine max]
Seq. No.
                  230862
Seq. ID
                  LIB3197-010-P1-M1-H3
Method
                  BLASTX
NCBI GI
                  g2129825
BLAST score
                  459
E value
                  5.0e-46
Match length
                  107
% identity
                  83
NCBI Description
                  dynamin-like protein phragmoplastin 12 - soybean
                  >gi 1217994 (U25547) SDL [Glycine max]
Seq. No.
                  230863
Seq. ID
                  LIB3197-010-P1-M1-H5
Method
                  BLASTX
NCBI GI
                  g2104959
BLAST score
                  460
E value
                  4.0e-46
Match length
                  109
                  77
% identity
NCBI Description
                  (U96925) immunophilin [Vicia faba]
Seq. No.
                  230864
Seq. ID
                  LIB3197-010-P1-M1-H6
Method
                  BLASTX
NCBI GI
                  g4454051
```

NCBI GI

BLAST score



```
% identity
                  (AL035394) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
                  230865
Seq. No.
                  LIB3197-010-P1-M1-H8
Seq. ID
                  BLASTX
Method
                  g267069
NCBI GI
                  583
BLAST score
                  2.0e-60
E value
Match length
                  108
                  99
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  230866
Seq. No.
                  LIB3197-010-P1-M1-H9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2500717
BLAST score
                  329
E value
                  1.0e-30
                  100
Match length
                  58
% identity
NCBI Description STS14 PROTEIN PRECURSOR >gi_2129995_pir__S65052
                  pistil-specific protein sts14 precursor - potato
                  >gi_1236785_emb_CAA57976_ (X82652) sts14 [Solanum
                  tuberosum] >gi 1589691 prf 2211417A sts14 gene [Solanum
                  tuberosum]
Seq. No.
                  230867
                  LIB3197-011-P1-M1-A11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4455208
BLAST score
                  357
E value
                  6.0e - 34
Match length
                  114
% identity
                  68
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  230868
                  LIB3197-011-P1-M1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3184082
BLAST score
                  338
E value
                  1.0e-31
Match length
                  117
% identity
                  51
NCBI Description
                  (AL023781) N-terminal acetyltransferase 1
                   [Schizosaccharomyces pombe]
Seq. No.
                  230869
                  LIB3197-011-P1-M1-A4
Seq. ID
Method
                  BLASTX
```

33175

g2252841



E value 6.0e-13 Match length 73 % identity 52

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 230870

Seq. ID LIB3197-011-P1-M1-A6

Method BLASTX
NCBI GI g3738257
BLAST score 493
E value 7.0e-50
Match length 105
% identity 92

NCBI Description (AB018410) cytosolic phosphoglycerate kinase 1 [Populus

nigra]

Seq. No. 230871

Seq. ID LIB3197-011-P1-M1-B10

Method BLASTX
NCBI GI g2398679
BLAST score 709
E value 3.0e-75
Match length 146
% identity 93

NCBI Description (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate

synthase [Morinda citrifolia]

Seq. No. 230872

Seq. ID LIB3197-011-P1-M1-B11

Method BLASTX
NCBI GI g2702281
BLAST score 379
E value 1.0e-36
Match length 100
% identity 42

NCBI Description (AC003033) putative protein disulfide isomerase precursor

[Arabidopsis thaliana]

Seq. No. 230873

Seq. ID LIB3197-011-P1-M1-B4

Method BLASTX
NCBI GI g3023847
BLAST score 560
E value 9.0e-58
Match length 115
% identity 36

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE

PROTEIN >gi\_2385376\_emb\_CAA69934\_ (Y08678) G protein beta

subunit-like [Medicago sativa]

Seq. No. 230874

Seq. ID LIB3197-011-P1-M1-C10

Method BLASTX
NCBI GI g2827710
BLAST score 173
E value 2.0e-12
Match length 65

% identity (AL021684) lysosomal Pro-X carboxypeptidase - like protein NCBI Description [Arabidopsis thaliana] Seq. No. 230875 Seq. ID LIB3197-011-P1-M1-C11 BLASTX Method NCBI GI q3914431 BLAST score 599 2.0e-62 E value Match length 135 85 % identity PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8) NCBI Description (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8) >gi 2285802 dbj BAA21651 (D78173) 26S proteasome alpha subunit [Spinacia oleracea] 230876

 Seq. No.
 230876

 Seq. ID
 LIB3197-011-P1-M1-C2

 Method
 BLASTX

 NCBI GI
 g3650032

 BLAST score
 237

 E value
 7.0e-20

 Match length
 49

 % identity
 73

NCBI Description (AC005396) gibberellin-regulated protein GAST1-like

[Arabidopsis thaliana]

 Seq. No.
 230877

 Seq. ID
 LIB3197-011-P1-M1-C3

 Method
 BLASTX

 NCBI GI
 g2286153

 BLAST score
 529

 Examples
 3.00-54

BLAST score 529
E value 3.0e-54
Match length 126
% identity 80

NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No. 230878

Seq. ID LIB3197-011-P1-M1-C5

Method BLASTX
NCBI GI g1586940
BLAST score 425
E value 6.0e-42
Match length 122
% identity 68

NCBI Description Ser/Thr kinase [Lycopersicon esculentum]

Seq. No. 230879

Seq. ID LIB3197-011-P1-M1-C7

Method BLASTX
NCBI GI g2245000
BLAST score 335
E value 2.0e-31
Match length 91
% identity 75

NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

BLAST score

Match length

E value

318

66

1.0e-29

```
230880
Seq. No.
Seq. ID
                  LIB3197-011-P1-M1-C9
Method
                  BLASTX
NCBI GI
                  g1703108
BLAST score
                  489
E value
                  2.0e-49
Match length
                  93
                  98
% identity
                 ACTIN 2/7 >gi_2129525_pir S71210 actin 2 - Arabidopsis
NCBI Description
                  thaliana >gi 2129528 pir S68107 actin 7 - Arabidopsis
                  thaliana >gi 1049307 (U37281) actin-2 [Arabidopsis
                  thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis
                  thaliana]
Seq. No.
                  230881
                  LIB3197-011-P1-M1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1710780
BLAST score
                  193
                  7.0e-29
E value
Match length
                  114
% identity
                  58
                  40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433
NCBI Description
                  (X96613) cytoplasmic ribosomal protein S7 [Podospora
                  anserina]
Seq. No.
                  230882
Seq. ID
                  LIB3197-011-P1-M1-D7
Method
                  BLASTX
NCBI GI
                  q131529
BLAST score
                  186
                  6.0e-14
E value
                  82
Match length
                  22
% identity
                 POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS
NCBI Description
                  NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I)
                  >gi 53553_emb_CAA36321_ (X52101) 25kDa nuclear protein [Mus
                  musculus]
                  230883
Seq. No.
                  LIB3197-011-P1-M1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455194
BLAST score
                  290
E value
                  2.0e-26
Match length
                  68
% identity
                  79
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
                  230884
Seq. No.
                  LIB3197-011-P1-M1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1703375
```

E value

Match length

% identity

4.0e-58

110



```
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 965483 dbj BAA08259 (D45420)
                  DcARF1 [Daucus carota]
                  230885
Seq. No.
                  LIB3197-011-P1-M1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462825
BLAST score
                  271
                  5.0e-24
E value
Match length
                  85
% identity
                  61
                  (AF000657) contains Procite 'RNP1' putative RNA-binding
NCBI Description
                  region [Arabidopsis thaliana]
                  230886
Seq. No.
                  LIB3197-011-P1-M1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q267069
BLAST score
                  440
                  8.0e-44
E value
Match length
                  81
                  99
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  230887
Seq. No.
                  LIB3197-011-P1-M1-G1
Seq. ID
Method
                  BLASTX
                  g4467146
NCBI GI
BLAST score
                  388
E value
                  1.0e-37
Match length
                  142
                  52
% identity
NCBI Description
                  (AL035540) galactosidase like protein [Arabidopsis
                  thaliana]
                  230888
Seq. No.
                  LIB3197-011-P1-M1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q280523
BLAST score
                  258
E value
                  2.0e-22
Match length
                  83
% identity
                  61
NCBI Description hypothetical protein B0464.5 - Caenorhabditis elegans
Seq. No.
                  230889
Seq. ID
                  LIB3197-011-P1-M1-G8
Method
                  BLASTX
NCBI GI
                  g1174592
BLAST score
                  563
```



NCBI Description TUBULIN ALPHA-1 CHAIN >gi\_2119270\_pir\_\_S60233 alpha-tubulin - garden pea >gi\_525332 (U12589) alpha-tubulin [Pisum

sativum]

Seq. No. 230890

Seq. ID LIB3197-011-P1-M1-G9

Method BLASTX
NCBI GI g3341681
BLAST score 381
E value 9.0e-37
Match length 80
% identity 96

NCBI Description (AC003672) small GTP-binding protein [Arabidopsis thaliana]

>gi 741994 prf 2008312A GTP-binding protein [Arabidopsis

thaliana]

Seq. No. 230891

Seq. ID LIB3197-011-P1-M1-H2

Method BLASTX
NCBI GI g4490332
BLAST score 184
E value 9.0e-14
Match length 77
% identity 53

NCBI Description (AL035656) putative protein [Arabidopsis thaliana]

Seq. No. 230892

Seq. ID LIB3197-011-P1-M1-H3

Method BLASTX
NCBI GI g3548803
BLAST score 300
E value 2.0e-27
Match length 85
% identity 66

NCBI Description (ACO05313) putative DNA-binding protein [Arabidopsis

thaliana] >gi\_4335770\_gb\_AAD17447\_ (AC006284) putative

SMUBP-2 [mouse] DNA-binding protein [Arabidopsis thaliana]

Seq. No. 230893

Seq. ID LIB3197-012-P1-M1-A10

Method BLASTX
NCBI GI g2827143
BLAST score 649
E value 3.0e-68
Match length 127
% identity 93

NCBI Description (AF027174) cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Seq. No. 230894

Seq. ID LIB3197-012-P1-M1-A11

Method BLASTX
NCBI GI g4580460
BLAST score 471
E value 2.0e-47
Match length 101
% identity 92

Match length

% identity

113

83



```
(AC006081) putative 26S Protease Subunit 4 [Arabidopsis
NCBI Description
                  thaliana]
                  230895
Seq. No.
                  LIB3197-012-P1-M1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q267069
                  531
BLAST score
                  2.0e-54
E value
Match length
                  98
                  99
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  230896
Seq. No.
                  LIB3197-012-P1-M1-A5
Seq. ID
                  BLASTX
Method
                  q4580460
NCBI GI
                  162
BLAST score
                  1.0e-11
E value
Match length
                  56
% identity
                  62
                  (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  230897
                  LIB3197-012-P1-M1-A6
Seq. ID
Method
                  BLASTX
                  q172383
NCBI GI
                  304
BLAST score
                  9.0e-28
E value
                  96
Match length
                   60
% identity
NCBI Description (M38723) RNA polymerase III [Saccharomyces cerevisiae]
Seq. No.
                  230898
                  LIB3197-012-P1-M1-B10
Seq. ID
                  BLASTX
Method
                  q4098521
NCBI GI
BLAST score
                   634
                   2.0e-66
E value
                  131
Match length
                   91
% identity
                  (U79160) HMG-CoA synthase [Arabidopsis thaliana]
NCBI Description
                   >gi 4098523 (U79161) HMG-CoA synthase [Arabidopsis
                   thaliana]
Seq. No.
                   230899
                  LIB3197-012-P1-M1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1351014
BLAST score
                   474
                   1.0e-47
E value
```



NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi\_968902\_dbj\_BAA07207\_ (D38010) ribosomal protein S8 [Oryza sativa]

Seq. No. 230900

Seq. ID LIB3197-012-P1-M1-B6

Method BLASTX
NCBI GI g3643602
BLAST score 322
E value 7.0e-30
Match length 115
% identity 59

NCBI Description (AC005395) putative tonoplast intrinsic protein

[Arabidopsis thaliana]

Seq. No. 230901

Seq. ID LIB3197-012-P1-M1-C10

Method BLASTX
NCBI GI g3914192
BLAST score 269
E value 1.0e-23
Match length 131
% identity 51

NCBI Description DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE

DEHYDROGENASE COMPLEX PRECURSOR (E2) (PDC-E2)

>gi\_3150120\_emb\_CAA19134\_ (AL023595) dihydrolipoamide acetyltransferase component [Schizosaccharomyces pombe]

Seq. No. 230902

Seq. ID LIB3197-012-P1-M1-C11

Method BLASTX
NCBI GI 94574320
BLAST score 157
E value 2.0e-10
Match length 53
% identity 60

NCBI Description (AF117224) wound-induced protein WI12 [Mesembryanthemum

crystallinum]

Seq. No. 230903

Seq. ID LIB3197-012-P1-M1-C4

Method BLASTX
NCBI GI g120669
BLAST score 578
E value 7.0e-60
Match length 134
% identity 83

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 230904

Seq. ID LIB3197-012-P1-M1-C5

Method BLASTX NCBI GI g3309170 BLAST score 280

E value

Match length

% identity

2.0e-63

138



```
E value
                  6.0e-25
Match length
                  115
                  48
% identity
                  (AF071314) COP9 complex subunit 4 [Mus musculus]
NCBI Description
                  230905
Seq. No.
                  LIB3197-012-P1-M1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4539301
BLAST score
                  211
                  7.0e-17
E value
Match length
                  108
% identity
                  43
                  (AL049480) putative mitochondrial protein [Arabidopsis
NCBI Description
                  thaliana]
                  230906
Seq. No.
Seq. ID
                  LIB3197-012-P1-M1-D11
Method
                  BLASTX
NCBI GI
                  q3063396
BLAST score
                  533
                  1.0e-54
E value
Match length
                  119
% identity
                  84
NCBI Description (AB012947) vcCyP [Vicia faba]
                  230907
Seq. No.
Seq. ID
                  LIB3197-012-P1-M1-D4
Method
                  BLASTX
NCBI GI
                  q4191778
BLAST score
                  320
                  1.0e-29
E value
Match length
                  105
% identity
                  63
                  (AC005917) putative nucleosome assembly protein I
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  230908
                  LIB3197-012-P1-M1-D5
Seq. ID
Method
                  BLASTX
                  g2909781
NCBI GI
BLAST score
                  549
E value
                  2.0e-56
                  139
Match length
% identity
                  78
NCBI Description (AF020288) MgATP-energized glutathione S-conjugate pump
                   [Arabidopsis thaliana]
                  230909
Seq. No.
                  LIB3197-012-P1-M1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3915866
BLAST score
                  608
```

NCBI Description GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)

33183





## >gi\_2995455\_emb\_CAA62901\_ (X91787) tRNA-glutamine synthetase [Lupinus luteus]

```
Seq. No.
                  230910
Seq. ID
                  LIB3197-012-P1-M1-E4
Method
                  BLASTX
NCBI GI
                  g2062167
BLAST score
                  206
E value
                  2.0e-16
                  78
Match length
% identity
                  51
                  (ACO01645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  230911
                  LIB3197-012-P1-M1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3493172
BLAST score
                  515
E value
                  1.0e-52
Match length
                  111
                  91
% identity
NCBI Description (U89609) fiber annexin [Gossypium hirsutum]
Seq. No.
                  230912
                  LIB3197-012-P1-M1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4469023
BLAST score
                  551
E value
                  1.0e-56
Match length
                  124
% identity
                  84
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
                  230913
Seq. No.
Seq. ID
                  LIB3197-012-P1-M1-F11
Method
                  BLASTX
NCBI GI
                  g2104219
BLAST score
                  743
E value
                  3.0e-79
Match length
                  144
% identity
                  100
NCBI Description (D21853) KIAA0111 [Homo sapiens]
Seq. No.
                  230914
                  LIB3197-012-P1-M1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076627
                  330
BLAST score
E value
                  8.0e-31
Match length
                  110
% identity
                  63
```

Seq. No. 230915

NCBI Description

[Nicotiana tabacum]

inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco

>gi\_790479\_emb\_CAA58701\_ (X83730) inorganic pyrophosphatase



65

NCBI Description (D64004) NifS [Synechocystis sp.]

% identity

```
Seq. ID
                  LIB3197-012-P1-M1-F3
Method
                  BLASTX
NCBI GI
                  g71532
BLAST score
                  677
E value
                  2.0e-71
Match length
                  138
                  99
% identity
NCBI Description
                  keratin, type II cytoskeletal - human (fragment)
                  >qi 34069 emb CAA24760 (V01516) keratin [Homo sapiens]
                  >gi 386847 (J00269) keratin [Homo sapiens]
                  230916
Seq. No.
Seq. ID
                  LIB3197-012-P1-M1-F5
                  BLASTX
Method
NCBI GI
                  q267069
BLAST score
                  566
E value
                  2.0e-58
                  105
Match length
% identity
                  99
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >qi 320183 pir JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >qi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  230917
Seq. No.
Seq. ID
                  LIB3197-012-P1-M1-F7
                  BLASTX
Method
NCBI GI
                  q1814424
BLAST score
                  184
E value
                  4.0e-14
Match length
                  47
% identity
                  83
                  (U85254) homeodomain protein AHDP [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  230918
                  LIB3197-012-P1-M1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267069
                  531
BLAST score
                  2.0e-54
E value
                  98
Match length
                  99
% identity
NCBI Description
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                  230919
                  LIB3197-012-P1-M1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1001708
BLAST score
                  273
E value
                  4.0e-24
Match length
                  85
```



230920

LIB3197-012-P1-M1-G10

Seq. No.

```
Seq. ID
Method
                  BLASTX
                  q4204260
NCBI GI
                  164
BLAST score
                  2.0e-11
E value
Match length
                  51
                  59
% identity
                  (AC005223) 25568 [Arabidopsis thaliana]
NCBI Description
                  230921
Seq. No.
                  LIB3197-012-P1-M1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1495273
BLAST score
                  546
                  4.0e-56
E value
                  124
Match length
% identity
                  84
                  (Z50752) sugar transporter [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  230922
                  LIB3197-012-P1-M1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3702641
BLAST score
                  214
                  3.0e-17
E value
Match length
                  88
% identity
                   44
                  (AL031825) similar to human 75k autoantigen
NCBI Description
                   [Schizosaccharomyces pombe]
                  230923
Seq. No.
                  LIB3197-012-P1-M1-G5
Seq. ID
Method
                  BLASTX
                   g3660467
NCBI GI
                   398
BLAST score
                   9.0e-39
E value
Match length
                   90
                   88
% identity
                  (AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   230924
                  LIB3197-012-P1-M1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2642157
BLAST score
                   267
E value
                   2.0e-23
Match length
                   76
% identity
                   65
NCBI Description (AC003000) ankyrin-like protein [Arabidopsis thaliana]
                   230925
Seq. No.
Seq. ID
                   LIB3197-012-P1-M1-H1
                   BLASTX
Method
NCBI GI
                   g2833386
BLAST score
                   537
```



E value 4.0e-55 Match length 128 % identity 85

NCBI Description RIBULOSE-PHOSPHATE 3-EPIMERASE PRECURSOR

(PENTOSE-5-PHOSPHATE 3-EPIMERASE) (PPE) (RPE) (R5P3E) >gi 2129493 pir S62724 ribulose-phosphate 3-epimerase (EC

5.1.3.1) precursor - spinach >gi\_1162980 (L42328) ribulose-5-phosphate 3-epimerase [Spinacia oleracea] >gi\_3264788 (AF070941) ribulose-phosphate 3-epimerase

[Spinacia oleracea] >gi\_1587969\_prf\_\_2207382A

D-ribulose-5-phosphate 3-epimerase [Sorghum bicolor]

Seq. No. 230926

Seq. ID LIB3197-012-P1-M1-H11

Method BLASTX
NCBI GI g1255951
BLAST score 598
E value 3.0e-62
Match length 128
% identity 83

NCBI Description (X96932) PS60 [Nicotiana tabacum]

Seq. No. 230927

Seq. ID LIB3197-012-P1-M1-H3

Method BLASTX
NCBI GI g1168410
BLAST score 574
E value 2.0e-59
Match length 135
% identity 83

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 2

>gi\_2118267\_pir\_\_S58167 fructose-bisphosphate aldolase (EC
4.1.2.13) - garden pea >gi\_927505\_emb\_CAA61947\_ (X89829)

fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No. 230928

Seq. ID LIB3197-012-P1-M1-H4

Method BLASTX
NCBI GI g629602
BLAST score 182
E value 2.0e-13
Match length 57
% identity 65

NCBI Description probable imbibition protein - wild cabbage

>gi 488787 emb CAA55893 (X79330) putative imbibition

protein [Brassica oleracea]

Seq. No. 230929

Seq. ID LIB3197-012-P1-M1-H5

Method BLASTX
NCBI GI g3738339
BLAST score 627
E value 1.0e-65
Match length 139
% identity 85

NCBI Description (AC005170) putative kinase [Arabidopsis thaliana]



230930 Seq. No. LIB3197-012-P1-M1-H6 Seq. ID BLASTX Method NCBI GI q1066859 426 BLAST score E value 4.0e-42Match length 121 67 % identity (L49020) acetyl-CoA carboxylase [Glycine max] NCBI Description Seq. No. 230931 LIB3197-012-P1-M1-H9 Seq. ID Method BLASTX NCBI GI g3451075 BLAST score 613 E value 5.0e-64 Match length 137 % identity 82 (AL031326) putative protein [Arabidopsis thaliana] NCBI Description 230932 Seq. No. LIB3197-013-P1-M1-A1 Seq. ID Method BLASTX NCBI GI g3335226 255 BLAST score E value 3.0e-22 Match length 53 % identity 18 NCBI Description (AF077374) small proline-rich protein [Homo sapiens] 230933 Seq. No. LIB3197-013-P1-M1-A11 Seq. ID Method BLASTX NCBI GI q1731146 291 BLAST score E value 3.0e-26 Match length 82 % identity 62 NCBI Description HYPOTHETICAL 42.1 KD PROTEIN ZK1307.9 IN CHROMOSOME III >gi\_3881615\_emb\_CAA87435\_ (Z47358) similar to YJU2 protein [Caenorhabditis elegans] 230934 Seq. No. LIB3197-013-P1-M1-A2 Seq. ID Method BLASTX NCBI GI q4105472 BLAST score 151 E value 2.0e-12 Match length 122 49 % identity NCBI Description (AF046059) cytokine receptor related protein 4 [Homo

sapiens]

Seq. No. 230935

Seq. ID LIB3197-013-P1-M1-A4

Method BLASTX NCBI GI g3582436



```
201
BLAST score
                   1.0e-15
E value
Match length
                   69
                   61
% identity
                  (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]
NCBI Description
                  230936
Seq. No.
                  LIB3197-013-P1-M1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3024516
BLAST score
                   628
                   9.0e-66
E value
                  124
Match length
                   98
% identity
                  RAS-RELATED PROTEIN RAB11C >gi_2160157 (AC000132) Strong
NCBI Description
                   similarity to A. thaliana ara-\overline{2} (gb_ATHARA2). ESTs
                   gb ATTS2483,gb ATTS2484,gb AA042159 come from this gene.
                   [Arabidopsis thaliana] >gi_2231303 (U74669) ras-related
                   small GTPase [Arabidopsis thaliana]
                   230937
Seq. No.
                  LIB3197-013-P1-M1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1762144
                   349
BLAST score
                   6.0e-33
E value
Match length
                   123
% identity
                   59
                  (U48435) putative cytochrome P450 [Solanum chacoense]
NCBI Description
                   230938
Seq. No.
                   LIB3197-013-P1-M1-B2
Seq. ID
Method
                   BLASTX
                   g3599491
NCBI GI
                   478
BLAST score
                   3.0e-48
E value
Match length
                   123
% identity
                   72
                  (AF085149) putative aminotransferase [Capsicum chinense]
NCBI Description
                   230939
Seq. No.
Seq. ID
                   LIB3197-013-P1-M1-B3
Method
                   BLASTX
NCBI GI
                   g2384671
                   361
BLAST score
                   2.0e-34
E value
Match length
                   88
% identity
                   82
NCBI Description
                   (AF012657) putative potassium transporter AtKT2p
                   [Arabidopsis thaliana]
```

Seq. No. 230940

Seq. ID LIB3197-013-P1-M1-B5

Method BLASTX
NCBI GI g533084
BLAST score 544
E value 2.0e-65



```
Match length
                  146
                  86
% identity
                  (U07597) delta-9 stearoyl-acyl carrier protein desaturase
NCBI Description
                  precursor [Thunbergia alata]
Seq. No.
                  230941
                  LIB3197-013-P1-M1-C11
Seq. ID
                  BLASTX
Method
                  g2827039
NCBI GI
BLAST score
                  344
E value
                  1.0e-32
                  92
Match length
                  72
% identity
                  (AF008444) chloroplast processing enzyme [Arabidopsis
NCBI Description
                  thaliana]
                  230942
Seq. No.
                  LIB3197-013-P1-M1-C2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1345785
BLAST score
                  704
                  1.0e-74
E value
Match length
                  142
                  96
% identity
                  CHALCONE SYNTHASE 1 (NARINGENIN-CHALCONE SYNTHASE 1)
NCBI Description
                  >gi 567935 dbj BAA05640 (D26593) chalcone synthase
                  [Camellia sinensis]
                  230943
Seq. No.
                  LIB3197-013-P1-M1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267069
                  579
BLAST score
                  6.0e-60
E value
                  118
Match length
                  90
% identity
NCBI Description
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  230944
Seq. No.
                  LIB3197-013-P1-M1-D4
Seq. ID
Method
                  BLASTX
                  g1173027
NCBI GI
                  181
BLAST score
                  3.0e-13
E value
Match length
                  48
                  77
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L31 >gi 915313 (U23784) ribosomal
                  protein L31 [Nicotiana glutinosa]
```

Seq. No. 230945 LIB3197-013-P1-M1-E1 Seq. ID

Method BLASTX NCBI GI g2980794

BLAST score 240



E value

1.0e-34

```
Match length
                  104
                  69
% identity
                  (AL022197) myb - like protein [Arabidopsis thaliana]
NCBI Description
                  230946
Seq. No.
                  LIB3197-013-P1-M1-E2
Seq. ID
                  BLASTX
Method
                  g2129578
NCBI GI
BLAST score
                  248
                  4.0e-21
E value
                  102
Match length
                  55
% identity
                  dTDP-glucose 4-6-dehydratases homolog - Arabidopsis
NCBI Description
                  thaliana >gi 928932_emb_CAA89205_ (Z49239) homolog of
                  dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana]
                  >gi_1585435_prf__2124427B diamide resistance gene
                  [Arabidopsis thaliana]
                  230947
Seq. No.
                  LIB3197-013-P1-M1-F3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g267069
                  422
BLAST score
                  2.0e-61
E value
Match length
                  118
                  97
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  230948
Seq. No.
                  LIB3197-013-P1-M1-G1
Seq. ID
                  BLASTX
Method
                  g2244866
NCBI GI
BLAST score
                  251
E value
                  4.0e-25
                  99
Match length
% identity
                  54
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
                  230949
Seq. No.
                  LIB3197-013-P1-M1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2982259
BLAST score
                  556
E value
                   3.0e-57
Match length
                  128
% identity
                  (AF051212) probable 60s ribosomal protein L13a [Picea
NCBI Description
                  mariana]
Seq. No.
                   230950
                  LIB3197-013-P1-M1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454012
```



```
BLAST score
                  217
E value
                  1.0e-17
                  83
Match length
% identity
                  55
                  (AL035396) Pollen-specific protein precursor like
NCBI Description
                  [Arabidopsis thaliana]
                  230951
Seq. No.
                  LIB3197-013-P1-M1-G9
Seq. ID
                  BLASTX
Method
                  g3851636
NCBI GI
BLAST score
                  315
                  3.0e-29
E value
                  77
Match length
                  77
% identity
                  (AF098519) unknown [Avicennia marina] >gi_4128206
NCBI Description
                  (AF056316) 40S ribosome protein S7 [Avicennia marina]
                  230952
Seq. No.
                  LIB3197-013-P1-M1-H10
Seq. ID
                  BLASTX
Method
                  g2501432
NCBI GI
                  237
BLAST score
                  4.0e-20
E value
                  71
Match length
                  69
% identity
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_2146981_pir__JC4894
                  ubiquitin-conjugating enzyme (EC 6.3.2.-) E2 - human
                  >gi_1181558_dbj_BAA11675_ (D83004) ubiquitin-conjugating
                  enzyme E2 UbcH-ben [Homo sapiens]
                  >gi 4507793 ref NP 003339.1 pUBE2N ubiquitin-conjugating
                  enzyme E2N (homologous to yeast UBC13)
                  230953
Seq. No.
                  LIB3197-013-P1-M1-H2
Seq. ID
Method
                  BLASTX
                  g2853081
NCBI GI
                  366
BLAST score
                  5.0e-35
E value
Match length
                  83
                  83
% identity
                  (AL021768) ATP binding protein - like [Arabidopsis
NCBI Description
                  thaliana]
                  230954
Seq. No.
Seq. ID
                  LIB3197-013-P1-M1-H3
Method
                  BLASTX
NCBI GI
                  q3914449
```

Method BLASTX
NCBI GI g391444
BLAST score 614
E value 5.0e-64
Match length 141
% identity 87

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi 3172331 (AF041258) 26S proteasome subunit 7 [Prunus

persica]



```
230955
Seq. No.
Seq. ID
                  LIB3197-013-P1-M1-H9
Method
                  BLASTX
NCBI GI
                  q3860247
BLAST score
                  556
                  3.0e-57
E value
                  116
Match length
% identity
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                  230956
Seq. No.
                  LIB3197-014-P1-M1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1362086
BLAST score
                  429
                  2.0e-42
E value
                  115
Match length
                  75
% identity
NCBI Description
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919 pir S65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                  [Catharanthus roseus]
Seq. No.
                  230957
                  LIB3197-014-P1-M1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1362086
BLAST score
                  408
                  4.0e-40
E value
                  105
Match length
                  77
% identity
                  5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919 pir S65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                   [Catharanthus roseus]
Seq. No.
                  230958
Seq. ID
                  LIB3197-014-P1-M1-A3
Method
                  BLASTX
NCBI GI
                  g3176874
BLAST score
                  182
E value
                  1.0e-13
                  58
Match length
% identity
```

NCBI Description (AF065639) cucumisin-like serine protease [Arabidopsis

thaliana]

Seq. No. 230959

Seq. ID LIB3197-014-P1-M1-C11

Method BLASTX NCBI GI g2738949



BLAST score 481
E value 1.0e-48
Match length 100
% identity 90
NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x ananassa]

Seq. No. 230960
Seq. ID LIB3197-014-P1-M1-C12

Method BLASTX
NCBI GI g2501578
BLAST score 165
E value 2.0e-11
Match length 55
% identity 64

NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi 2129913 pir S60047

ethylene-responsive protein 1 - Para rubber tree

>gi 1209317 (M88254) ethylene-inducible protein [Hevea

brasiliensis]

Seq. No. 230961

Seq. ID LIB3197-014-P1-M1-C2

Method BLASTX
NCBI GI g3023857
BLAST score 311
E value 1.0e-39
Match length 105
% identity 41

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE

PROTEIN >gi\_629591\_pir\_\_S48839 guanine nucleotide

regulatory protein - rape >gi\_563335\_emb\_CAA83924\_ (Z33643) guanine nucleotide regulatory protein [Brassica napus]

Seq. No. 230962

Seq. ID LIB3197-014-P1-M1-C6

Method BLASTX
NCBI GI 94049341
BLAST score 209
E value 6.0e-30
Match length 100
% identity 75

NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 230963

Seq. ID LIB3197-014-P1-M1-D1

Method BLASTX
NCBI GI g1345971
BLAST score 304
E value 7.0e-28
Match length 118
% identity 52

NCBI Description OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR

>gi\_541947\_pir\_\_JQ2339 omega-3 fatty acid desaturase (EC
1.14.99.-) GMD - soybean >gi\_408792 (L22965) omega-3 fatty

acid desaturase [Glycine soja]

Seq. No. 230964



```
LIB3197-014-P1-M1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1724102
BLAST score
                  418
E value
                  3.0e-41
Match length
                  99
% identity
                  84
                  (U79766) S-adenosyl-L-homocystein hydrolase; SAH
NCBI Description
                   [Mesembryanthemum crystallinum]
Seq. No.
                  230965
                  LIB3197-014-P1-M1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2982262
BLAST score
                  197
E value
                  3.0e-15
Match length
                  108
                  44
% identity
NCBI Description
                  (AF051214) probable glutathione S-transferase [Picea
                  mariana]
                  230966
Seq. No.
Seq. ID
                  LIB3197-014-P1-M1-D6
Method
                  BLASTX
NCBI GI
                  g2982466
BLAST score
                  145
E value
                  3.0e-09
Match length
                  49
% identity
NCBI Description (AL022223) putative protein [Arabidopsis thaliana]
                  230967
Seq. No.
Seq. ID
                  LIB3197-014-P1-M1-E1
                  BLASTX
Method
NCBI GI
                  g2160156
BLAST score
                  496
                  2.0e-50
E value
Match length
                  113
                  81
% identity
                 (AC000132) Strong similarity to S. pombe leucyl-tRNA
NCBI Description
                  synthetase (gb_Z73100). [Arabidopsis thaliana]
                  230968
Seq. No.
                  LIB3197-014-P1-M1-E2
Seq. ID
Method
                  {\tt BLASTX}
NCBI GI
                  g2811278
BLAST score
                  382
                  2.0e-37
E value
                  77
Match length
                   88
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
                   230969
Seq. No.
Seq. ID
                  LIB3197-014-P1-M1-F1
Method
                  BLASTX
```

33195

g1169009

323

NCBI GI

BLAST score



```
4.0e-30
E value
Match length
                   118
                   51
% identity
                   CAFFEIC ACID 3-O-METHYLTRANSFERASE
NCBI Description
                   (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                   3-O-METHYLTRANSFERASE) (COMT) >gi_542009_pir__S40146 catechol O-methyltransferase (EC 2.1.1.6) - cider tree
                   >gi_437777_emb_CAA52814_ (X74814) 0-Methyltransferase
                   [Eucalyptus gunnii]
                   230970
Seq. No.
                   LIB3197-014-P1-M1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1888485
BLAST score
                   252
                   3.0e-23
E value
                   77
Match length
                   73
% identity
NCBI Description (Y11749) dihydroflavonol 4-reductase [Vitis vinifera]
                   230971
Seq. No.
                   LIB3197-014-P1-M1-G11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2739168
BLAST score
                   217
                   1.0e-17
E value
Match length
                   76
                   57
% identity
                  (AF032386) aldose-1-epimerase-like protein [Nicotiana
NCBI Description
                   tabacum]
                   230972
Seq. No.
                   LIB3197-014-P1-M1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q136107
BLAST score
                   153
E value
                    3.0e-10
                   87
Match length
                    31
% identity
NCBI Description TRIPEPTIDYL-PEPTIDASE II (TPP II) (TRIPEPTIDYL
                   AMINOPEPTIDASE) >gi 1082875 pir S54376
                   tripeptidyl-peptidase II (EC 3.4.14.10) - human >gi_339880
                    (M73047) tripeptidyl peptidase II [Homo sapiens]
                   >gi 4507657_ref_NP_003282.1_pTPP2_ tripeptidyl peptidase II
                    230973
Seq. No.
Seq. ID
                    LIB3197-014-P1-M1-H1
Method
                    BLASTX
NCBI GI
                    g729470
BLAST score
                    183
E value
                    1.0e-13
Match length
                    83
                    49
% identity
NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR -
```

(NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)

>gi\_542089\_pir\_\_JQ2272 formate dehydrogenase (EC 1.2.1.2)
precursor, mitochondrial - potato >gi 297798\_emb\_CAA79702\_



(Z21493) mitochondrial formate dehydrogenase precursor [Solanum tuberosum]

230974 Seq. No. LIB3197-014-P1-M1-H10 Seq. ID BLASTX Method NCBI GI q2832625 273 BLAST score 2.0e-24 E value

101 Match length 57 % identity

(AL021711) putative protein [Arabidopsis thaliana] NCBI Description

230975 Seq. No.

Seq. ID LIB3197-014-P1-M1-H2

Method BLASTX g3913002 NCBI GI BLAST score 110 1.0e-08 E value Match length 62 56 % identity

FLORAL HOMEOTIC PROTEIN AGL9 HOMOLOG (TM5) NCBI Description

>gi 629674 pir\_\_S23728 TDR5 protein - tomato

>gi 19358 emb CAA43010 (X60480) TDR5 [Lycopersicon esculentum] >gi 19384 emb CAA43170 (X60758) TDR5

[Lycopersicon esculentum]

Seq. No. 230976

LIB3197-015-P1-M1-A10 Seq. ID

BLASTX Method g3152594 NCBI GI BLAST score 370 8.0e-36 E value 87 Match length

11 % identity

(AC002986) Contains repeats similar to RECA protein NCBI Description

gb L26100 from Acinetobacter calcoaceticus. [Arabidopsis

thaliana]

230977 Seq. No.

LIB3197-015-P1-M1-A3 Seq. ID

Method BLASTX NCBI GI g1747296 BLAST score 343 2.0e-32 E value Match length 95 68 % identity

(D45384) vacuolar H+-pyrophosphatase [Oryza sativa] NCBI Description

>gi 3298476 dbj\_BAA31524\_ (AB012766) ovp2 [Oryza sativa]

230978 Seq. No.

Seq. ID LIB3197-015-P1-M1-A6

Method BLASTX NCBI GI g1362107 BLAST score 218 E value 8.0e-18 Match length 44



% identity 95 NCBI Description GUT8-2a protein - common tobacco 230979 Seq. No. LIB3197-015-P1-M1-B1 Seq. ID Method BLASTX NCBI GI g2262164 329 BLAST score 1.0e-30 E value 105 Match length 65 % identity (AC002329) putative obtusifoliol 14-alpha demethylase NCBI Description [Arabidopsis thaliana] Seq. No. 230980 LIB3197-015-P1-M1-B2 Seq. ID Method BLASTX NCBI GI g1703108 BLAST score 732 7.0e-78E value 145 Match length 98 % identity ACTIN 2/7 >gi\_2129525\_pir\_\_S71210 actin 2 - Arabidopsis thaliana >gi\_2129528\_pir\_\_S68107 actin 7 - Arabidopsis NCBI Description thaliana >gi\_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi\_1943863 (U27811) actin7 [Arabidopsis thaliana] 230981 Seq. No. LIB3197-015-P1-M1-B3 Seq. ID BLASTX Method NCBI GI g116054 469 BLAST score 3.0e-47E value 102 Match length 90 % identity NCBI Description CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK) >gi\_280393\_pir\_\_A43713 calcium-dependent protein kinase (EC 2.7.1.-) - soybean >gi 169931 (M64987) Glycine max calcium dependent protein kinase mRNA. [Glycine max] 230982 Seq. No. LIB3197-015-P1-M1-B6 Seq. ID Method BLASTX NCBI GI g4262151 BLAST score 403 E value 2.0e-39 Match length 116 % identity 66 (AC005275) putative receptor kinase [Arabidopsis thaliana] NCBI Description

Seq. No. 230983

Seq. ID LIB3197-015-P1-M1-B7

Method BLASTX
NCBI GI g2129698
BLAST score 225
E value 2.0e-18



Match length 54 % identity 74

NCBI Description protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana

>gi\_1054633\_emb\_CAA63387\_ (X92728) protein kinase

[Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3197-015-P1-M1-B8

230984

Method BLASTX
NCBI GI g1061040
BLAST score 617
E value 2.0e-64
Match length 130
% identity 85

NCBI Description (X89867) sterol-C-methyltransferase [Arabidopsis thaliana]

>gi\_1587694 prf 2207220A sterol C-methyltransferase

[Arabidopsis thaliana]

Seq. No. 230985

Seq. ID LIB3197-015-P1-M1-B9

Method BLASTX
NCBI GI g3694872
BLAST score 527
E value 7.0e-54
Match length 124
% identity 81

NCBI Description (AF092547) profilin [Ricinus communis]

Seq. No. 230986

Seq. ID LIB3197-015-P1-M1-C1

Method BLASTX
NCBI GI g1666228
BLAST score 391
E value 3.0e-38
Match length 75
% identity 99

NCBI Description (U76190) actin [Pisum sativum] >gi\_1666230 (U76191) actin

[Pisum sativum] >gi\_1724137 (U81046) actin [Pisum sativum]

>gi 1724139 (U81047) actin [Pisum sativum]

Seq. No. 230987

Seq. ID LIB3197-015-P1-M1-C2

Method BLASTX
NCBI GI g3914501
BLAST score 531
E value 2.0e-54
Match length 120
% identity 86

NCBI Description ASPARTATE CARBAMOYLTRANSFERASE 3 PRECURSOR (ASPARTATE

TRANSCARBAMYLASE 3) (ATCASE 3) >gi\_609344 (U05293)

aspartate carbamoyltransferase [Pisum sativum]

Seq. No. 230988

Seq. ID LIB3197-015-P1-M1-C4

Method BLASTX NCBI GI g267069 BLAST score 362

E value Match length

% identity

122

58



```
8.0e-35
E value
                  69
Match length
                  96
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  230989
Seq. No.
                  LIB3197-015-P1-M1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4098128
                   393
BLAST score
                   2.0e-38
E value
Match length
                   91
% identity
                   85
                  (U73588) sucrose synthase [Gossypium hirsutum]
NCBI Description
                   230990
Seq. No.
                   LIB3197-015-P1-M1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1944216
BLAST score
                   379
                   8.0e-37
E value
Match length
                   82
% identity
                   87
                  (D84246) alcohol dehydrogenase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   230991
                   LIB3197-015-P1-M1-D4
Seq. ID
                   BLASTX
Method
                   g1724102
NCBI GI
BLAST score
                   209
                   3.0e-17
E value
                   45
Match length
                   91
% identity
                  (U79766) S-adenosyl-L-homocystein hydrolase; SAH
NCBI Description
                   [Mesembryanthemum crystallinum]
                   230992
Seq. No.
                   LIB3197-015-P1-M1-E11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3097321
BLAST score
                   243
                   1.0e-20
E value
                   114
Match length
                   46
% identity
NCBI Description (AB013289) Bd 30K [Glycine max]
                   230993
Seq. No.
Seq. ID
                   LIB3197-015-P1-M1-F11
Method
                   BLASTX
NCBI GI
                   q4263711
BLAST score
                   341
                   4.0e-32
```



```
(AC006223) putative CCR4-associated transcription factor
NCBI Description
                  [Arabidopsis thaliana]
                  230994
Seq. No.
                  LIB3197-015-P1-M1-F3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3212871
BLAST score
                  169
                  6.0e-12
E value
                  90
Match length
                  48
% identity
                  (AC004005) putative translation initiation factor
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  230995
                  LIB3197-015-P1-M1-F6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3757514
                  589
BLAST score
                  4.0e-61
E value
Match length
                  128
% identity
                  88
NCBI Description
                  (AC005167) putative plasma membrane intrinsic protein
                  [Arabidopsis thaliana]
                  230996
Seq. No.
                  LIB3197-015-P1-M1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                  261
                  6.0e-23
E value
                  71
Match length
                  77
% identity
                  (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                  230997
Seq. No.
Seq. ID
                  LIB3197-015-P1-M1-G1
Method
                  BLASTX
NCBI GI
                  q346685
BLAST score
                  353
E value
                  8.0e-34
Match length
                  88
% identity
                  77
NCBI Description developmentally-regulated GTP-binding protein - mouse
                  230998
Seq. No.
Seq. ID
                  LIB3197-015-P1-M1-G10
Method
                  BLASTX
NCBI GI
                  q2392025
BLAST score
                  211
                  8.0e-17
E value
Match length
                  45
% identity
                  84
NCBI Description
                  (D88420) stromal ascorbate peroxidase [Cucurbita sp.]
```

33201

230999

LIB3197-015-P1-M1-G11

Seq. No. Seq. ID

% identity



```
Method
                  BLASTX
NCBI GI
                  q4263519
BLAST score
                  463
E value
                  2.0e-46
Match length
                  96
                  93
% identity
NCBI Description
                  (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis
                  thaliana]
                  231000
Seq. No.
Seq. ID
                  LIB3197-015-P1-M1-G7
Method
                  BLASTX
                  q4508073
NCBI GI
                  463
BLAST score
E value
                  2.0e-46
Match length
                  141
                   62
% identity
NCBI Description
                 (AC005882) 43220 [Arabidopsis thaliana]
Seq. No.
                  231001
                  LIB3197-015-P1-M1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829911
BLAST score
                   375
                   3.0e - 36
E value
Match length
                  103
                   30
% identity
NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]
                   231002
Seq. No.
Seq. ID
                  LIB3197-015-P1-M1-H10
Method
                  BLASTX
NCBI GI
                   g4056502
BLAST score
                   338
E value
                   1.0e-33
Match length
                  95
                  80
% identity
NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
                   231003
Seq. No.
                  LIB3197-015-P1-M1-H11
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3097321
BLAST score
                   190
E value
                   2.0e-14
Match length
                  83
% identity
                   45
NCBI Description (AB013289) Bd 30K [Glycine max]
                   231004
Seq. No.
                   LIB3197-015-P1-M1-H3
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3757514
BLAST score
                   252
E value
                   8.0e-22
Match length
                   64
```



```
(AC005167) putative plasma membrane intrinsic protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   231005
                   LIB3197-015-P1-M1-H4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2828291
BLAST score
                   393
                   4.0e-38
E value
                   115
Match length
                   72
% identity
NCBI Description
                   (AL021687) putative protein [Arabidopsis thaliana]
                   231006
Seq. No.
                   LIB3197-015-P1-M1-H8
Seq. ID
Method
                   BLASTX
                   q3757514
NCBI GI
BLAST score
                   220
                   5.0e-18
E value
                   89
Match length
                   57
% identity
                   (AC005167) putative plasma membrane intrinsic protein
NCBI Description
                   [Arabidopsis thaliana]
                   231007
Seq. No.
                   LIB3197-015-P1-M1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2887459
                   511
BLAST score
                   3.0e-52
E value
                   102
Match length
                   99
% identity
                   (AB010922) actin [Cucumis sativus]
NCBI Description
                   231008
Seq. No.
                   LIB3197-016-P1-M1-A10
Seq. ID
Method
                   BLASTX
                   g3193306
NCBI GI
BLAST score
                   334
                   3.0e - 31
E value
Match length
                   132
                   56
 % identity
NCBI Description
                   (AF069300) contains similarity to Arabidopsis
                   membrane-associated salt-inducible-like protein
                   (GB:AL021637) [Arabidopsis thaliana]
                   231009
 Seq. No.
 Seq. ID
                   LIB3197-016-P1-M1-A11
Method
                   BLASTX
NCBI GI
                   a267069
BLAST score
                   466
E value
                   7.0e-47
Match length
                   86
                   99
 % identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
```

33203

tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916

Seq. No.

231015



## (M84697) alpha-4 tubulin [Arabidopsis thaliana]

```
Seq. No.
                   231010
Seq. ID
                   LIB3197-016-P1-M1-A12
Method
                   BLASTX
NCBI GI
                   g3560264
BLAST score
                   168
E value
                   1.0e-11
Match length
                   102
                   38
% identity
NCBI Description (AL031535) soll family protein [Schizosaccharomyces pombe]
                   231011
Seq. No.
Seq. ID
                   LIB3197-016-P1-M1-A5
Method
                   BLASTX
NCBI GI
                   g120669
BLAST score
                   592
E value
                   2.0e-61
Match length
                   116
% identity
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                   231012
Seq. ID
                   LIB3197-016-P1-M1-A6
Method
                   BLASTX
NCBI GI
                   g2739387
BLAST score
                   147
E value
                   2.0e-09
Match length
                   114
% identity
NCBI Description (AC002505) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   231013
Seq. ID
                   LIB3197-016-P1-M1-A7
Method
                   BLASTX
NCBI GI
                   g2811278
BLAST score
                   420
                   2.0e-41
E value
                   84
Match length
                   94
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                   231014
Seq. ID
                   LIB3197-016-P1-M1-B11
Method
                   BLASTX
NCBI GI
                   g3953471
BLAST score
                   371
                   6.0e-36
E value
Match length
                   92
% identity
NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]
```



```
LIB3197-016-P1-M1-B12
 Seq. ID
 Method
                   BLASTX
                   q3540182
 NCBI GI
 BLAST score
                   162
 E value
                   1.0e-18
                   101
 Match length
                    58
 % identity
                   (AC004122) Unknown protein [Arabidopsis thaliana]
 NCBI Description
                   231016
 Seq. No.
                   LIB3197-016-P1-M1-B2
Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g3287696
                   159
 BLAST score
                   8.0e-14
 E value
 Match length
                   50
                    76
 % identity
                    (AC003979) Strong similarity to phosphoribosylanthranilate
 NCBI Description
                    transferase gb D86180 from Pisum sativum. This ORF may be
                   part of a larger gene that lies in the overlapping region.
                    [Arabidopsis thaliana]
                    231017
 Seq. No.
                   LIB3197-016-P1-M1-B6
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                    g1657382
 BLAST score
                    675
                    3.0e-71
 E value
                    136
 Match length
                    90
 % identity
                   (Y09101) cholinephosphate cytidylyltransferase [Pisum
 NCBI Description
                    sativum]
                    231018
 Seq. No.
                    LIB3197-016-P1-M1-C10
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q4138209
 BLAST score
                    155
                    3.0e-10
 E value
                    67
 Match length
                    42
 % identity
 NCBI Description
                    (AJ223071) serine/threonine kinase protein MSTK2L,long-form
                    [Mus musculus]
 Seq. No.
                    231019
                    LIB3197-016-P1-M1-C4
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3211975
 BLAST score
                    336
                    2.0e-31
 E value
 Match length
                    72
 % identity
                    94
 NCBI Description
                    (AF068195) putative glialblastoma cell
                    differentiation-related protein [Homo sapiens]
```

Seq. No. 231020

Seq. ID LIB3197-016-P1-M1-C6



```
BLASTX
Method
                    g1408471
NCBI GI
                    492
BLAST score
                    9.0e-50
E value
                    113
Match length
                    78
% identity
                    (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                    thaliana] >gi_3851707 (AF102173) actin depolymerizing
                    factor 1 [Arabidopsis thaliana]
                    231021
Seq. No.
                    LIB3197-016-P1-M1-D10
Seq. ID
                    BLASTX
Method
                    g4263695
NCBI GI
BLAST score
                    231
                    3.0e-19
E value
                    126
Match length
% identity
                    11
                    (AC006223) putative myosin II heavy chain [Arabidopsis
NCBI Description
                    thaliana]
                    231022
Seq. No.
                    LIB3197-016-P1-M1-D12
Seq. ID
Method
                    BLASTX
                    g132939
NCBI GI
                    432
BLAST score
                    5.0e-43
E value
Match length
                    99
                    83
% identity
                    60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal
NCBI Description
                    protein L3 (ARP1) - Arabidopsis thaliana >gi_166858
                    (M32654) ribosomal protein [Arabidopsis thaliana]
                    231023
Seq. No.
                    LIB3197-016-P1-M1-D4
Seq. ID
                    BLASTX
Method
NCBI GI
                    g116602
                    186
BLAST score
                    2.0e-14
E value
Match length
                    63
                     68
% identity
NCBI Description COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN]
                     231024
Seq. No.
                    LIB3197-016-P1-M1-E5
Seq. ID
                    BLASTX
Method
NCBI GI
                     g122097
BLAST score
                     296
                     1.0e-29
E value
Match length
                    82
% identity
                     86
NCBI Description HISTONE H4 >gi_103010_pir___S18003 histone H4 - midge (Chironomus thummi thummi) >gi_103052_pir__S09656 histone H4 - fruit fly (Drosophila hydei) >gi_103199_pir__S10098
```

histone H4 - fruit fly (Drosophila melanogaster)
>gi\_542539\_pir\_\_S40437 histone H4 - midge (Chironomus thummi thummi) >gi\_1085859\_pir\_\_B56654 histone H4 -



Tigriopus californicus >gi\_2119026\_pir\_\_B56580 histone H4 -midge (Chironomus thummi thummi) >gi\_7084\_emb\_CAA39772\_
(X56335) histone H4 [Chironomus thummi]
>gi\_7434\_emb\_CAA36806\_ (X52576) histone H4 [Drosophila hydei] >gi\_7440\_emb\_CAA34920\_ (X17072) histone H4
[Drosophila hydei] >gi\_8071\_emb\_CAA32435\_ (X14215) H4
histone [Drosophila melanogaster] >gi\_10616\_emb\_CAA36639\_
(X52393) histone H4 [Tigriopus californicus] >gi\_161896
(M84797) histone H4 [Tigriopus californicus]
>gi\_297562\_emb\_CAA51323\_ (X72803) histone H4 [Chironomus thummi] >gi\_1419478\_emb\_CAA66066\_ (X97436) histone H4
[Drosophila hydei] >gi\_1419480\_emb\_CAA66067\_ (X97437) histone H4 [Drosophila melanogaster]
>gi\_1419482\_emb\_CAA66068\_ (X97438) histone H4 [Drosophila melanogaster] >gi\_1882999\_emb\_CAA62808\_ (X91508) histone H4
[Acrolepiopsis assectella] >gi\_1885324\_emb\_CAA62814\_ (X91514) histone H4 [Myrmica ruginodis]

 Seq. No.
 231025

 Seq. ID
 LIB3197-016-P1-M1-F11

 Method
 BLASTX

 NCBI GI
 g1370190

 BLAST score
 177

 E value
 1.0e-19

E value 1.06
Match length 86
% identity 64

NCBI Description (Z73944) RAB8A [Lotus japonicus]

Seq. No. 231026

Seq. ID LIB3197-016-P1-M1-F4

Method BLASTX
NCBI GI g232024
BLAST score 251
E value 8.0e-22
Match length 81
% identity 64

NCBI Description PROTEIN E6 >gi\_421806\_pir\_A46130 fiber protein - upland cotton >gi\_2129498\_pir\_S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi\_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi\_1000084

(U30505) E6 [Gossypium hirsutum]

Seq. No. 231027

Seq. ID LIB3197-016-P1-M1-F6

Method BLASTX
NCBI GI g2289961
BLAST score 346
E value 1.0e-32
Match length 90
% identity 79

NCBI Description (U82434) AtRAB8 [Arabidopsis thaliana]

Seq. No. 231028

Seq. ID LIB3197-016-P1-M1-G12

Method BLASTX NCBI GI g2062167 BLAST score 348



```
4.0e-33
E value
Match length
                  71
                  89
% identity
                  (ACO01645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                  thaliana]
                  231029
Seq. No.
                  LIB3197-016-P1-M1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263790
BLAST score
                  202
                  4.0e-16
E value
                  70
Match length
% identity
                  59
                  (AC006068) putative ch-TOG protein [Arabidopsis thaliana]
NCBI Description
                  231030
Seq. No.
                  LIB3197-016-P1-M1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1168256
BLAST score
                  210
E value
                  4.0e-17
                  53
Match length
                  70
% identity
                  ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                  (TRANSAMINASE A) >gi_693688 (U15026) aspartate
                  aminotransferase [Arabidopsis thaliana] >gi 3201622
                   (AC004669) aspartate aminotransferase [Arabidopsis
                  thaliana]
                  231031
Seq. No.
Seq. ID
                  LIB3197-016-P1-M1-H5
Method
                  BLASTX
NCBI GI
                  g81811
BLAST score
                  145
E value
                  4.0e-09
Match length
                  31
                  90
% identity
                  ribosomal protein S11 - soybean (fragment) >gi 170054
NCBI Description
                   (M31024) ribosomal protein S11 [Glycine max]
Seq. No.
                  231032
                  LIB3197-016-P1-M1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1168256
BLAST score
                  594
E value
                  9.0e-62
Match length
                  127
% identity
NCBI Description ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR
                   (TRANSAMINASE A) >gi_693688 (U15026) aspartate
                  aminotransferase [Arabidopsis thaliana] >gi 3201622
```

Seq. No. 231033

Seq. ID LIB3197-016-P1-M1-H9

thaliana]

(AC004669) aspartate aminotransferase [Arabidopsis

Method

BLASTX



```
Method
                  BLASTX
                  g2160169
NCBI GI
BLAST score
                  184
                  1.0e-13
E value
Match length
                  73
                  55
% identity
                  (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                  231034
Seq. No.
                  LIB3197-017-P1-M1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1174162
BLAST score
                  593
                  1.0e-61
E value
Match length
                  111
% identity
                  93
                  (U44976) ubiquitin-conjugating enzyme [Arabidopsis
NCBI Description
                  thaliana] >gi 3746915 (AF091106) E2
                  ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
                  231035
Seq. No.
                  LIB3197-017-P1-M1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g125080
BLAST score
                  744
                  3.0e-79
E value
Match length
                  151
% identity
                  99
                  KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK
NCBI Description
                  14) >gi 2144816 pir KRHUE keratin, 50K type I cytoskeletal
                  - human >gi_386848 (J00124) keratin [Homo sapiens]
                  >gi 4504913 ref NP 000517.1 pKRT14 keratin 14
                   (epidermolysis bullosa simplex, Dowling-Meara, Koebner)
Seq. No.
                  231036
                  LIB3197-017-P1-M1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244850
BLAST score
                  190
                  9.0e-22
E value
                  109
Match length
                  64
% identity
NCBI Description
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
                  231037
Seq. No.
                  LIB3197-017-P1-M1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4056479
BLAST score
                  266
                  2.0e-23
E value
                  80
Match length
% identity
                  66
NCBI Description
                  (AC005896) unknown protein [Arabidopsis thaliana]
                  231038
Seq. No.
                  LIB3197-017-P1-M1-B6
Seq. ID
```



```
NCBI GI
                   q2244750
BLAST score
                   611
E value
                   2.0e-64
Match length
                   129
% identity
                   94
NCBI Description
                   (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                   >gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                   [Arabidopsis thaliana]
Seq. No.
                   231039
                   LIB3197-017-P1-M1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2760334
BLAST score
                   413
                   2.0e-40
E value
Match length
                   87
                   83
% identity
NCBI Description (AC002130) F1N21.5 [Arabidopsis thaliana]
Seq. No.
                   231040
Seq. ID
                   LIB3197-017-P1-M1-E12
Method
                   BLASTX
NCBI GI
                   g2154715
BLAST score
                   208
                   7.0e-17
E value
Match length
                   67
% identity
                   69
NCBI Description (Y09418) CDPK-related protein kinase [Arabidopsis thaliana]
                   231041
Seq. No.
Seq. ID
                   LIB3197-017-P1-M1-E5
Method
                   BLASTX
NCBI GI
                   g464621
BLAST score
                   261
                   8.0e-23
E value
Match length
                   96
% identity
                   54
NCBI Description
                  60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir S28586
                   ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
Seq. No.
                   231042
                   LIB3197-017-P1-M1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4337175
BLAST score
                   454
E value
                   2.0e-45
Match length
                   127
% identity
```

NCBI Description (AC006416) ESTs gb T20589, gb T04648, gb AA597906,

gb\_T04111, gb\_R841\(\bar{8}\)0, gb\_R654\(\bar{2}\)8, gb\_T444\(\bar{3}\)9, gb\_T76570, gb\_R90004, gb\_T45020, gb\_T42457, gb\_T20921, gb\_AA042762 and gb\_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No. 231043

Seq. ID LIB3197-017-P1-M1-F12



```
Method
                  BLASTX
                  g2213595
NCBI GI
BLAST score
                  350
                  3.0e-33
E value
Match length
                  109
                  60
% identity
                  (AC000348) T7N9.15 [Arabidopsis thaliana]
NCBI Description
                  231044
Seq. No.
Seq. ID
                  LIB3197-017-P1-M1-F4
                  BLASTX
Method
NCBI GI
                  g82264
BLAST score
                  210
                  1.0e-16
E value
                  43
Match length
                   91
% identity
                  ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
NCBI Description
                   c1 precursor (clone pC(1)8I) - potato (fragment)
                   >qi 498789 emb CAA56109 (X79597) cytochrome c1 [Solanum
                   tuberosum]
                   231045
Seq. No.
Seq. ID
                  LIB3197-017-P1-M1-G10
Method
                  BLASTX
NCBI GI
                   g1495251
BLAST score
                   348
                   3.0e-33
E value
Match length
                   91
% identity
                   70
                  (270314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                   231046
Seq. No.
                   LIB3197-017-P1-M1-G12
Seq. ID
Method
                   BLASTX
                   g1771162
NCBI GI
                   260
BLAST score
                   1.0e-22
E value
Match length
                   118
                   48
% identity
                  (X98930) SBT2 [Lycopersicon esculentum]
NCBI Description
                   >gi 3687307 emb CAA07000_ (AJ006379) subtilisin-like
                   protease [Lycopersicon esculentum]
                   231047
Seq. No.
                   LIB3197-017-P1-M1-G4
Seq. ID
                   BLASTX
Method
                   g2654208
NCBI GI
                   97
BLAST score
                   1.0e-08
E value
Match length
                   40
                   88
% identity
                   (AF035456) heat shock 70 protein [Spinacia oleracea]
NCBI Description
                   >gi 2773050 (AF039083) heat shock 70 protein [Spinacia
                   oleracea]
```

231048

LIB3197-017-P1-M1-G6

Seq. No.

Seq. ID



```
BLASTX
Method
                   q4204300
NCBI GI
                   202
BLAST score
                   9.0e-16
E value
                   79
Match length
                   52
% identity
                   (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   231049
Seq. No.
                   LIB3197-019-Q1-M1-A10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3097321
                   185
BLAST score
                   9.0e-14
E value
                   89
Match length
                   44
% identity
                   (AB013289) Bd 30K [Glycine max]
NCBI Description
                   231050
Seq. No.
                   LIB3197-019-Q1-M1-A11
Seq. ID
Method
                   BLASTX
                   g3097321
NCBI GI
                   191
BLAST score
                   2.0e-14
E value
                   104
Match length
                   38
% identity
NCBI Description
                   (AB013289) Bd 30K [Glycine max]
                   231051
Seq. No.
                   LIB3197-019-Q1-M1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g120669
BLAST score
                   425
E value
                   5.0e-42
                   87
Match length
                   90
% identity
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
                   231052
Seq. No.
                   LIB3197-019-Q1-M1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2829902
BLAST score
                   399
E value
                   5.0e-39
Match length
                   109
                   73
% identity
                   (AC002311) Putative sulphate transporter protein#protein
NCBI Description
                    [Arabidopsis thaliana]
```

Seq. No. 231053

Seq. ID LIB3197-019-Q1-M1-A6

Method BLASTX NCBI GI g4510344



```
BLAST score
                  149
                  1.0e-09
E value
Match length
                  84
% identity
                  42
                  (AC006921) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  231054
Seq. No.
Seq. ID
                  LIB3197-019-Q1-M1-A7
Method
                  BLASTX
NCBI GI
                  g1703115
BLAST score
                  510
                  6.0e-52
E value
Match length
                  93
                  100
% identity
                  ACTIN 3 >gi_2129526_pir__S68112 actin 3 - Arabidopsis
NCBI Description
                  thaliana >gi 1145695 (U39480) actin [Arabidopsis thaliana]
                  >qi 3236244 (AC004684) actin 3 protein [Arabidopsis
                  thaliana]
                  231055
Seq. No.
                  LIB3197-019-Q1-M1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1486472
BLAST score
                   421
                   2.0e-41
E value
                   96
Match length
% identity
                   84
                  (X99853) oxoglutarate malate translocator [Solanum
NCBI Description
                  tuberosum]
Seq. No.
                   231056
                   LIB3197-019-Q1-M1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2811278
BLAST score
                   333
                   4.0e-31
E value
Match length
                   123
% identity
                   78
                  (AF043284) expansin [Gossypium hirsutum]
NCBI Description
Seq. No.
                   231057
                   LIB3197-019-Q1-M1-B2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2832625
                   307
BLAST score
                   2.0e-28
E value
                   69
Match length
                   81
% identity
                  (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
                   231058
Seq. No.
                   LIB3197-019-Q1-M1-B7
Seq. ID
Method
                   BLASTX
                   g1209756
NCBI GI
BLAST score
                   147
```

1.0e-09

54

E value

Match length



```
% identity
                   63
                   (U43629) integral membrane protein [Beta vulgaris]
NCBI Description
                   231059
Seq. No.
                   LIB3197-019-Q1-M1-B8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2244734
                   545
BLAST score
                   4.0e-56
E value
                   121
Match length
                   89
% identity
                   (D88414) actin [Gossypium hirsutum]
NCBI Description
                   231060
Seq. No.
                   LIB3197-019-Q1-M1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3914740
BLAST score
                   190
                   6.0e-15
E value
                   50
Match length
                   76
% identity
                   60S RIBOSOMAL PROTEIN L26 >gi 2160300 dbj BAA18941
NCBI Description
                   (D78495) ribosomal protein [Brassica rapa]
                   231061
Seq. No.
                   LIB3197-019-Q1-M1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2623296
BLAST score
                   141
                   1.0e-08
E value
Match length
                   50
                   58
% identity
NCBI Description
                   (AC002409) hypothetical protein [Arabidopsis thaliana]
                   231062
Seq. No.
                   LIB3197-019-Q1-M1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3924611
                   187
BLAST score
E value
                   4.0e-14
                   123
Match length
                   36
% identity
NCBI Description
                   (AF069442) hypothetical protein [Arabidopsis thaliana]
                   231063
Seq. No.
                   LIB3197-019-Q1-M1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g400384
BLAST score
                   149
E value
                   1.0e-09
Match length
                   104
                   35
% identity
NCBI Description
                   NADH-UBIQUINONE OXIDOREDUCTASE B14 SUBUNIT (COMPLEX I-B14)
                   (CI-B14) >gi_346536_pir__S28245 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B14 - bovine
```

33214

taurus]

>gi 240 emb CAA44896 (X63211) NADH dehydrogenase [Bos

NCBI GI

E value

BLAST score

q4204300

7.0e-15

194



```
231064
Seq. No.
                  LIB3197-019-Q1-M1-C9
Seq. ID
                  BLASTX
Method
                  g2129559
NCBI GI
                  496
BLAST score
                  3.0e-50
E value
                  110
Match length
                  87
% identity
                  cellulase homolog OR16pep - Arabidopsis thaliana
NCBI Description
                  >gi 1022807 (U37702) cellulase [Arabidopsis thaliana]
                  >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana]
                  >gi 3598956 (AF074375) cellulase [Arabidopsis thaliana]
                  >gi 3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN
                  [Arabidopsis thaliana]
Seq. No.
                  231065
Seq. ID
                  LIB3197-019-Q1-M1-D1
Method
                  BLASTX
NCBI GI
                  q4490756
BLAST score
                  339
E value
                  6.0e-32
Match length
                  86
% identity
                  78
                  (AL035708) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  231066
Seq. ID
                  LIB3197-019-Q1-M1-D10
Method
                  BLASTX
NCBI GI
                  q3024017
BLAST score
                  468
                  6.0e-47
E value
Match length
                  99
                  92
% identity
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)
NCBI Description
                   (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation
                  initiation factor eIF-1A [Onobrychis viciifolia]
                  231067
Seq. No.
                  LIB3197-019-Q1-M1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913295
BLAST score
                  704
                  1.0e-74
E value
Match length
                  138
                  91
% identity
NCBI Description
                  CAFFEIC ACID 3-O-METHYLTRANSFERASE
                   (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                  3-O-METHYLTRANSFERASE) (COMT) >gi_602588_emb_CAA58218_
                   (X83217) caffeic O-methyltransferase [Prunus dulcis]
Seq. No.
                  231068
Seq. ID
                  LIB3197-019-Q1-M1-D12
Method
                  BLASTX
```



```
Match length
                  75
% identity
                  52
                  (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  231069
                  LIB3197-019-Q1-M1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q120668
BLAST score
                  531
                  2.0e-54
E value
                  116
Match length
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 82399 pir A24159 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)
                  >gi 167044 (M36650) glyceraldehyde-3-phosphate
                  dehydrogenase [Hordeum vulgare] >gi 225347 prf 1301218A
                  dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var.
                  distichum]
                  231070
Seq. No.
                  LIB3197-019-Q1-M1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3334113
                  192
BLAST score
                  1.0e-14
E value
                  37
Match length
% identity
                  97
NCBI Description
                  ACYL-COA-BINDING PROTEIN (ACBP) >gi 1006831 (U35015)
                  acyl-CoA-binding protein [Gossypium hirsutum]
Seq. No.
                  231071
                  LIB3197-019-Q1-M1-D9
Seq. ID
Method
                  BLASTX
                  g4335864
NCBI GI
BLAST score
                  562
                   4.0e-58
E value
                  116
Match length
% identity
                  85
                  (AF052040) calreticulin [Berberis stolonifera]
NCBI Description
                  231072
Seq. No.
                  LIB3197-019-Q1-M1-E1
Seq. ID
                  BLASTX
Method
                  q88052
NCBI GI
                   290
BLAST score
                   5.0e-35
E value
                   83
Match length
                   95
% identity
                  keratin K5, 58K type II, epidermal (version 2) - human
NCBI Description
                   (fragment)
                   231073
Seq. No.
                  LIB3197-019-Q1-M1-E2
Seq. ID
```

BLASTX

g3236237 274

Method NCBI GI

BLAST score

NCBI Description



```
2.0e-24
E value
Match length
                  90
                  60
% identity
                  (AC004684) putative ribotol dehydrogenase [Arabidopsis
NCBI Description
                  231074
Seq. No.
                  LIB3197-019-Q1-M1-E3
Seq. ID
                  BLASTX
Method
                  g1174600
NCBI GI
                  379
BLAST score
E value
                  1.0e-36
Match length
                  72
                  96
% identity
                  TUBULIN BETA CHAIN >gi_493710_dbj_BAA06382_ (D30717)
NCBI Description
                  beta-tubulin [Oryza sativa]
                  231075
Seq. No.
Seq. ID
                  LIB3197-019-Q1-M1-E4
                  BLASTX
Method
                  q4314378
NCBI GI
                  251
BLAST score
                  1.0e-21
E value
Match length
                  101
                  52
% identity
                  (AC006232) putative lipase [Arabidopsis thaliana]
NCBI Description
                  231076
Seq. No.
Seq. ID
                  LIB3197-019-Q1-M1-E5
Method
                  BLASTX
                  q1587206
NCBI GI
BLAST score
                   443
                   3.0e-44
E value
Match length
                  93
                   95
% identity
NCBI Description T complex protein [Cucumis sativus]
                   231077
Seq. No.
                  LIB3197-019-Q1-M1-E9
Seq. ID
Method .
                  BLASTX
                   g3242728
NCBI GI
                   215
BLAST score
                   3.0e-17
E value
Match length
                   134
% identity
                   36
NCBI Description (AC003040) unknown protein [Arabidopsis thaliana]
                   231078
Seq. No.
                   LIB3197-019-Q1-M1-F1
Seq. ID
                   BLASTX
Method
                   g1362086
NCBI GI
BLAST score
                   458
                   7.0e-46
E value
Match length
                   96
                   91
% identity
                  5-methyltetrahydropteroyltriglutamate--homocysteine
```

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle



>gi 2129919 pir\_\_S65957  $\verb§5-methyltetrahyd \\ \hline \texttt{ropteroyltriglutamate--homocysteine}$ S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi 886471\_emb\_CAA58474\_ (X83499) methionine synthase [Catharanthus roseus] 231079 LIB3197-019-Q1-M1-F10

Seq. ID Method BLASTX NCBI GI g1843527 BLAST score 472 2.0e-47 E value Match length 124 43 % identity

Seq. No.

NCBI Description (U73747) annexin [Gossypium hirsutum]

Seq. No. Seq. ID LIB3197-019-Q1-M1-F12 Method BLASTX NCBI GI g4490737 BLAST score 336 2.0e-31 E value Match length 122

% identity 59 (AL035708) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 231081

Seq. ID LIB3197-019-Q1-M1-F5

231080

Method BLASTX q4521249 NCBI GI 289 BLAST score 4.0e-26 E value Match length 75

73 % identity

(AB013912) DNA helicase [Mus musculus] NCBI Description

231082 Seq. No.

Seq. ID LIB3197-019-Q1-M1-G10

BLASTX Method NCBI GI g1168728 485 BLAST score 6.0e-49E value 114 Match length 82 % identity

CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi\_598071 (L37883) NCBI Description

cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

231083 Seq. No.

LIB3197-019-Q1-M1-G11 Seq. ID

BLASTX Method NCBI GI q585451 BLAST score 264 4.0e-23 E value 91 Match length 58 % identity

NCBI Description MALATE OXIDOREDUCTASE (NAD), MITOCHONDRIAL 62 KD ISOFORM PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME)



(NAD-ME) >gi\_1076667\_pir\_B53318 malate dehydrogenase (decarboxylating) (EC 1.1.1.39) 62K chain precursor, mitochondrial - potato >gi\_438249\_emb\_CAA80559\_ (Z23023) malate dehydrogenase [Solanum tuberosum]

```
Seq. No.
                  231084
Seq. ID
                  LIB3197-019-Q1-M1-G12
Method
                  BLASTX
NCBI GI
                  q1843527
BLAST score
                  484
E value
                  8.0e-49
Match length
                  127
% identity
                  44
NCBI Description (U73747) annexin [Gossypium hirsutum]
                  231085
Seq. No.
Seq. ID
                  LIB3197-019-Q1-M1-G2
Method
                  BLASTX
NCBI GI
                  g232024
BLAST score
                  454
E value
                  2.0e-45
Match length
                  109
                  82
% identity
NCBI Description
                 PROTEIN E6 >gi 421806 pir A46130 fiber protein - upland
                  cotton >gi_2129498_pir__S65061 fiber protein E6 (clone
                  CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site
                  is putative; putative [Gossypium hirsutum] >gi 1000084
                  (U30505) E6 [Gossypium hirsutum]
Seq. No.
                  231086
                  LIB3197-019-Q1-M1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2653446
BLAST score
                  278
E value
                  8.0e-25
                  95
Match length
                  63
% identity
NCBI Description (AB009077) proton pyrophosphatase [Vigna radiata]
Seq. No.
                  231087
                  LIB3197-019-Q1-M1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g464775
BLAST score
                  430
                  1.0e-42
E value
                  86
Match length
                  92
% identity
                  SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_542013 pir_S39492
NCBI Description
                  superoxide dismutase - Para rubber tree >gi 348137 (L11707)
                  superoxide dismutase (manganese) [Hevea brasiliensis]
```

Seq. No. 231088

Seq. ID LIB3197-019-Q1-M1-G5

Method BLASTX
NCBI GI g2501448
BLAST score 248
E value 8.0e-26



```
72
Match length
% identity
                  86
                  UBIQUITIN-LIKE PROTEIN SMT3 >gi 1707372 emb CAA67923
NCBI Description
                  (X99609) ubiquitin-like protein [Arabidopsis thaliana]
Seq. No.
                  231089
                  LIB3197-019-Q1-M1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023858
                  566
BLAST score
                  2.0e-58
E value
                  114
Match length
                  33
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                  PROTEIN >gi 1256608 (U44850) G protein beta subunit
                  [Glycine max]
                  231090
Seq. No.
                  LIB3197-019-Q1-M1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g629806
                  291
BLAST score
                  8.0e-40
E value
                  96
Match length
                  86
% identity
                  tubulin beta chain - rice >gi_493725_emb_CAA55912_ (X79367)
NCBI Description
                  beta tubulin [Oryza sativa]
                  231091
Seq. No.
                  LIB3197-019-Q1-M1-G8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3892051
BLAST score
                  234
                  3.0e-29
E value
                  82
Match length
                  80
% identity
NCBI Description
                   (AC002330) predicted NADH dehydrogenase 24 kD subunit
                   [Arabidopsis thaliana]
                  231092
Seq. No.
                  LIB3197-019-Q1-M1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g119354
                   530
BLAST score
E value
                   3.0e-54
Match length
                  115
                   88
% identity
NCBI Description
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi 82082 pir__JQ1185
                  phosphopyruvate hydratase (EC 4.2.1.11) - tomato
                  >gi_19281 emb_CAA41115_ (X58108) enolase [Lycopersicon
```

esculentum]

Seq. No. 231093

Seq. ID LIB3197-019-Q1-M1-H11

Method BLASTX NCBI GI g4220537



```
BLAST score
                  548
                  2.0e-56
E value
Match length
                  126
                  81
% identity
                  (AL035356) PsRT17-1 like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  231094
                  LIB3197-019-Q1-M1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023841
BLAST score
                  170
                  5.0e-12
E value
                  56
Match length
                  62
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT
NCBI Description
                  >gi 1695179 emb CAA70704 (Y09513) G protein beta subunit
                  [Nicotiana plumbaginifol\overline{a}]
                  231095
Seq. No.
                  LIB3197-019-Q1-M1-H2
Seq. ID
Method
                  BLASTX
                  q1710581
NCBI GI
BLAST score
                  400
                  4.0e-39
E value
                  97
Match length
                  76
% identity
                  60S RIBOSOMAL PROTEIN L9 >gi 2129720 pir S71255 ribosomal
NCBI Description
                  protein L9 - Arabidopsis thaliana >gi_1107489 emb CAA63024
                   (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]
Seq. No.
                  231096
                  LIB3197-019-Q1-M1-H4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2661840
BLAST score
                  380
                  1.0e-36
E value
                  105
Match length
                   67
% identity
NCBI Description
                  (Y15430) adenosine kinase [Physcomitrella patens]
                   231097
Seq. No.
                  LIB3197-019-Q1-M1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244847
BLAST score
                   304
                   9.0e-28
E value
                  103
Match length
                   57.
% identity
NCBI Description
                  (Z97337) hydroxyproline-rich glycoprotein homolog
                   [Arabidopsis thaliana]
Seq. No.
                   231098
Seq. ID
                  LIB3197-020-Q1-M1-A11
Method
                  BLASTX
NCBI GI
                   g2062167
BLAST score
                   468
```

6.0e-47

E value



```
99
Match length
                  87
% identity
                  (ACO01645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                  thaliana]
                  231099
Seq. No.
                  LIB3197-020-Q1-M1-A12
Seq. ID
                  BLASTX
Method
                  g2853087
NCBI GI
                  172
BLAST score
                  3.0e-12
E value
Match length
                  74
                  50
% identity
                  (AL021768) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  231100
                  LIB3197-020-Q1-M1-B10
Seq. ID
Method
                  BLASTX
                  q1524370
NCBI GI
BLAST score
                  242
                  4.0e-38
E value
Match length
                  115
                  73
% identity
                  (X92491) TOM20 [Solanum tuberosum]
NCBI Description
                  231101
Seq. No.
                  LIB3197-020-Q1-M1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q267069
BLAST score
                  591
                  2.0e-61
E value
                  109
Match length
                  98
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                  231102
                  LIB3197-020-Q1-M1-B5
Seq. ID
Method
                  BLASTX
                  g3063710
NCBI GI
BLAST score
                   306
                   5.0e-28
E value
                  71
Match length
                   75
% identity
                  (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  231103
                  LIB3197-020-Q1-M1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1703129
BLAST score
                  620
E value
                   9.0e-65
Match length
                  117
                   100
% identity
NCBI Description ACTIN 11 >gi_2129522 pir__S68109 actin 11 - Arabidopsis
```

33222



thaliana >gi\_1002533 (U27981) actin-11 [Arabidopsis

thaliana] 231104 Seq. No. LIB3197-020-Q1-M1-C12 Seq. ID Method BLASTX g2677828 NCBI GI 398 BLAST score 1.0e-38 E value Match length 116 66 % identity (U93166) cysteine protease [Prunus armeniaca] NCBI Description 231105 Seq. No. LIB3197-020-Q1-M1-D12 Seq. ID Method BLASTX q3914449 NCBI GI BLAST score 735 3.0e-78 E value 145 Match length 99 % identity 26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT NCBI Description 7) >gi 3172331 (AF041258) 26S proteasome subunit 7 [Prunus persica] 231106 Seq. No. LIB3197-020-Q1-M1-E10 Seq. ID Method BLASTX NCBI GI g3386614 BLAST score 445 3.0e-44E value Match length 118

% identity 40 (AC004665) putative transcription factor SF3 [Arabidopsis NCBI Description

thaliana]

231107 Seq. No.

LIB3197-020-Q1-M1-E11 Seq. ID

Method BLASTX g464849 NCBI GI BLAST score 763 1.0e-81 E value Match length 143 100 % identity

TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha NCBI Description

chain - almond  $>gi_2041\overline{3}_{emb_C\overline{A}A47\overline{63}5_{emb_CX}}$  (X67162)

alpha-tubulin [Prunus dulcis]

231108 Seq. No.

Seq. ID LIB3197-020-Q1-M1-E12

Method BLASTX NCBI GI g2832625 BLAST score 429 2.0e-42E value Match length 101 % identity 81

(AL021711) putative protein [Arabidopsis thaliana] NCBI Description



```
Seq. No.
                  231109
                  LIB3197-020-Q1-M1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1053047
                  232
BLAST score
E value
                  7.0e-20
Match length
                  52
                  88
% identity
NCBI Description
                  (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)
                  histone H3 [Glycine max] >gi_1053051 (U38427) histone H3
                  [Glycine max]
                  231110
Seq. No.
                  LIB3197-020-Q1-M1-E6
Seq. ID
Method
                  BLASTX
                  g267069
NCBI GI
BLAST score
                  265
                  1.0e-23
E value
                  52
Match length
% identity
                  88
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                  231111
                  LIB3197-020-Q1-M1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2213595
BLAST score
                  363
E value
                  1.0e-34
                  134
Match length
% identity
                  53
NCBI Description (AC000348) T7N9.15 [Arabidopsis thaliana]
Seq. No.
                  231112
Seq. ID
                  LIB3197-020-Q1-M1-F11
Method
                  BLASTX
NCBI GI
                  q231496
BLAST score
                  355
E value
                  1.0e-33
Match length
                  70
                  97
% identity
NCBI Description
                  ACTIN 58 >gi_100421_pir__S20094 actin - potato
                  >gi_21536_emb_CAA39278_ (X55749) actin [Solanum tuberosum]
Seq. No.
                  231113
Seq. ID
                  LIB3197-020-Q1-M1-F12
Method
                  BLASTX
NCBI GI
                  g231683
BLAST score
                  381
E value
                  1.0e-36
```

Match length 114 % identity 61

CALNEXIN HOMOLOG PRECURSOR >gi 421825 pir JN0597 NCBI Description

calnexin-like protein - Arabidopsis thaliana



>gi 16211 emb CAA79144 (Z18242) calnexin homolog [Arabidopsis thaliana]

Seq. No. 231114

LIB3197-020-Q1-M1-F4 Seq. ID

Method BLASTX NCBI GI q3821730 BLAST score 223 3.0e-18E value Match length 69 % identity 67

NCBI Description (Z99991) formate dehydrogenase [Solanum tuberosum]

Seq. No. 231115

Seq. ID LIB3197-020-Q1-M1-F5

Method BLASTX g3695059 NCBI GI BLAST score 452 4.0e-45 E value Match length 134 % identity 69

(AF064787) rac GTPase activating protein 1 [Lotus NCBI Description

japonicus]

231116 Seq. No.

LIB3197-020-Q1-M1-G12 Seq. ID

Method BLASTX NCBI GI g3885328 BLAST score 201 9.0e-16 E value Match length 63 57 % identity

NCBI Description (AC005623) putative serine/threonine protein kinase

[Arabidopsis thaliana]

231117 Seq. No.

LIB3197-020-Q1-M1-G4 Seq. ID

Method BLASTX g3024764 NCBI GI 234 BLAST score 1.0e-19 E value Match length 116 49 % identity

UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T (UBIQUITIN NCBI Description

THIOLESTERASE T) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE T)

(DEUBIQUITINATING ENZYME T) (ISOPEPTIDASE T) >gi 3287373

(AC002397) ISOT [Mus musculus]

231118 Seq. No.

Seq. ID LIB3197-020-Q1-M1-G5

Method BLASTX g3881780 NCBI GI BLAST score 173 2.0e-12 E value Match length 116 % identity

(Z48638) similar to lipid transfer protein [Caenorhabditis NCBI Description

% identity

100



## elegans]

```
231119
Seq. No.
                  LIB3197-020-Q1-M1-G9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2213595
BLAST score
                  357
                  5.0e-34
E value
                  106
Match length
% identity
                  63
                  (AC000348) T7N9.15 [Arabidopsis thaliana]
NCBI Description
                  231120
Seq. No.
                  LIB3197-020-Q1-M1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3643598
                  419
BLAST score
E value
                  9.0e-44
                  106
Match length
% identity
                  86
                  (AC005395) putative poly(A) polymerase [Arabidopsis
NCBI Description
                  thaliana]
                  231121
Seq. No.
                  LIB3197-020-Q1-M1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g232024
BLAST score
                  184
                  3.0e-14
E value
Match length
                  55
                  67
% identity
                  PROTEIN E6 >gi 421806 pir A46130 fiber protein - upland
NCBI Description
                  cotton >gi_2129498_pir__S65061 fiber protein E6 (clone
                  CKE6-1A) - upland cotton >gi 167323 (M92051) 5' start site
                  is putative; putative [Gossypium hirsutum] >gi_1000084
                   (U30505) E6 [Gossypium hirsutum]
Seq. No.
                  231122
                  LIB3197-020-Q1-M1-H5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3212877
                  437
BLAST score
E value
                  2.0e-43
                  101
Match length
                  79
% identity
NCBI Description (AC004005) Lea-like protein [Arabidopsis thaliana]
Seq. No.
                  231123
                  LIB3197-020-Q1-M1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3869088
BLAST score
                  605
E value
                  5.0e-63
Match length
                  11.6
```

NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]



```
Seq. No.
                  231124
Seq. ID
                  LIB3197-020-Q1-M1-H9
Method
                  BLASTX
NCBI GI
                  q131770
BLAST score
                  378
E value
                  2.0e-36
Match length
                  105
                  66
% identity
                  40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
NCBI Description
                   (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3D024
                  ribosomal protein S9.e - slime mold (Dictyostelium
                  discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein
                   [Dictyostelium discoideum]
Seq. No.
                  231125
                  LIB3197-021-Q1-M1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913008
BLAST score
                  299
                  2.0e-30
E value
Match length
                  86
% identity
                  84
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
NCBI Description
                  >gi_3021338_emb_CAA06308_ (AJ005041) cytosolic
                  fructose-1,6-bisphosphate aldolase [Cicer arietinum]
Seq. No.
                  231126
                  LIB3197-021-Q1-M1-A11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1666228
BLAST score
                  374
E value
                  3.0e-47
Match length
                  95
                  99
% identity
                 (U76190) actin [Pisum sativum] >gi_1666230 (U76191) actin
NCBI Description
                   [Pisum sativum] >gi_1724137 (U8104\overline{6}) actin [Pisum sativum]
                  >gi_1724139 (U81047) actin [Pisum sativum]
Seq. No.
                  231127
                  LIB3197-021-Q1-M1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3212869
BLAST score
                  512
                  4.0e-52
E value
Match length
                  111
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  231128
Seq. ID
                  LIB3197-021-Q1-M1-A2
Method
                  BLASTX
NCBI GI
                  q4033468
BLAST score
                  401
```

Method BLASTX
NCBI GI g4033468
BLAST score 401
E value 4.0e-39
Match length 112
% identity 46

NCBI Description ARGININE/SERINE-RICH SPLICING FACTOR RSP40



>gi\_2582641\_emb\_CAA67800\_ (X99437) splicing factor
[Arabidopsis thaliana] >gi\_2980800\_emb\_CAA18176\_ (AL022197)
splicing factor At-SRp40 [Arabidopsis thaliana]

231129 Seq. No. Seq. ID LIB3197-021-Q1-M1-A5 BLASTX Method NCBI GI q4204300 BLAST score 149 1.0e-09 E value Match length 56 57 % identity

NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana]

Seq. ID 231130 Seq. ID LIB319

Seq. ID LIB3197-021-Q1-M1-A6

Method BLASTX
NCBI GI 94098331
BLAST score 620
E value 8.0e-65
Match length 114
% identity 97

NCBI Description (U76896) beta-tubulin 5 [Triticum aestivum]

Seq. No. 231131

Seq. ID LIB3197-021-Q1-M1-A8

Method BLASTX
NCBI GI g4455199
BLAST score 210
E value 3.0e-17
Match length 49
% identity 80

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 231132

Seq. ID LIB3197-021-Q1-M1-B1

Method BLASTX
NCBI GI g3176098
BLAST score 383
E value 5.0e-37
Match length 127
% identity 35

NCBI Description (Y15036) annexin [Medicago truncatula]

Seq. No. 231133

Seq. ID LIB3197-021-Q1-M1-B10

Method BLASTX
NCBI GI g2827755
BLAST score 278
E value 1.0e-24
Match length 96
% identity 62

NCBI Description INORGANIC PYROPHOSPHATASE, VACUOLAR (PYROPHOSPHATE

PHOSPHOHYDROLASE) (PPASE) >gi 951323 (U31467)

pyrophosphatase [Vigna radiata]

Seq. No. 231134



65

% identity

```
LIB3197-021-Q1-M1-B11
Seq. ID
                  BLASTX
Method
                  q3377797
NCBI GI
BLAST score
                  556
                  3.0e-57
E. value
                  123
Match length
                  86
% identity
                  (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
                  231135
Seq. No.
                  LIB3197-021-Q1-M1-B12
Seq. ID
                  BLASTX
Method
                  q2664210
NCBI GI
                   300
BLAST score
                   7.0e-32
E value
                  109
Match length
                   66
% identity
                   (AJ222644) asparaginyl-tRNA synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   231136
Seq. No.
                   LIB3197-021-Q1-M1-B4
Seq. ID
                   BLASTX
Method
                   q2626840
NCBI GI
                   282
BLAST score
E value
                   3.0e-25
                   130
Match length
% identity
                   (D89729) CRM1 protein [Homo sapiens]
NCBI Description
                   >gi_4507943_ref_NP_003391.1_pXP01_ exportin 1 (CRM1, yeast,
                   homolog)
                   231137
Seq. No.
                   LIB3197-021-Q1-M1-B5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3776560
                   289
BLAST score
                   5.0e-26
E value
                   132
Match length
                   48
% identity
                   (AC005388) Similar to gb_U51990 hPrp18 (splicing factor)
NCBI Description
                   gene from Homo sapiens. [Arabidopsis thaliana]
                   231138
Seq. No.
                   LIB3197-021-Q1-M1-B6
Seq. ID
Method
                   BLASTX
                   g131770
NCBI GI
                   409
BLAST score
                   5.0e-40
E value
                   115
Match length
```

(VEGETATIVE SPECIFIC PROTEIN V12) >gi\_70880\_pir\_\_R3D024

NCBI Description 40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)



ribosomal protein S9.e - slime mold (Dictyostelium discoideum) >gi\_7353\_emb\_CAA29844\_ (X06636) rp1024 protein [Dictyostelium discoideum]

231139 Seq. No. Seq. ID LIB3197-021-Q1-M1-B7 BLASTX Method NCBI GI q2119934 446 BLAST score 2.0e-44 E value 92 Match length 93 % identity translation initiation factor eIF-4A.7 - common tobacco NCBI Description 231140 Seq. No. Seq. ID LIB3197-021-Q1-M1-B9 Method BLASTX q2738949 NCBI GI BLAST score 540 2.0e-55 E value 113 Match length 88 % identity (AF022213) cytosolic ascorbate peroxidase [Fragaria x NCBI Description ananassa] 231141 Seq. No. LIB3197-021-Q1-M1-C1 Seq. ID BLASTX Method NCBI GI g1724102 BLAST score 502 6.0e-51E value Match length 114 84 % identity (U79766) S-adenosyl-L-homocystein hydrolase; SAH NCBI Description [Mesembryanthemum crystallinum] 231142 Seq. No. LIB3197-021-Q1-M1-C2 Seq. ID Method BLASTX g4371285 NCBI GI 485 BLAST score 5.0e-49 E value 133 Match length 69 % identity (AC006260) hypothetical protein [Arabidopsis thaliana] NCBI Description 231143 Seq. No. LIB3197-021-Q1-M1-C3 Seq. ID BLASTX Method g3337349 NCBI GI 148 BLAST score 9.0e-10 E value 41 Match length 61 % identity

Seq. No. 231144

NCBI Description (AC004481) putative protein kinase [Arabidopsis thaliana]



```
LIB3197-021-Q1-M1-C4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1174536
BLAST score
                  139
                  5.0e-09
E value
                  40
Match length
                  62
% identity
                  ASPARAGINYL-TRNA SYNTHETASE (ASPARAGINE--TRNA LIGASE)
NCBI Description
                   (ASNRS) >gi_1073865_pir__B64115 asparagine--tRNA ligase (EC
                   6.1.1.22) - Haemophilus influenzae (strain Rd KW20)
                  >qi 1574761 (U32810) asparaginyl-tRNA synthetase (asnS)
                   [Haemophilus influenzae Rd]
                  231145
Seq. No.
Seq. ID
                  LIB3197-021-Q1-M1-C7
                  BLASTX
Method
                  g3249066
NCBI GI
BLAST score
                   340
                   5.0e-32
E value
Match length
                  121
% identity
                   61
                   (AC004473) Similar to S. cerevisiae SIK1P protein
NCBI Description
                   gb 984964. ESTs gb_F15433 and gb_AA395158 come from this
                   gene. [Arabidopsis thaliana]
                   231146
Seq. No.
Seq. ID
                   LIB3197-021-Q1-M1-C9
                   BLASTX
Method
NCBI GI
                   q3885328
BLAST score
                   178
                   5.0e-13
E value
                   43
Match length
                   72
% identity
                  (AC005623) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   231147
                   LIB3197-021-Q1-M1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4206124
BLAST score
                   660
                   2.0e-69
E value
Match length
                   135
                   95
% identity
                   (AF097668) T-complex protein 1 epsilon subunit
NCBI Description
                   [Mesembryanthemum crystallinum]
                   231148
Seq. No.
                   LIB3197-021-Q1-M1-D10
Seq. ID
Method
                   BLASTX
                   g2443348
NCBI GI
                   282
BLAST score
                   3.0e-25
E value
                   117
Match length
                   44
% identity
```

NCBI Description (AB001379) cytochrome P450 [Glycyrrhiza echinata]



```
Seq. No.
                  231149
                  LIB3197-021-Q1-M1-D3
Seq. ID
                  BLASTX
Method
                  q3319457
NCBI GI
                  172
BLAST score
                  3.0e-12
E value
                  98
Match length
                  39
% identity
                  (AF077542) contains similarity to O-linked GlcNAc
NCBI Description
                  transferases [Caenorhabditis elegans]
Seq. No.
                  231150
                  LIB3197-021-Q1-M1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4469005
BLAST score
                  150
                  3.0e-15
E value
Match length
                  84
                  57
% identity
                  (AL035602) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  231151
Seq. No.
                  LIB3197-021-Q1-M1-D7
Seq. ID
                  BLASTX
Method
                  g4454012
NCBI GI
                  457
BLAST score
                  1.0e-45
E value
Match length
                  123
% identity
                  67
                  (AL035396) Pollen-specific protein precursor like
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  231152
                  LIB3197-021-Q1-M1-D9
Seq. ID
                  BLASTX
Method
                  g586076
NCBI GI
                  557
BLAST score
                   2.0e-57
E value
                  109
Match length
                   89
% identity
                  TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta
NCBI Description
                   chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta
                   tubulin 1 [Lupinus albus]
                   231153
Seq. No.
                  LIB3197-021-Q1-M1-E1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g113621
                   298
BLAST score
                   3.0e-27
E value
Match length
                   90
                   72
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
NCBI Description
```

>gi\_68196\_pir\_\_ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi\_168420 (M16220) aldolase
[Zea mays] >gi\_295850\_emb\_CAA31366\_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi\_225624\_prf\_\_1307278A

Match length

% identity

104 98



## cytoplasmic aldolase [Zea mays]

```
Seq. No.
                  231154
                  LIB3197-021-Q1-M1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q464444
                  546
BLAST score
                  4.0e-56
E value
                  118
Match length
                  90
% identity
                  PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                  COMPLEX 30 KD SUBUNIT) >gi_541889_pir__S39900 proteasome -
                  Arabidopsis thaliana >gi 166830 (M98495) proteasome
                   [Arabidopsis thaliana]
Seq. No.
                  231155
                  LIB3197-021-Q1-M1-E11
Seq. ID
Method
                  BLASTX
                  g2811278
NCBI GI
BLAST score
                  257
                  7.0e-40
E value
Match length
                  118
% identity
                  73
                  (AF043284) expansin [Gossypium hirsutum]
NCBI Description
Seq. No.
                  231156
                  LIB3197-021-Q1-M1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1703129
BLAST score
                   561
                  7.0e-58
E value
Match length
                  105
                   98
% identity
                  ACTIN 11 >gi_2129522_pir__S68109 actin 11 - Arabidopsis
NCBI Description
                   thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis
                   thaliana]
                   231157
Seq. No.
Seq. ID
                  LIB3197-021-Q1-M1-E3
Method
                  BLASTX
                   g3367534
NCBI GI
BLAST score
                   282
                   8.0e-52
E value
                   132
Match length
                   77
% identity
                  (AC004392) Strong similarity to coatamer alpha subunit
NCBI Description
                   (HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis
                   thaliana]
                   231158
Seq. No.
                   LIB3197-021-Q1-M1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q267069
BLAST score
                   560
                   9.0e-58
E value
```



TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi\_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

231159 Seq. No.

NCBI Description

LIB3197-021-Q1-M1-E7 Seq. ID

BLASTX Method g1346349 NCBI GI 500 BLAST score 1.0e-50 E value 102 Match length 97 % identity

KERATIN, TYPE II CYTOSKELETAL 6F (CYTOKERATIN 6F) (CK 6F) NCBI Description (K6F KERATIN) >gi\_2119219\_pir\_\_I61771 keratin type II -

human >gi 908805 (L42612) keratin type II [Homo sapiens]

Seq. No. 231160

LIB3197-021-Q1-M1-E8 Seq. ID

Method BLASTX g2811278 NCBI GI 558 BLAST score 1.0e-57 E value Match length 119 87 % identity

(AF043284) expansin [Gossypium hirsutum] NCBI Description

Seq. No. 231161

LIB3197-021-Q1-M1-E9 Seq. ID

BLASTX Method g1843525 NCBI GI 250 BLAST score 1.0e-21 E value 50 Match length 98 % identity

(U73746) annexin [Gossypium hirsutum] NCBI Description

Seq. No. 231162

LIB3197-021-Q1-M1-F1 Seq. ID

BLASTX Method NCBI GI g1170567 350 BLAST score E value 2.0e-33 72 Match length 88 % identity

MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) NCBI Description

>gi\_1085960\_pir\_\_S52648 INO1 protein - Citrus paradisi >gi 602565 emb CAA83565 (Z32632) INO1 [Citrus x paradisi]

Seq. No. 231163

LIB3197-021-Q1-M1-F10 Seq. ID

Method BLASTX NCBI GI a3881976 BLAST score 223 7.0e-19 E value Match length 64 % identity 64

33234

```
(AJ012409) hypothetical protein [Homo sapiens]
NCBI Description
                  231164
Seq. No.
Seq. ID
                  LIB3197-021-Q1-M1-F12
                  BLASTX
Method
                  g3269289
NCBI GI
                  177
BLAST score
                  7.0e-13
E value
                  50
Match length
                  68
% identity
                  (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                  231165
Seq. No.
                  LIB3197-021-Q1-M1-F3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g112863
BLAST score
                  596
                  5.0e-62
E value
                  135
Match length
                  81
% identity
                  STYLE DEVELOPMENT-SPECIFIC PROTEIN 9612 PRECURSOR
NCBI Description
                  >gi 100227 pir S12209 hypothetical protein - tomato
                  >gi_19162_emb_CAA38979_ (X55193) 9612 [Lycopersicon
                  esculentum]
```

Seq. No. 231166

Seq. ID LIB3197-021-Q1-M1-F4

Method BLASTX
NCBI GI 94512705
BLAST score 537
E value 3.0e-55
Match length 117
% identity 87

NCBI Description (AC006569) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 231167

Seq. ID LIB3197-021-Q1-M1-F5

Method BLASTX
NCBI GI g339878
BLAST score 198
E value 6.0e-16
Match length 64
% identity 59

NCBI Description (M55169) tripeptidyl peptidase II [Homo sapiens]

Seq. No. 231168

Seq. ID LIB3197-021-Q1-M1-F6

Method BLASTX
NCBI GI g2062172
BLAST score 351
E value 3.0e-33
Match length 73
% identity 89

NCBI Description (AC001645) unknown protein [Arabidopsis thaliana]

Seq. No. 231169



```
LIB3197-021-Q1-M1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2435519
BLAST score
                  385
                  3.0e-37
E value
                  133
Match length
                  58
% identity
                   (AF024504) similar to mouse MEM3 (GB:U47024 and S.
NCBI Description
                  cerevisiae vacuolar sorting protein 35 (SW; P34110)
                   [Arabidopsis thaliana]
                   231170
Seq. No.
                   LIB3197-021-Q1-M1-F9
Seq. ID
                   BLASTX
Method
                   q3128228
NCBI GI
BLAST score
                   640
                   4.0e-67
E value
Match length
                   133
% identity
                   90
                   (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                   thaliana] >gi 3337376 (AC004481) putative ribosomal protein
                   L18A [Arabidopsis thaliana]
                   231171
Seq. No.
                   LIB3197-021-Q1-M1-G1
Seq. ID
                   BLASTX
Method
                   g2326345
NCBI GI
                   223
BLAST score
E value
                   3.0e-18
Match length
                   109
                   43
% identity
                  (Y11187) PRL1 protein [Arabidopsis thaliana]
NCBI Description
                   231172
Seq. No.
                   LIB3197-021-Q1-M1-G12
Seq. ID
                   BLASTX
Method
                   g586076
NCBI GI
                   643
BLAST score
E value
                   2.0e-67
Match length
                   122
                   97
 % identity
                   TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta
NCBI Description
                   chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta
                   tubulin 1 [Lupinus albus]
                   231173
 Seq. No.
                   LIB3197-021-Q1-M1-G2
 Seq. ID
                   BLASTX
Method
                   q1708401
 NCBI GI
                   493
 BLAST score
                   6.0e-50
 E value
 Match length
                   105
                   91
 % identity
                   ISOCITRATE DEHYDROGENASE (NADP) (OXALOSUCCINATE
 NCBI Description
                   DECARBOXYLASE) (IDH) (NADP+-SPECIFIC ICDH) (IDP)
```

Seq. No. 231174



```
LIB3197-021-Q1-M1-G3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g231496
BLAST score
                  572
                  3.0e-59
E value
                  108
Match length
% identity
                  98
                  ACTIN 58 >gi 100421 pir S20094 actin - potato
NCBI Description
                  >qi 21536 emb CAA39278 (X55749) actin [Solanum tuberosum]
                  231175
Seq. No.
                  LIB3197-021-Q1-M1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2580440
BLAST score
                  158
                  1.0e-10
E value
Match length
                  60
                  53
% identity
                  (D87261) PCF2 [Oryza sativa]
NCBI Description
Seq. No.
                  231176
                  LIB3197-021-Q1-M1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2119934
BLAST score
                  446
                  2.0e-44
E value
Match length
                  92
                   93
% identity
NCBI Description translation initiation factor eIF-4A.7 - common tobacco
                   231177
Seq. No.
                  LIB3197-021-Q1-M1-G9
Seq. ID
                  BLASTX
Method
                   g2598575
NCBI GI
                   249
BLAST score
                   3.0e-21
E value
                   124
Match length
                   40
% identity
                  (Y15293) MtN21 [Medicago truncatula]
NCBI Description
                   231178
Seq. No.
                   LIB3197-021-Q1-M1-H11
Seq. ID
                   BLASTX
Method
                   g309557
NCBI GI
                   555
BLAST score
                   3.0e-57
E value
                   119
Match length
                   91
% identity
NCBI Description (L21007) chaperonin 60 [Zea mays]
                   231179
Seq. No.
                   LIB3197-021-Q1-M1-H12
Seq. ID
                   BLASTX
Method
                   g3860272
NCBI GI
                   660
BLAST score
                   2.0e-69
E value
                   132
Match length
```

Match length

% identity

63

92



```
% identity
                  98
                  (AC005824) putative suppressor protein [Arabidopsis
NCBI Description
                  thaliana] >gi 4314399 gb AAD15609 (AC006232) putative skd1
                  protein [Arabidopsis thaliana]
                  231180
Seq. No.
                  LIB3197-021-Q1-M1-H4
Seq. ID
                  BLASTX
Method
                  g1931639
NCBI GI
BLAST score
                  172
                  2.0e-12
E value
                  91
Match length
                  37
% identity
                  (U95973) lysophospholipase isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  231181
                  LIB3197-021-Q1-M1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1710663
                  188
BLAST score
                  4.0e-15
E value
Match length
                  99
                  48
% identity
                  PUTATIVE DNA-DIRECTED RNA POLYMERASE III 130 KD POLYPEPTIDE
NCBI Description
                   (RNA POLYMERASE III SUBUNIT 2) >gi_1204209_emb_CAA93558
                   (Z69727) putative DNA-directed RNA polymerase III 130 kd
                  subunit [Schizosaccharomyces pombe]
                  231182
Seq. No.
                  LIB3197-022-Q1-M1-A3
Seq. ID
                  BLASTX
Method
                  g3493172
NCBI GI
                   411
BLAST score
                   2.0e-40
E value
                   91
Match length
                   89
% identity
                  (U89609) fiber annexin [Gossypium hirsutum]
NCBI Description
                   231183
Seq. No.
                  LIB3197-022-Q1-M1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1724102
                   493
BLAST score
                   7.0e-50
E value
                   112
Match length
                   84
% identity
NCBI Description
                   (U79766) S-adenosyl-L-homocystein hydrolase; SAH
                   [Mesembryanthemum crystallinum]
                   231184
Seq. No.
Seq. ID
                   LIB3197-022-Q1-M1-A7
Method
                   BLASTX
NCBI GI
                   q4539327
BLAST score
                   312
E value
                   5.0e-29
```



```
NCBI Description (AL035679) putative proton pump [Arabidopsis thaliana]
                    231185
Seq. No.
Seq. ID
                    LIB3197-022-Q1-M1-A8
Method
                    BLASTX
                    q3212869
NCBI GI
                    439
BLAST score
                    1.0e-43
E value
                    93
Match length
                    87
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
                    231186
Seq. No.
                    LIB3197-022-Q1-M1-A9
Seq. ID
                    BLASTX
Method
                    q4389512
NCBI GI
BLAST score
                    255
                    3.0e-22
E value
Match length
                    101
                    54
% identity
                    (AC007059) Human homolog of Mus musculus wizS protein [AA
NCBI Description
                    64-934] [Homo sapiens]
                    231187
Seq. No.
                    LIB3197-022-Q1-M1-B11
Seq. ID
                    BLASTX
Method
NCBI GI
                    g2462746
BLAST score
                    563
                    4.0e-58
E value
Match length
                    124
                    84
% identity
                    (AC002292) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                    thaliana]
                     231188
Seq. No.
                    LIB3197-022-Q1-M1-B3
Seq. ID
                    BLASTX
Method
                    g3319921
NCBI GI
BLAST score
                     271
                     7.0e-24
E value
                    97
Match length
                     61
 % identity
                    (AJ223388) Hev b 3 [Hevea brasiliensis]
NCBI Description
                    >gi_3319923_emb_CAA11304_ (AJ223389) Hev b 3 [Hevea
brasiliensis] >gi_3319925_emb_CAA11305_ (AJ223390) Hev b 3
[Hevea brasiliensis] >gi_3818475 (AF051317) small rubber
                     particle protein [Hevea brasiliensis]
 Seq. No.
                     231189
                     LIB3197-022-Q1-M1-B6
 Seq. ID
                     BLASTX
 Method
                     g2209358
 NCBI GI
                     567
 BLAST score
                     1.0e-58
 E value `
                     138
 Match length
 % identity
 NCBI Description (AF004812) beta-D-galactosidase [Mangifera indica]
```



```
231190
Seq. No.
Seq. ID
                  LIB3197-022-Q1-M1-B8
Method
                  BLASTX
                  q3420006
NCBI GI
                  259
BLAST score
E value
                  2.0e-22
Match length
                  89
                  55
% identity
                  (AF000306) steroid sulfotransferase 2 [Brassica napus]
NCBI Description
Seq. No.
                  231191
                  LIB3197-022-Q1-M1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3095111
BLAST score
                  143
                   6.0e-09
E value
Match length
                  91
% identity
                   37
                  (AF051894) 15 kDa selenoprotein [Homo sapiens]
NCBI Description
                  231192
Seq. No.
Seq. ID
                  LIB3197-022-Q1-M1-C10
Method
                  BLASTX
NCBI GI
                  g4455158
BLAST score
                  216
E value
                   1.0e-17
Match length
                   60
% identity
                   68
                  (AL021687) kinase-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  231193
                  LIB3197-022-Q1-M1-C12
Seq. ID
Method
                  BLASTX
                   g2341034
NCBI GI
                   556
BLAST score
                   3.0e-57
E value
Match length
                  113
% identity
                   97
                  (AC000104) F19P19.13 [Arabidopsis thaliana]
NCBI Description
                  231194
Seq. No.
                  LIB3197-022-Q1-M1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2493131
                   537
BLAST score
                   3.0e-55
E value
Match length
                  112
                   96
% identity
                  VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B
NCBI Description
                   SUBUNIT) >gi 167108 (L11862) vacuolar ATPase B subunit
                   [Hordeum vulgare]
```

Seq. No. 231195

Seq. ID LIB3197-022-Q1-M1-C3

Method BLASTX NCBI GI g2853219

% identity



```
577
BLAST score
                  8.0e-60
E value
                  127
Match length
% identity
                  82
                  (AJ000923) glutathione transferase [Carica papaya]
NCBI Description
                  231196
Seq. No.
                  LIB3197-022-Q1-M1-C7
Seq. ID
                  BLASTX
Method
                  g1170567
NCBI GI
BLAST score
                  541
                  2.0e-55
E value
Match length
                  111
                  89
% identity
                  MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)
NCBI Description
                  >qi 1085960 pir S52648 INO1 protein - Citrus paradisi
                  >gi_602565_emb_CAA83565_ (Z32632) INO1 [Citrus x paradisi]
Seq. No.
                  231197
                  LIB3197-022-Q1-M1-D1
Seq. ID
                  BLASTX
Method
                  g4335763
NCBI GI
                  225
BLAST score
                   2.0e-18
E value
                  81
Match length
                   49
% identity
                  (AC006284) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   231198
                  LIB3197-022-Q1-M1-D10
Seq. ID
                   BLASTX
Method
                   q4508073
NCBI GI
                   435
BLAST score
                   4.0e-43
E value
                   113
Match length
                   69
% identity
                  (AC005882) 43220 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   231199
                   LIB3197-022-Q1-M1-D11
Seq. ID
                   BLASTX
Method
                   g3550982
NCBI GI
                   501
BLAST score
                   1.0e-52
E value
                   123
Match length
                   86
% identity
NCBI Description (AB010690) mutM homologue-1 [Arabidopsis thaliana]
                   231200
Seq. No.
                   LIB3197-022-Q1-M1-D12
Seq. ID
                   BLASTX
Method
                   q2738949
NCBI GI
                   579
BLAST score .
                   5.0e-60
E value
                   119
Match length
                   89
```

NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x



## ananassa]

```
231201
Seq. No.
                   LIB3197-022-Q1-M1-D4
 Seq. ID
 Method
                   BLASTX
                   g2062167
 NCBI GI
BLAST score
                   267
                   1.0e-23
 E value
                   57
Match length
                   84
 % identity
                   (AC001645) Proline-rich protein APG isolog [Arabidopsis
 NCBI Description
                   thaliana]
                   231202
 Seq. No.
                   LIB3197-022-Q1-M1-D5
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2104681
 BLAST score
                   146
                   3.0e-09
 E value
                   129
 Match length
 % identity
                   37
 NCBI Description (X97907) transcription factor [Vicia faba]
                   231203
 Seq. No.
                   LIB3197-022-Q1-M1-D6
 Seq. ID
 Method
                   BLASTX
                   g1703375
 NCBI GI
 BLAST score
                   384
                   3.0e - 37
 E value
                   88
 Match length
 % identity
                   86
 NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483 dbj_BAA08259 (D45420)
                   DcARF1 [Daucus carota]
 Seq. No.
                   231204
 Seq. ID
                   LIB3197-022-Q1-M1-D8
 Method
                   BLASTX
 NCBI GI
                   g2454184
 BLAST score
                   577
                   9.0e-60
 E value
 Match length
                   117
 % identity
                   (U80186) pyruvate dehydrogenase E1 beta subunit
 NCBI Description
                    [Arabidopsis thaliana]
                   231205
 Seq. No.
 Seq. ID
                   LIB3197-022-Q1-M1-E1
 Method
                   BLASTX
 NCBI GI
                   q4454463
 BLAST score
                   192
 E value
                   3.0e-15
 Match length
                   48
 % identity
                   28
                   (AC006234) putative leucine rich protein kinase
 NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 231206



```
LIB3197-022-Q1-M1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351856
                  617
BLAST score
                  2.0e-64
E value
                  127
Match length
                  91
% identity
                  ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
NCBI Description
                   (ACONITASE) >gi 868003 dbj BAA06108_ (D29629) aconitase
                   [Cucurbita sp.]
                  231207
Seq. No.
                  LIB3197-022-Q1-M1-E3
Seq. ID
Method
                  BLASTX
                  g2924509
NCBI GI
BLAST score
                  233
                  2.0e-19
E value
                  91
Match length
                   51
% identity
                  (AL022023) subtilisin proteinase - like [Arabidopsis
NCBI Description
                  thaliana]
                  231208
Seq. No.
                  LIB3197-022-Q1-M1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3668089
                  234
BLAST score
                  2.0e-19
E value
                   83
Match length
% identity
                   51
                  (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
                   231209
Seq. No.
                  LIB3197-022-Q1-M1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3128186
BLAST score
                   236
E value
                   9.0e-20
                   67
Match length
                   67
% identity
                  (AC004521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   231210
                   LIB3197-022-Q1-M1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2811278
BLAST score
                   424
E value
                   8.0e-42
Match length
                   122
% identity
                   65
                  (AF043284) expansin [Gossypium hirsutum]
NCBI Description
Seq. No.
                   231211
                   LIB3197-022-Q1-M1-F4
Seq. ID
```

Method BLASTX NCBI GI g3668097 BLAST score 425

NCBI GI

E value

BLAST score

q1076738

461 4.0e-46



```
E value
                  4.0e-42
Match length
                  101
% identity
                  82
                  (ACO04667) putative glycine cleavage system protein H
NCBI Description
                  precursor [Arabidopsis thaliana]
Seq. No.
                  231212
                  LIB3197-022-Q1-M1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832625
BLAST score
                  378
                  2.0e-36
E value
Match length
                  90
                  80
% identity
                  (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
                  231213
Seq. No.
                  LIB3197-022-Q1-M1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2827552
BLAST score
                  332
                  4.0e-31
E value
Match length
                  91
% identity
                  58
                  (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  231214
Seq. ID
                  LIB3197-022-Q1-M1-G10
Method
                  BLASTX
                  q1711532
NCBI GI
                  282
BLAST score
                   3.0e - 26
E value
                  123
Match length
                   54
% identity
                  SSU72 PROTEIN >gi_2131928_pir__S63180 hypothetical protein
NCBI Description
                   YNL222w - yeast (Saccharomyces cerevisiae) >gi_1173490
                   (U20390) Ssu72p [Saccharomyces cerevisiae]
                   >gi_1302241_emb_CAA96125_ (Z71498) ORF YNL222w
                   [Saccharomyces cerevisiae] >gi_1589662 prf__2211396A SSU72
                   protein [Saccharomyces cerevisiae]
                   231215
Seq. No.
Seq. ID
                  LIB3197-022-Q1-M1-G11
                   BLASTX
Method
                   g2583108
NCBI GI
BLAST score
                   225
E value
                   1.0e-18
Match length
                   90
                   54
% identity
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]
                   231216
Seq. No.
                   LIB3197-022-Q1-M1-G2
Seq. ID
Method
                   BLASTX
```

33244

% identity

98

NCBI Description actin 1 - rice



```
Match length
                  89
                  96
% identity
                  beta-tubulin R2242 - rice
NCBI Description
                  231217
Seq. No.
                  LIB3197-022-Q1-M1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3641837
                  440
BLAST score
                  9.0e-44
E value
                  124
Match length
% identity
                  73
                  (AL023094) Nonclathrin coat protein gamma - like protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  231218
                  LIB3197-022-Q1-M1-G5
Seq. ID
Method
                  BLASTX
                  q3249098
NCBI GI
BLAST score
                  162
                  4.0e-11
E value
                  105
Match length
% identity
                  44
                  (AC003114) ESTs gb_T04610, gb_N38459, gb_T45174, gb_R30481
NCBI Description
                  and gb N64971 come from this gene. [Arabidopsis thaliana]
                  231219
Seq. No.
Seq. ID
                  LIB3197-022-Q1-M1-G7
Method
                  BLASTX
NCBI GI
                  q4038043
                  174
BLAST score
                  2.0e-12
E value
Match length
                  115
                   34
% identity
                  (AC005936) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  231220
                  LIB3197-022-Q1-M1-G8
Seq. ID
                  BLASTX
Method
                  g100488
NCBI GI
BLAST score
                   331
                   7.0e-31
E value
Match length
                  124
                   53
% identity
NCBI Description TNP2 protein - garden snapdragon
Seq. No.
                   231221
Seq. ID
                  LIB3197-022-Q1-M1-H1
Method
                  BLASTX
                   g71634
NCBI GI
BLAST score
                   332
E value
                   3.0e-31
Match length
                   65
```



```
231222
Seq. No.
Seq. ID
                   LIB3197-022-Q1-M1-H10
Method
                   BLASTX
NCBI GI
                   g3334322
BLAST score
                   431
                   9.0e-43
E value
                   82
Match length
 % identity
                   GTP-BINDING PROTEIN SAR1B >qi 2108347 (U55036) small
NCBI Description
                   GTP-binding protein Bsarlb [Brassica rapa]
                   231223
 Seq. No.
 Seq. ID
                   LIB3197-022-Q1-M1-H7
                   BLASTX
Method
                   g2895576
NCBI GI
                   162
 BLAST score
                   4.0e-11
 E value
                   130
Match length
                   25
 % identity
                   (AF041337) vacuolar proton pump subunit SFD beta isoform
NCBI Description
                   [Bos taurus]
                   231224
 Seq. No.
 Seq. ID
                   LIB3197-022-Q1-M1-H8
 Method
                   BLASTX
                   g1174592
 NCBI GI
 BLAST score
                   614
                   4.0e-64
 E value
 Match length
                   138
 % identity
                   90
                   TUBULIN ALPHA-1 CHAIN >qi 2119270 pir S60233 alpha-tubulin
 NCBI Description
                    - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
                   sativum]
 Seq. No.
                    231225
                    LIB3197-023-Q1-M1-A4
 Seq. ID
                    BLASTX
 Methód
 NCBI GI
                    q475048
 BLAST score
                    614
                    5.0e-64
 E value
 Match length
                    131
 % identity
                    63
                    (X72581) tonoplast intrinsic protein gamma (gamma-TIP)
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                    231226
                    LIB3197-023-Q1-M1-A5
 Seq. ID
 Method
                    BLASTX
                    g1408471
 NCBI GI
 BLAST score
                    523
                    2.0e-53
 E value
                    116
 Match length
 % identity
                    81
                   (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
```

factor 1 [Arabidopsis thaliana]

thaliana] >gi\_3851707 (AF102173) actin depolymerizing

Seq. ID



```
231227
Seq. No.
Seq. ID
                  LIB3197-023-Q1-M1-A8
Method
                  BLASTX
NCBI GI
                  q4580394
BLAST score
                  410
                  4.0e-40
E value
                  137
Match length
                  53
% identity
                  (AC007171) putative fatty acid elongase [Arabidopsis
NCBI Description
                  thaliana]
                  231228
Seq. No.
Seq. ID
                  LIB3197-023-Q1-M1-B4
Method
                  BLASTX
                  q1330401
NCBI GI
BLAST score
                  200
E value
                  2.0e-15
                  81
Match length
% identity
                  46
                  (U58762) T27F7.1 gene product [Caenorhabditis elegans]
NCBI Description
                  231229
Seq. No.
                  LIB3197-023-Q1-M1-B8
Seq. ID
Method
                  BLASTX
                  q464849
NCBI ĞI
                  593
BLAST score
                  1.0e-61
E value
                  120
Match length
% identity
                   97
                  TUBULIN ALPHA CHAIN >gi_486847_pir__$336232 tubulin alpha
NCBI Description
                  chain - almond >gi 20413 emb CAA47635 (X67162)
                   alpha-tubulin [Prunus dulcis]
Seq. No.
                   231230
                  LIB3197-023-Q1-M1-C1
Seq. ID
Method
                   BLASTX
                   g4220537
NCBI GI
BLAST score
                   363
E value
                   1.0e-34
Match length
                   140
% identity
                   51
                  (AL035356) PsRT17-1 like protein [Arabidopsis thaliana]
NCBI Description
                   231231
Seq. No.
                  LIB3197-023-Q1-M1-C7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4240116
                   373
BLAST score
E value
                   8.0e-36
                   107
Match length
                   73
% identity
                  (AB007799) NADH-cytochrome b5 reductase [Arabidopsis
NCBI Description
                   thaliana] >gi_4240118_dbj_BAA74838_ (AB007800)
                   NADH-cytochrome b5 reductase [Arabidopsis thaliana]
Seq. No.
                   231232
```

LIB3197-023-Q1-M1-C9



```
Method
                  BLASTX
NCBI GI
                  g3603401
BLAST score
                  347
                  5.0e-33
E value
Match length
                  96
                   68
% identity
                  (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]
NCBI Description
                  231233
Seq. No.
                  LIB3197-023-Q1-M1-D1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3122703
BLAST score
                  173
                   5.0e-13
E value
                   66
Match length
% identity
                   53
                  60S RIBOSOMAL PROTEIN L23A >gi 2641201 (AF031542) ribosomal
NCBI Description
                  protein L23a [Fritillaria agrestis]
                   231234
Seq. No.
Seq. ID
                  LIB3197-023-Q1-M1-D3
                   BLASTX
Method
NCBI GI
                   g2662343
BLAST score
                   644
                   1.0e-67
E value
Match length
                   123
                   100
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                   231235
Seq. No.
                   LIB3197-023-Q1-M1-D7
Seg. ID
Method
                   BLASTX
                   g3122703
NCBI GI
BLAST score
                   327
                   2.0e-30
E value
                   86
Match length
                   76
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L23A >gi 2641201 (AF031542) ribosomal
                   protein L23a [Fritillaria agrestis]
                   231236
Seq. No.
                   LIB3197-023-Q1-M1-D9
Seq. ID
                   BLASTX
Method
                   g3420801
NCBI GI
                   473
BLAST score
                   1.0e-47
E value
                   140
Match length
                   66
% identity
                  (AF081066) IAA-amino acid hydrolase homolog ILL3
NCBI Description
                   [Arabidopsis thaliana]
                   231237
Seq. No.
                   LIB3197-023-Q1-M1-E1
Seq. ID
Method
                   BLASTX
                   q4455223
NCBI GI
                   236
BLAST score
```

9.0e-20

E value

NCBI Description



```
64
Match length
% identity
                  (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  231238
                  LIB3197-023-Q1-M1-E2
Seq. ID
Method
                  BLASTX
                  a541954
NCBI GI
BLAST score
                  583
                  2.0e-60
E value
                  140
Match length
                  84
% identity
                  ubiquitin extension protein - white lupine
NCBI Description
                  >qi 438111 emb CAA80334 (Z22613) ubiquitin extension
                  protein [Lupinus albus]
                  231239
Seq. No.
Seq. ID
                  LIB3197-023-Q1-M1-E7
                  BLASTX
Method
                  q2811278
NCBI GI
                  572
BLAST score
                  3.0e-59
E value
Match length
                  119
                  88
% identity
                  (AF043284) expansin [Gossypium hirsutum]
NCBI Description
                  231240
Seq. No.
Seq. ID
                  LIB3197-023-Q1-M1-E9
Method
                  BLASTX
                  q2811278
NCBI GI
BLAST score
                   665
                   5.0e-70
E value
Match length
                  135
% identity
                  89
                  (AF043284) expansin [Gossypium hirsutum]
NCBI Description
                   231241
Seq. No.
Seq. ID
                  LIB3197-023-Q1-M1-F1
Method
                  BLASTX
NCBI GI
                   q2829910
                   147
BLAST score
                   3.0e-09
E value
Match length
                   99
                   11
% identity
                  (AC002291) Unknown protein, contains regulator of
NCBI Description
                   chromosome condensation motifs [Arabidopsis thaliana]
Seq. No.
                   231242
                   LIB3197-023-Q1-M1-F7
Seq. ID
                   BLASTX
Method
                   g3986750
NCBI GI
                   470
BLAST score
                   4.0e-47
E value
Match length
                   94
                   89
% identity
```

(AF107464) serine/threonine protein phosphatase type 2A



## [Hevea brasiliensis]

```
231243
Seq. No.
                   LIB3197-023-Q1-M1-G2
Seq. ID
Method
                   BLASTX
                   q2996012
NCBI GI
                   451
BLAST score
                   6.0e-45
E value
                   113
Match length
                   75
% identity
                   (AF054455) cytosolic phosphoglucose isomerase; PgiC
NCBI Description
                   [Leavenworthia crassa]
Seq. No.
                   231244
                   LIB3197-023-Q1-M1-G7
Seq. ID
                   BLASTX
Method
                   g3355471
NCBI GI
                   181
BLAST score
                   2.0e-13
E value
                   96
Match length
                   38
% identity
                   (AC004218) putative lysophospholipase [Arabidopsis
NCBI Description
                   thaliana]
                   231245
Seq. No.
                   LIB3197-023-Q1-M1-G8
Seq. ID
Method
                   BLASTX
                   g4454012
NCBI GI
                   566
BLAST score
                   2.0e-58
E value
                   147
Match length
                   71
% identity
                   (AL035396) Pollen-specific protein precursor like
NCBI Description
                   [Arabidopsis thaliana]
                   231246
Seq. No.
                   LIB3197-023-Q1-M1-H10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3122572
                   297
BLAST score
                   2.0e-27
E value
Match length
                   74
                   77
% identity
                   NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR
NCBI Description
                    (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I
                   SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato
                   >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial
                   complex I subunit [Solanum tuberosum]
Seq. No.
                   231247
                   LIB3197-023-Q1-M1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1370162
BLAST score
                    469
                    3.0e-47
E value
```

99

Match length

Seq. No.

231253



```
92
% identity
NCBI Description (X97853) RAB1A [Lotus japonicus]
                  231248
Seq. No.
                  LIB3197-023-Q1-M1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2493416
BLAST score
                  148
E value
                  1.0e-09
Match length
                  76
% identity
                  38
NCBI Description S100 CALCIUM-BINDING PROTEIN Al3 >gi 2134853 pir JC5064
                  calcium-binding protein S100 A13 - human
                  >gi 1694828 emb CAA68188 (X99920) S100 calcium-binding
                  protein A13 (S100A13) [Homo sapiens]
                  231249
Seq. No.
Seq. ID
                  LIB3197-023-Q1-M1-H3
                  BLASTX
Method
NCBI GI
                  q3551249
BLAST score
                  155
E value
                  3.0e-10
                  65
Match length
% identity
                  48
NCBI Description (AB012704) 184 [Daucus carota]
Seq. No.
                  231250
Seq. ID
                  LIB3197-023-Q1-M1-H5
Method
                  BLASTX
                  g3059131
NCBI GI
                  291
BLAST score
E value
                  3.0e-26
Match length
                  94
                  57
% identity
NCBI Description (AJ000478) cytochrome P450 [Helianthus tuberosus]
Seq. No.
                  231251
                  LIB3197-023-Q1-M1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1781103
                  250
BLAST score
                  2.0e-21
E value
                  110
Match length
                  43
% identity
NCBI Description (Z83864) menG [Mycobacterium tuberculosis]
Seq. No.
                  231252
Seq. ID
                  LIB3197-023-Q1-M1-H7
Method
                  BLASTX
NCBI GI
                  g1644427
BLAST score
                  334
                  3.0e-31
E value
Match length
                  74
% identity
                  85
NCBI Description (U74610) glyoxalase II [Arabidopsis thaliana]
```

33251



```
LIB3197-024-Q1-M1-A2
Seq. ID
Method
                  BLASTX
                  g1171866
NCBI GI
BLAST score
                  215
                  2.0e-17
E value
                  83
Match length
                  54
% identity
                  NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR
NCBI Description
                   (COMPLEX I-20KD) (CI-20KD) >gi 629601_pir__S48826 NADH
                  dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild
                  cabbage >gi 562282 emb_CAA57725_ (X82274) PSST subunit of
                  NADH: ubiquinone oxidoreductase [Brassica oleracea]
Seq. No.
                  231254
                  LIB3197-024-Q1-M1-A7
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4006875
BLAST score
                   180
                   3.0e-13
E value
                   74
Match length
                   49
% identity
                  (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
                   231255
Seq. No.
                   LIB3197-024-Q1-M1-A9
Seq. ID
                   BLASTX
Method
                   q4510348
NCBI GI
                   205
BLAST score
                   2.0e-16
E value
Match length
                   60
                   67
% identity
                  (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                   231256
Seq. No.
                   LIB3197-024-Q1-M1-B1
Seq. ID
                   BLASTX
Method
                   g4455202
NCBI GI
                   217
BLAST score
                   1.0e-17
E value
                   74
Match length
                   58
% identity
                  (AL035440) putative APG protein [Arabidopsis thaliana]
NCBI Description
                   231257
Seq. No.
                   LIB3197-024-Q1-M1-B8
Seq. ID
                   BLASTX
Method
                   g1856971
NCBI GI
                   346
BLAST score
                   8.0e-33
E value
                   88
Match length
                   81
% identity
                   (D26058) This gene is specifically expressed at the S phase
NCBI Description
                   during the cell cycle in the synchronous culture of
                   periwinkle cells. [Catharanthus roseus]
```

Seq. No. 231258

Seq. ID LIB3197-024-Q1-M1-C1



```
Method
                  BLASTX
                  g3059131
NCBI GI
                  305
BLAST score
                  6.0e-28
E value
                  97
Match length
                  57
% identity
                  (AJ000478) cytochrome P450 [Helianthus tuberosus]
NCBI Description
                  231259
Seq. No.
                  LIB3197-024-Q1-M1-C8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g232024
BLAST score
                  670
                  1.0e-70
E value
                  129
Match length
                  98
% identity
                  PROTEIN E6 >gi 421806 pir A46130 fiber protein - upland
NCBI Description
                  cotton >qi 2129498 pir S65061 fiber protein E6 (clone
                  CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site
                  is putative; putative [Gossypium hirsutum] >gi_1000084
                   (U30505) E6 [Gossypium hirsutum]
                  231260
Seq. No.
                  LIB3197-024-Q1-M1-C9
Seq. ID
                  BLASTX
Method
                  g3122673
NCBI GI
                   409
BLAST score
                   3.0e-40
E value
Match length
                   105
% identity
                   76
                   60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb_CAB10447_
NCBI Description
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                   231261
                  LIB3197-024-Q1-M1-D1
Seq. ID
                   BLASTX
Method
                   g232024
NCBI GI
                   609
BLAST score
E value
                   1.0e-63
Match length
                   114
                   100
% identity
                  PROTEIN E6 >gi 421806 pir A46130 fiber protein - upland
NCBI Description
                   cotton >gi_2129498_pir__S65061 fiber protein E6 (clone
                   CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site
                   is putative; putative [Gossypium hirsutum] >gi 1000084
                   (U30505) E6 [Gossypium hirsutum]
                   231262
Seq. No.
                   LIB3197-024-Q1-M1-D2
Seq. ID
                   BLASTX
Method
                   q2507281
NCBI GI
                   621
BLAST score
                   6.0e-65
E value
Match length
                   112
% identity
                   98
```

33253

NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi\_1668706\_emb\_CAA66048\_ (X97380) atran2 [Arabidopsis thaliana]

BLAST score

Match length

E value

1.0e-34

98



```
Seq. No.
                  231263
Seq. ID
                  LIB3197-024-Q1-M1-D7
                  BLASTX
Method
NCBI GI
                  g1173198
BLAST score
                  412
                  1.0e-40
E value
Match length
                  88
                   90
% identity
                  40S RIBOSOMAL PROTEIN S13 >gi_480095_pir__S36423 ribosomal
NCBI Description
                  protein S13.e - garden pea >gi_396639_emb_CAA80974_
                   (Z25509) ribosomal protein S13 [Pisum sativum]
                   231264
Seq. No.
                   LIB3197-024-Q1-M1-D8
Seq. ID
                   BLASTX
Method
                   q114121
NCBI GI
BLAST score
                   257
                   3.0e-22
E value
                   81
Match length
                   62
% identity
                   ADP-RIBOSYLATION FACTOR 1 >gi_101185_pir__B36167
NCBI Description
                   ADP-ribosylation factor 1 - yeast (Saccharomyces
                   cerevisiae) >gi_171073 (J03276) ADP-ribosylation factor
                   [Saccharomyces cerevisiae] >gi_1004303_emb_CAA58255_
                   (X83276) ADP-ribosylationfactor 2 [Saccharomyces
                   cerevisiae] >gi 1431314_emb_CAA98769_ (Z74240) ORF YDL192w
                   [Saccharomyces cerevisiae]
Seq. No.
                   231265
Seq. ID
                   LIB3197-024-Q1-M1-D9
                   BLASTX
Method
                   q4538897
NCBI GI
BLAST score
                   327
                   1.0e-30
E value
Match length
                   90
                   69
 % identity
NCBI Description (AL049482) AX110P-like protein [Arabidopsis thaliana]
Seq. No.
                   231266
                   LIB3197-024-Q1-M1-E2
Seq. ID
Method
                   BLASTX
                   g2062167
NCBI GI
                   465
 BLAST score
                   1.0e-46
 E value
                   97
Match length
                   88
 % identity
                   (AC001645) Proline-rich protein APG isolog [Arabidopsis
 NCBI Description
                   thaliana]
                   231267
 Seq. No.
                   LIB3197-024-Q1-M1-E6
 Seq. ID
                   BLASTX
 Method
                   g82040
 NCBI GI
                   361
```



```
% identity
                  ubiquitin precursor - flax (fragment) >gi_168304 (M57895)
NCBI Description
                  ubiquitin [Linum usitatissimum]
                  231268
Seq. No.
                  LIB3197-024-Q1-M1-E8
Seq. ID
                  BLASTX
Method
                  q1710585
NCBI GI
                  360
BLAST score
                  2.0e - 34
E value
                  84
Match length
                  85
% identity
                  60S ACIDIC RIBOSOMAL PROTEIN PO >gi_1143507_emb_CAA63786_
NCBI Description
                   (X93587) PO ribosomal protein [Lupinus luteus]
                  231269
Seq. No.
Seq. ID
                  LIB3197-024-Q1-M1-F10
                  BLASTX
Method
                  g267069
NCBI GI
BLAST score
                   430
                   1.0e-42
E value
                   79
Match length
                   100
% identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                   231270
Seq. No.
                   LIB3197-024-Q1-M1-F11
Seq. ID
                   BLASTX
Method
                   q4455309
NCBI GI
                   495
BLAST score
                   4.0e-50
E value
                   137
Match length
 % identity
NCBI Description (AL035528) hypothetical protein [Arabidopsis thaliana]
                   231271
 Seq. No.
                   LIB3197-024-Q1-M1-F12
 Seq. ID
                   BLASTX
Method
                   q2459445
 NCBI GI
 BLAST score
                   314
                   7.0e-29
 E value
                   111
 Match length
 % identity
                   31
 NCBI Description (AC002332) putative ribonucleoprotein [Arabidopsis
                   thaliana]
                   231272
 Seq. No.
                   LIB3197-024-Q1-M1-F2
 Seq. ID
                   BLASTX
 Method
                   q120669
 NCBI GI
                   446
 BLAST score
                   2.0e-44
 E value
 Match length
                   89
```

33255

92

% identity



```
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi 19566 emb CAA42905 (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                   231273
Seq. ID
                  LIB3197-024-Q1-M1-F3
Method
                  BLASTX
NCBI GI
                   q120672
BLAST score
                   223
                   1.0e-18
E value
                   58
Match length
                   76
% identity
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_66016_pir__DEPZG glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) - parsley
                   >gi 20549 emb CAA42902 (X60344) glyceraldehyde 3-phosphate
                   dehydrogenase [Petroselinum crispum]
                   231274
Seq. No.
Seq. ID
                   LIB3197-024-Q1-M1-F4
                   BLASTX
Method
NCBI GI
                   g2493318
BLAST score
                   211
                   5.0e-17
E value
Match length
                   67
% identity
                   57
NCBI Description BLUE COPPER PROTEIN PRECURSOR >gi 562779 emb CAA80963
                   (Z25471) blue copper protein [Pisum sativum]
                   >gi 1098264 prf 2115352A blue Cu protein [Pisum sativum]
                   231275
Seq. No.
                   LIB3197-024-Q1-M1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q586076
BLAST score
                   584
E value
                   1.0e-60
Match length
                   107
% identity
                   98
                   TUBULIN BETA-1 CHAIN >gi_486734_pir_S35142 tubulin beta
NCBI Description
                   chain - white lupine >gi 402636 emb CAA49736 (X70184) Beta
                   tubulin 1 [Lupinus albus]
Seq. No.
                   231276
Seq. ID
                   LIB3197-024-Q1-M1-F9
Method
                   BLASTX
NCBI GI
                   g1694976
BLAST score
                   354
E value
                   1.0e-33
                   100
Match length
% identity
NCBI Description
                  (Y09482) HMG1 [Arabidopsis thaliana]
                   >gi 2832361 emb CAA74402 (Y14073) HMG protein [Arabidopsis
```

33256

thaliana]

231277

Seq. No.

NCBI GI

BLAST score

253



```
LIB3197-024-Q1-M1-G1
Seq. ID
                  BLASTX
Method
                  g2811278
NCBI GI
                  551
BLAST score
                  1.0e-56
E value
                  133
Match length
                  76
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
                  231278
Seq. No.
Seq. ID
                  LIB3197-024-Q1-M1-G11
                  BLASTX
Method
                   g4544399
NCBI GI
                   303
BLAST score
                   1.0e-27
E value
                   124
Match length
                   44
% identity
                   (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
                   231279
Seq. No.
                   LIB3197-024-Q1-M1-G12
Seq. ID
                   BLASTX
Method
                   q3395422
NGBI GI
                   375
BLAST score
                   5.0e-36
E value
                   138
Match length
                   54
% identity
                   (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3786022 (AC005499) hypothetical protein [Arabidopsis
                   thaliana]
                   231280
Seq. No.
                   LIB3197-024-Q1-M1-G2
Seq. ID
Method
                   BLASTX
                   g2764732
NCBI GI
BLAST score
                   392
                   4.0e-38
E value
Match length
                   87
 % identity
                   93
NCBI Description (AJ002490) ndhB [Arabidopsis thaliana]
                   231281
 Seq. No.
                   LIB3197-024-Q1-M1-G5
 Seq. ID
                   BLASTX
Method
                   g3953471
 NCBI GI
                   328
 BLAST score
                   1.0e-30
 E value
                   75
 Match length
 % identity
                   81
 NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]
                   231282
 Seq. No.
                   LIB3197-024-Q1-M1-G6
 Seq. ID
                   BLASTX
 Method
                   g2760839
```

33257



```
8.0e-22
E value
Match length
                   72
                   61
% identity
                   (AC003105) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
                   231283
Seq. No.
Seq. ID
                   LIB3197-024-Q1-M1-G7
                   BLASTX
Method
                   q231757
NCBI GI
BLAST score
                   575
                   2.0e-59
E value
Match length
                   131
                   87
% identity
                   CAFFEIC ACID 3-O-METHYLTRANSFERASE
NCBI Description
                   (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                   3-O-METHYLTRANSFERASE) (COMT) >gi_99653_pir__S18568
                   lignin-bispecific O-methyltransferase (EC 2.1.1.-) -
                   quaking aspen >gi_20951_emb_CAA44006_ (X62096) lignin
                   bispecific acid/5-hydroxyferulic acid methyltransferase
                   [Populus tremuloides] >gi_2226267 (U13171) caffeic
                   acid/5-hydroxyferulic aci\overline{d} O-methyltransferase [Populus
                   tremuloides]
                   231284
'Seq. No.
                   LIB3197-024-Q1-M1-G8
Seq. ID
                   BLASTX
Method
                   q1928981
NCBI GI
                   529
BLAST score
                   4.0e-54
E value
Match length
                   113
                   93
% identity
                   (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                   oleracea var. botrytis]
                   231285
Seq. No.
                   LIB3197-024-Q1-M1-G9
Seq. ID
Method
                   BLASTX
                   g416758
NCBI GI
BLAST score
                   184
                   9.0e-14
E value
                   92
Match length
                   42
 % identity
                   SERINE CARBOXYPEPTIDASE PRECURSOR >gi 166674 (M81130)
NCBI Description
                   carboxypeptidase Y-like protein [Arabidopsis thaliana]
                   >gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis
                   thaliana]
                   231286
 Seq. No.
                   LIB3197-024-Q1-M1-H11
 Seq. ID
 Method
                   BLASTX
                   g1708191
 NCBI GI
                    351
 BLAST score
                    3.0e - 33
 E value
                   126
 Match length
                    55
 % identity
```

NCBI Description HEXOSE CARRIER PROTEIN HEX6 >gi\_467319 (L08188) hexose carrier protein [Ricinus communis]

% identity

```
Seq. No.
                  231287
Seq. ID
                  LIB3197-024-Q1-M1-H2
Method
                  BLASTX
NCBI GI
                  q3097321
                  199
BLAST score
                  2.0e-15
E value
Match length
                  104
                  39
% identity
                  (AB013289) Bd 30K [Glycine max]
NCBI Description
                  231288
Seq. No.
Seq. ID
                  LIB3197-024-Q1-M1-H4
                  BLASTX
Method
                  q2811031
NCBI GI
BLAST score
                  127
E value
                  7.0e-13
Match length
                  72
% identity
                  58
                  BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (BADH)
NCBI Description
                  >gi 2109299 gb_AAB58165.1 (AF000132) betaine aldehyde
                  dehydrogenase [Amaranthus hypochondriacus]
                  231289
Seq. No.
                  LIB3197-024-Q1-M1-H6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4567262
                   301
BLAST score
                   9.0e-49
E value
Match length
                  107
                   86
% identity
                  (AC006841) putative ubiquitin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   231290
                  LIB3197-024-Q1-M1-H7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q547684
BLAST score
                   558
                   2.0e-57
E value
Match length
                   112
                   96
% identity
                  HEAT SHOCK PROTEIN 82 >gi 100336 pir S18865 heat shock
NCBI Description
                   protein 82 - common tobacco (fragment)
                   >gi_19880_emb_CAA44877_ (X63195) heat shock protein 82
                   [Nicotiana tabacum]
                   231291
Seq. No.
                   LIB3197-025-Q1-M1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2507281
BLAST score
                   675
                   3.0e-71
E value
                   122
Match length
                   99
```

NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi\_1668706\_emb\_CAA66048\_ (X97380) atran2 [Arabidopsis thaliana]



```
Seq. No.
                  231292
                  LIB3197-025-Q1-M1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2739046
BLAST score
                  162
                  3.0e-11
E value
Match length
                  89
% identity
                  37
                  (AF024652) polyphosphoinositide binding protein Ssh2p
NCBI Description
                  [Glycine max]
                  231293
Seq. No.
                  LIB3197-025-Q1-M1-A9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3283893
BLAST score
                  192
E value
                  1.0e-14
Match length
                  110
% identity
                  36
                  (AF070626) unknown [Homo sapiens]
NCBI Description
                  231294
Seq. No.
                  LIB3197-025-Q1-M1-B12
Seq. ID
Method
                  BLASTX
                  g2738949
NCBI GI
BLAST score
                  568
                   1.0e-58
E value
Match length
                  118
% identity
                   88
                  (AF022213) cytosolic ascorbate peroxidase [Fragaria x
NCBI Description
                   ananassa]
                   231295
Seq. No.
                   LIB3197-025-Q1-M1-B2
Seq. ID
Method
                   BLASTX
                   g1408471
NCBI GI
                   505
BLAST score
                   3.0e-51
E value
Match length
                   113
% identity
                   81
                  (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                   thaliana] >gi 3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
                   231296
Seq. No.
                   LIB3197-025-Q1-M1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g123613
                   407
BLAST score
                   8.0e-40
E value
                   92
Match length
                   86
% identity
                  HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_100222_pir__S14949
NCBI Description
                   heat shock cognate protein 70 - tomato
```

70 [Lycopersicon esculentum]

>gi\_19256\_emb\_CAA37970\_ (X54029) heat shock protein cognate



```
231297
Seq. No.
Seq. ID
                  LIB3197-025-Q1-M1-B5
Method
                  BLASTX
                  g2129499
NCBI GI
                  605
BLAST score
                  5.0e-63
E value
                  126
Match length
% identity
                  fiber protein E6 (clone CKE6-4A) - upland cotton
NCBI Description
                  >gi 1000086 (U30506) E6 [Gossypium hirsutum]
                  231298
Seq. No.
                  LIB3197-025-Q1-M1-B6
Seq. ID
                  BLASTX
Method
                  q4235430
NCBI GI
                  426
BLAST score
                  4.0e-42
E value
                  134
Match length
                   67
% identity
                  (AF098458) latex-abundant protein [Hevea brasiliensis]
NCBI Description
                  231299
Seq. No.
                  LIB3197-025-Q1-M1-B7
Seq. ID
                   BLASTX
Method
                   q3176874
NCBI GI
                   417
BLAST score
                   6.0e-41
E value
                   134
Match length
                   61
% identity
                   (AF065639) cucumisin-like serine protease [Arabidopsis
NCBI Description
                   thaliana]
                   231300
Seq. No.
Seq. ID
                   LIB3197-025-Q1-M1-B9
                   BLASTX
Method
                   g2961357
NCBI GI
BLAST score
                   583
                   2.0e-60 -
E value
                   140
Match length
% identity
                   80
                  (AL022140) putative protein [Arabidopsis thaliana]
NCBI Description
                   231301
Seq. No.
                   LIB3197-025-Q1-M1-C1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1168328
BLAST score
                   141
                   1.0e-08
E value
                   51
Match length
                   61
% identity
                   ACTIN-LIKE PROTEIN 3 >gi_629878_pir__S48844 actin-like
NCBI Description
                   protein - slime mold (Dictyostelium discoideum)
                   >gi_2130164_pir__S69002 actin-like protein - slime mold
                   (Dictyostelium discoideum) >gi_563346_emb_CAA86553
                   (Z46418) actin-like protein [Dictyostelium discoideum]
```

Seq. ID Method

231307

BLASTX

LIB3197-025-Q1-M1-D6



```
LIB3197-025-Q1-M1-C12
Seq. ID
                  BLASTX
Method
                  g586076
NCBI GI
BLAST score
                  636
                  1.0e-66
E value
Match length
                  118
                  98
% identity
                  TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta
NCBI Description
                  chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta
                  tubulin 1 [Lupinus albus]
                  231303
Seq. No.
                  LIB3197-025-Q1-M1-C4
Seq. ID
                  BLASTX
Method
                  g3695023
NCBI GI
BLAST score
                  322
                  7.0e-30
E value
Match length
                  141
                  50
% identity
                  (AF055850) unknown [Arabidopsis thaliana]
NCBI Description
                  231304
Seq. No.
                  LIB3197-025-Q1-M1-C5
Seq. ID
                  BLASTX
Method
                  q2706450
NCBI GI
BLAST score
                   342
                   3.0e - 32
E value
Match length
                   85
% identity
                   81
                  (AJ225172) magnesium dependent soluble inorganic
NCBI Description
                  pyrophosphatase [Solanum tuberosum]
                   231305
Seq. No.
                   LIB3197-025-Q1-M1-C7
Seq. ID
                   BLASTX
Method
                   g3328240
NCBI GI
                   336
BLAST score
E value
                   2.0e-31
                   108
Match length
                   58
% identity
                  (AF064775) early nodule-specific protein [Medicago
NCBI Description
                   truncatula]
                   231306
Seq. No.
                   LIB3197-025-Q1-M1-D11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2462781
BLAST score
                   511
E value
                   5.0e-52
                   133
Match length
% identity
                   (U73175) carbamoyl phosphate synthetase small subunit
NCBI Description
                   [Arabidopsis thaliana]
```



```
NCBI GI
                  g3869088
BLAST score
                  637
E value
                  9.0e-67
Match length
                  122
                  100
% identity
                  (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
NCBI Description
                  231308
Seq. No.
                  LIB3197-025-Q1-M1-E10
Seq. ID
Method
                  BLASTX
                  g2160322
NCBI GI
BLAST score
                  465
                  1.0e-46
E value
Match length
                  92
% identity
                  92
                  (D16139) cytokinin binding protein CBP57 [Nicotiana
NCBI Description
                  sylvestris]
                  231309
Seq. No.
                  LIB3197-025-Q1-M1-E4
Seq. ID
Method
                  BLASTX
                  g3928099
NCBI GI
BLAST score
                  269
                  1.0e-23
E value
Match length
                  128
% identity
                  23
                  (AC005770) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  231310
                  LIB3197-025-Q1-M1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3695388
BLAST score
                  185
                  8.0e-14
E value
                  60
Match length
                  57
% identity
NCBI Description
                 (AF096371) No definition line found [Arabidopsis thaliana]
                  231311
Seq. No.
                  LIB3197-026-Q1-M1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q71634
BLAST score
                   517
                   1.0e-52
E value
                  95
Match length
% identity
                  100
NCBI Description actin 1 - rice
Seq. No.
                   231312
                  LIB3197-026-Q1-M1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267069
BLAST score
                  551
E value
                   1.0e-56
Match length
                  102
% identity
                   99
NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
```



tubulin alpha chain - Arabidopsis thaliana >gi\_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 231313

Seq. ID LIB3197-026-Q1-M1-A11

Method BLASTX
NCBI GI g4106515
BLAST score 513
E value 3.0e-52
Match length 123
% identity 77

NCBI Description (AF092743) CAK associated cyclinH homolog [Populus tremula

x Populus tremuloides]

Seq. No. 231314

Seq. ID LIB3197-026-Q1-M1-A12

Method BLASTX
NCBI GI g3915031
BLAST score 573
E value 2.0e-59
Match length 109
% identity 98

NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR

(STEAROYL-ACP DESATURASE) >gi\_1217628\_emb\_CAA65232\_

(X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase

[Gossypium hirsutum]

Seq. No. 231315

Seq. ID LIB3197-026-Q1-M1-A2

Method BLASTX
NCBI GI g267073
BLAST score 561
E value 7.0e-58
Match length 107
% identity 94

NCBI Description TUBULIN BETA-2/BETA-3 CHAIN >gi\_320184\_pir\_\_JQ1587 tubulin

beta chain - Arabidopsis thaliana >gi\_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi\_166900 (M84701)

beta-3 tubulin [Arabidopsis thaliana]

Seq. No. 231316

Seq. ID LIB3197-026-Q1-M1-A3

Method BLASTX
NCBI GI g2129499
BLAST score 379
E value 5.0e-37
Match length 78
% identity 87

NCBI Description fiber protein E6 (clone CKE6-4A) - upland cotton

>gi 1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No. 231317

Seq. ID LIB3197-026-Q1-M1-A5

Method BLASTX NCBI GI g267069 BLAST score 616

Seq. ID

231322

LIB3197-026-Q1-M1-B11



```
E value
                  3.0e-64
Match length
                  114
                  99
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  231318
Seq. No.
                  LIB3197-026-Q1-M1-A8
Seq. ID
                  BLASTX
Method
                  g267069
NCBI GI
                  640
BLAST score
                  4.0e-67
E value
                  121
Match length
% identity
                  97
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  231319
Seq. No.
                  LIB3197-026-Q1-M1-A9
Seq. ID
                  BLASTX
Method
                  g1168728
NCBI GI
                  373
BLAST score
                  3.0e - 36
E value
Match length
                  86
                  76
% identity
NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi 598071 (L37883)
                  cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]
                  231320
Seq. No.
                  LIB3197-026-Q1-M1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130073
BLAST score
                   525
E value
                  1.0e-53
                  121
Match length
% identity
                  fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
NCBI Description
                   cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
                   C-1 [Oryza sativa] >gi 790970 dbj BAA08830_ (D50301)
                   aldolase C-1 [Oryza sativa]
                   231321
Seq. No.
Seq. ID
                  LIB3197-026-Q1-M1-B10
Method
                   BLASTX
NCBI GI
                   q2290528
                   185
BLAST score
                   8.0e-14
E value
Match length
                   70
% identity
                   47
NCBI Description (U94746) ATAN11 [Arabidopsis thaliana]
```

33265



```
Method
                  BLASTX
NCBI GI
                  g2914706
BLAST score
                  410
                  3.0e-40
E value
Match length
                  85
                  85
% identity
                  (AC003974) putative homeobox protein [Arabidopsis thaliana]
NCBI Description
                  231323
Seq. No.
                  LIB3197-026-Q1-M1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g728938
                  589
BLAST score
                  3.0e-61
E value
Match length
                  130
% identity
                  87
                  PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP
NCBI Description
                   (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE)
                   (H+-PPASE) >gi 322841 pir JC1466 inorganic pyrophosphatase
                   (EC 3.6.1.1) - barley >gi 285638 dbj BAA02717 (D13472)
                  inorganic pyrophosphatse ase' [Hordeum vulgare]
Seq. No.
                  231324
                  LIB3197-026-Q1-M1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2661840
BLAST score
                  392
E value
                  4.0e-38
                  109
Match length
                  67
% identity
                  (Y15430) adenosine kinase [Physcomitrella patens]
NCBI Description
Seq. No.
                  231325
                  LIB3197-026-Q1-M1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2529683
BLAST score
                  556
E value
                  2.0e-57
Match length
                  129
                  78
% identity
                  (AC002535) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  231326
                  LIB3197-026-Q1-M1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82307
BLAST score
                  633
E value
                   3.0e-66
Match length
                  117
% identity
                   93
                  myb protein 306 - garden snapdragon >gi_256828_bbs_115017
NCBI Description
                  Myb oncoprotein homolog {clone 306} [Antirrhinum
                  majus=snapdragons, J1:522, flowers, Peptide, 316 aa]
```

Seq. ID LIB3197-026-Q1-M1-B6

Method BLASTX



```
NCBI GI
                  g1841870
                  155
BLAST score
                  7.0e-11
E value
                  37
Match length
                  84
% identity
NCBI Description
                  (U87222) elongation factor 1-beta [Pimpinella brachycarpa]
                  231328
Seq. No.
                  LIB3197-026-Q1-M1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2462929
BLAST score
                  455
                  2.0e-45
E value
                  119
Match length
% identity
                  69
                  (Y12295) glutathione transferase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  231329
                  LIB3197-026-Q1-M1-C10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4325345
BLAST score
                  489
                  2.0e-49
E value
Match length
                  137
                  25
% identity
                  (AF128393) similar to thioredoxin-like proteins (Pfam:
NCBI Description
                  PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity
                  to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42,
                  N=1) [Arabidopsis thaliana]
Seq. No.
                  231330
                  LIB3197-026-Q1-M1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3646373
                  534
BLAST score
E value
                  8.0e-55
Match length
                  105
% identity
                   92
NCBI Description
                  (AJ011078) RGP1 protein [Oryza sativa]
                  231331
Seq. No.
                  LIB3197-026-Q1-M1-C3
Seq. ID
Method
                  BLASTX
                  g461812
NCBI GI
BLAST score
                  178
E value
                   5.0e-13
Match length
                  73
% identity
                   48
                  CYTOCHROME P450 72 (CYPLXXII) (PROBABLE
NCBI Description
                  GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081)
                  Cytochrome P-450 protein [Catharanthus roseus]
                  >gi 445604 prf 1909351A cytochrome P450 [Catharanthus
                  roseus]
```

Seq. ID LIB3197-026-Q1-M1-C5

Method BLASTX



```
NCBI GI
                   q3763933
BLAST score
                   139
                   7.0e-09
E value
Match length
                   68
                   56
% identity
                  (AC004450) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   231333
Seq. ID
                   LIB3197-026-Q1-M1-C6
Method
                   BLASTX
NCBI GI
                   q267069
BLAST score
                   524
                   1.0e-53
E value
                   98
Match length
% identity
                   98
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                   231334
                   LIB3197-026-Q1-M1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3334115
BLAST score
                   286
E value
                   1.0e-25
Match length
                   81
                   75
% identity
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                   hirsutum]
                   231335
Seq. No.
                   LIB3197-026-Q1-M1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3212869
BLAST score
                   621
E value
                   6.0e-65
Match length
                   132
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
                   231336
Seq. No.
Seq. ID
                   LIB3197-026-Q1-M1-D12
Method
                   BLASTX
NCBI GI
                   g549060
BLAST score
                   504
E value
                   3.0e-51
Match length
                   137
% identity
                   67
                   T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA)
NCBI Description
                   >gi_631656_pir__S43058 CCTeta protein eta chain - mouse
>gi_468504_emb_CAA83274_ (Z31399) CCTeta, eta subunit of
```

the chaperonin containing TCP-1 (CCT) [Mus musculus]

Seq. ID



```
LIB3197-026-Q1-M1-D6
Seq. ID
                  BLASTX
Method
                  g1351974
NCBI GI
BLAST score
                  613
                  5.0e-64
E value
                  119
Match length
                  100
% identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi 1076788 pir S49325
                                                                    S53486
                  ADP-ribosylation factor - maize >gi 1076789 pir
                  ADP-ribosylation factor - maize >gi 556686 emb CAA56351
                  (X80042) ADP-ribosylation factor [Zea mays]
                  231338
Seq. No.
                  LIB3197-026-Q1-M1-E1
Seq. ID
Method
                  BLASTX
                  g132944
NCBI GI
BLAST score
                  564
                  3.0e-58
E value
Match length
                  115
% identity
                  90
                  60S RIBOSOMAL PROTEIN L3 >qi 81658 pir JQ0772 ribosomal
NCBI Description
                  protein L3 (ARP2) - Arabidopsis thaliana >gi 806279
                  (M32655) ribosomal protein [Arabidopsis thaliana]
                  231339
Seq. No.
Seq. ID
                  LIB3197-026-Q1-M1-E11
                  BLASTX
Method
                  g3062806
NCBI GI
BLAST score
                  434
E value
                  5.0e-43
                  135
Match length
                  57
% identity
                  (D86198) dolichol-phosphate-mannose synthase [Homo sapiens]
NCBI Description
                  >gi 4503363 ref NP 003850.1_pDPM1_ UNKNOWN
                  231340
Seq. No.
                  LIB3197-026-Q1-M1-E2
Seq. ID
                  BLASTX
Method
                  q2369766
NCBI GI
BLAST score
                   473
                  2.0e-47
E value
Match length
                  128
                   69
% identity
NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]
Seq. No.
                  231341
Seq. ID
                  LIB3197-026-Q1-M1-E3
Method
                  BLASTX
NCBI GI
                  g1694711
BLAST score
                  237
                  7.0e-20
E value
                  90
Match length
% identity
                   46
NCBI Description (Y09581) FRO1 [Arabidopsis thaliana]
Seq. No.
                   231342
```

LIB3197-026-Q1-M1-E4



```
BLASTX
Method
                  g3128228
NCBI GI
                  682
BLAST score
                  4.0e-72
E value
Match length
                  137
% identity
                  92
                  (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                  thaliana] >gi 3337376 (AC004481) putative ribosomal protein
                  L18A [Arabidopsis thaliana]
Seq. No.
                  231343
                  LIB3197-026-Q1-M1-E8
Seq. ID
Method
                  BLASTX
                  q3023847
NCBI GI
                  340
BLAST score
                  3.0e - 32
E value
Match length
                  72
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                  PROTEIN >gi 2385376 emb_CAA69934_ (Y08678) G protein beta
                  subunit-like [Medicago sativa]
Seq. No.
                  231344
                  LIB3197-026-Q1-M1-E9
Seq. ID
                  BLASTX
Method
                  q3334320
NCBI GI
                  473
BLAST score
                  1.0e-47
E value
                   104
Match length
                   93
% identity
                  40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
NCBI Description
                   ribosome-associated protein p40 [Glycine max]
Seq. No.
                   231345
                   LIB3197-026-Q1-M1-F1
Seq. ID
                   BLASTX
Method
                   q3170525
NCBI GI
                   160
BLAST score
                   6.0e-11
E value
                   56
Match length
                   57
% identity
NCBI Description (AF054615) cellulase [Fragaria x ananassa]
                   231346
Seq. No.
                   LIB3197-026-Q1-M1-F11
Seq. ID
                   BLASTX
Method
                   g4580461
NCBI GI
                   197
BLAST score
                   3.0e-15
E value
                   77
Match length
                   58
% identity
NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]
                   231347
Seq. No.
                   LIB3197-026-Q1-M1-F2
Seq. ID
                   BLASTX
Method
```

33270

g2914700

NCBI GI



```
BLAST score
                  8.0e-72
E value
                  142
Match length
% identity
                  (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
NCBI Description
                  thaliana]
                  231348
Seq. No.
                  LIB3197-026-Q1-M1-F3
Seq. ID
                  BLASTX
Method
                  g2982303
NCBI GI
BLAST score
                  297
                  4.0e-27
E value
                  66
Match length
% identity
NCBI Description (AF051236) hypothetical protein [Picea mariana]
                  231349
Seq. No.
                  LIB3197-026-Q1-M1-F7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g547683
                  510
BLAST score
                   4.0e-52
E value
                  104
Match length
                   93
% identity
NCBI Description HEAT SHOCK COGNATE PROTEIN 80 >gi 170456 (M96549) heat
                  shock cognate protein 80 [Solanum lycopersicum]
                  >gi_445601_prf__1909348A heat shock protein hsp80
                   [Lycopersicon esculentum]
                   231350
Seq. No.
Seq. ID
                  LIB3197-026-Q1-M1-F8
                  BLASTX
Method
NCBI GI
                   q3183088
                   209
BLAST score
                   1.0e-16
E value
                   71
Match length
                   56
% identity
NCBI Description PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
                   (LTP) >gi 629658 pir S47084 lipid transfer like protein -
                   cowpea >gi 499034 emb CAA56113 (X79604) lipid transfer
                   like protein [Vigna unguiculata]
Seq. No.
                   231351
                   LIB3197-026-Q1-M1-G1
Seq. ID
                   BLASTX
Method
                   q120669
NCBI GI
                   351
BLAST score
                   3.0e-33
E value
Match length
                   96
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
```

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde 3-phosphate\_dehydrogenase [Magnolia liliiflora]



```
Seq. No.
                  231352
                  LIB3197-026-Q1-M1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2213594
BLAST score
                  352
E value
                  2.0e-33
Match length
                  116
                  57
% identity
NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]
Seq. No.
                  231353
                  LIB3197-026-Q1-M1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1172874
BLAST score
                  139
                  1.0e-08
E value
Match length
                  52
                  50
% identity
                  DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
NCBI Description
                  >gi 479589 pir S34823 dehydration-induced protein RD22 -
                  Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22
                  [Arabidopsis thaliana] >gi_447134 prf_ 1913421A rd22 gene
                  [Arabidopsis thaliana]
Seq. No.
                  231354
Seq. ID
                  LIB3197-026-Q1-M1-G7
Method
                  BLASTX
NCBI GI
                  g120669
BLAST score
                  385
                  2.0e-37
E value
Match length
                  75
                  93
% identity
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                  >gi 19566 emb CAA42905 (X60347) glyceraldehyde
                  3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                  231355
Seq. ID
                  LIB3197-026-Q1-M1-G8
Method
                  BLASTX
NCBI GI
                  g3759177
BLAST score
                  364
                  7.0e-35
E value
Match length
                  121
% identity
                  70
NCBI Description
                  (AB018408) 3-phosphoserine phosphatase [Arabidopsis
                  thaliana] >gi 3759179 dbj BAA33807 (AB018409)
                  3-phosphoserin phosphatase [Arabidopsis thaliana]
Seq. No.
                  231356
```

Seq. ID LIB3197-026-Q1-M1-H10

Method BLASTX
NCBI GI g2894378
BLAST score 361
E value 2.0e-34
Match length 139



% identity NCBI Description (Y14573) putative ribophorin I homologue [Hordeum vulgare] Seq. No. 231357 LIB3197-026-Q1-M1-H12 Seq. ID Method BLASTX NCBI GI g2529685 BLAST score 527 E value 7.0e-54Match length 122 % identity NCBI Description (AC002535) putative dimethyladenosine transferase [Arabidopsis thaliana] Seq. No. 231358 Seq. ID LIB3197-026-Q1-M1-H3 Method BLASTX NCBI GI g135449 BLAST score 655 E value 7.0e-69 Match length 142 89 % identity NCBI Description TUBULIN BETA-1 CHAIN >gi\_100932\_pir\_\_S14701 tubulin beta-1 chain - maize >gi\_295851\_emb\_CAA37060\_ (X52878) beta 1 tubulin [Zea mays] Seq. No. 231359 Seq. ID LIB3197-026-Q1-M1-H5 Method BLASTX NCBI GI g99737 BLAST score 461 E value 4.0e-46 Match length 142 % identity 65 NCBI Description NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -Arabidopsis thaliana >gi\_16189\_emb\_CAA46815\_ (X66017) NADPH-ferrihemoprotein reductase [Arabidopsis thaliana] Seq. No. 231360 Seq. ID LIB3197-026-Q1-M1-H8 Method BLASTX NCBI GI g267069 BLAST score 245 E value 2.0e-21 56 Match length % identity NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183 pir JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >qi 166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana] Seq. No. 231361 Seq. ID LIB3197-027-Q1-M1-A1

BLASTX Method NCBI GI g3421094 BLAST score 247 E value 1.0e-21

BLAST score

E value Match length 426 5.0e-42

84



```
52
Match length
% identity
                  (AF043527) 20S proteasome subunit PAF2 [Arabidopsis
NCBI Description
                  thaliana]
                  231362
Seq. No.
                  LIB3197-027-Q1-M1-A10
Seq. ID
                  BLASTX
Method
                  g3269284
NCBI GI
BLAST score
                  381
                  8.0e-37
E value
                  114
Match length
                   69
% identity
                  (AL030978) histone H2A- like protein [Arabidopsis thaliana]
NCBI Description
                  231363
Seq. No.
                  LIB3197-027-Q1-M1-A11
Seq. ID
                  BLASTX
Method
                  g441457
NCBI GI
                   623
BLAST score
                   4.0e-65
E value
Match length
                  117
                   98
% identity
                   (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                  esculentum]
Seq. No.
                   231364
                  LIB3197-027-Q1-M1-A12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4580394
BLAST score
                   180
                   2.0e-13
E value
                   83
Match length
                   42
% identity
                   (AC007171) putative fatty acid elongase [Arabidopsis
NCBI Description
                   thaliana]
                   231365
Seq. No.
                   LIB3197-027-Q1-M1-A6
Seq. ID
Method
                   BLASTX
                   g1174470
NCBI GI
BLAST score
                   313
                   1.0e-28
E value
                   92
Match length
                   59
% identity
                  OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)
NCBI Description
                   (INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral
                   membrane protein 1 [Mus musculus] >gi_1588285 prf 2208301A
                   integral membrane protein [Mus musculus]
                   231366
Seq. No.
                   LIB3197-027-Q1-M1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g464846
```



% identity TUBULIN ALPHA-6 CHAIN >gi\_322880\_pir\_\_\$28983 tubulin
alpha-6 chain - maize >gi\_22158\_emb\_CAA44863\_ (X63178) NCBI Description alpha-tubulin #6 [Zea mays] 231367 Seq. No. LIB3197-027-Q1-M1-A8 Seq. ID BLASTX Method NCBI GI g1370198 BLAST score 286 E value 1.0e-25 77 Match length 77 % identity NCBI Description (Z73948) RAB8E [Lotus japonicus] Seq. No. 231368 LIB3197-027-Q1-M1-A9 Seq. ID Method BLASTX NCBI GI g2995384 BLAST score 159 8.0e-11 E value Match length 60 % identity 58 NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays] Seq. No. 231369 LIB3197-027-Q1-M1-B1 Seq. ID Method BLASTX NCBI GI g1170508 BLAST score 492 E value 7.0e-50 Match length 105 % identity 88 EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8) NCBI Description >gi\_2119931\_pir\_\_S60244 translation initiation factor eIF-4A.8, anther-specific - common tobacco >qi 475219 emb CAA55639 (X79004) translation initiation factor (eIF-4A) [Nicotiana tabacum] >gi 475221 emb CAA55640 (X79005) translation initiation factor (eIF-4A) [Nicotiana tabacum] 231370 Seq. No. LIB3197-027-Q1-M1-B12 Seq. ID Method BLASTX NCBI GI g2558655 BLAST score 237 7.0e-20 E value Match length 134 43 % identity NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]

231371

Seq. No.

Seq. ID LIB3197-027-Q1-M1-B2

BLASTX Method NCBI GI g1170508 BLAST score 182 E value 6.0e-14



```
Match length
                  60
% identity
                  EUKARYOTIC INITIATION FACTOR 4A-8 (EIF-4A-8)
NCBI Description
                  >gi_2119931_pir__S60244 translation initiation factor
                  eIF-4A.8, anther-specific - common tobacco
                  >gi 475219 emb CAA55639 (X79004) translation initiation
                  factor (eIF-4A) [Nicotiana tabacum]
                  >gi 475221 emb CAA55640 (X79005) translation initiation
                  factor (eIF-4A) [Nicotiana tabacum]
Seq. No.
                  231372
Seq. ID
                  LIB3197-027-Q1-M1-B5
Method
                  BLASTX
NCBI GI
                  q418854
                  757
BLAST score
E value
                  8.0e-81
Match length
                  152
% identity
                  18
NCBI Description
                  ubiquitin precursor - parsley >gi 288112 emb CAA45621
                  (X64344) polyubiquitin [Petroselinum crispum]
                  >gi_288114_emb_CAA45622_ (X64345) polyubiquitin
                  [Petroselinum crispum]
                  231373
Seq. No.
                  LIB3197-027-Q1-M1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3879145
BLAST score
                  164
E value
                  3.0e-11
Match length
                  80
% identity
                  44
                  (Z93386) predicted using Genefinder; Similarity to Human
NCBI Description
                  placenta (DIFF33) protein (TR:Q13530); cDNA EST yk198a11.5
                  comes from this gene [Caenorhabditis elegans]
Seq. No.
                  231374
Seq. ID
                  LIB3197-027-Q1-M1-B8
Method
                  BLASTX
NCBI GI
                  g3193222
BLAST score
                  164
E value
                  3.0e-11
Match length
                  36
% identity
NCBI Description (AF068687) malate dehydrogenase [Glycine max]
Seq. No.
                  231375
Seq. ID
                  LIB3197-027-Q1-M1-C1
Method
                  BLASTX
NCBI GI
                  g4309972
BLAST score
                  164
E value
                  2.0e-11
Match length
                  119
```

% identity

Seq. ID LIB3197-027-Q1-M1-C11

NCBI Description (AC002983) hypothetical protein [Arabidopsis thaliana]



```
Method
                  BLASTX
NCBI GI
                  g2253384
BLAST score
                  747
                  1.0e-79
E value
                  150
Match length
                   95
% identity
NCBI Description (AF007100) biotin carboxylase precursor [Glycine max]
Seq. No.
                   231377
                  LIB3197-027-Q1-M1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4105696
BLAST score
                   676
E value
                   3.0e-71
                  132
Match length
                   95
% identity
NCBI Description (AF049870) beta tubulin 1 [Arabidopsis thaliana]
Seq. No.
                   231378
Seq. ID
                  LIB3197-027-Q1-M1-C6
Method
                  BLASTX
NCBI GI
                   g3163946
BLAST score
                   565
E value
                   4.0e-67
Match length
                   151
% identity
                   89
NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]
Seq. No.
                   231379
                   LIB3197-027-Q1-M1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g529516
BLAST score
                   287
E value
                   1.0e-25
Match length
                   85
% identity
                   60
NCBI Description (L29099) beta-fructosidase [Solanum tuberosum]
Seq. No.
                   231380
                   LIB3197-027-Q1-M1-C9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2811278
BLAST score
                   587
E value
                   6.0e-61
Match length
                   123
% identity
                   88
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                   231381
Seq. ID
                   LIB3197-027-Q1-M1-D10
                   BLASTX
Method
NCBI GI
                   g3608137
BLAST score
                   264
E value
                   5.0e-23
Match length
                   125
% identity
```

NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. ID Method

NCBI GI



```
231382
 Seq. No.
 Seq. ID
                    LIB3197-027-Q1-M1-D11
 Method
                    BLASTX
. NCBI GI
                    g2924520
 BLAST score
                    649
 E value
                    4.0e-68
 Match length
                    144
                    85
 % identity
                    (AL022023) plasma membrane intrinsic protein (SIMIP)
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                    231383
 Seq. ID
                    LIB3197-027-Q1-M1-D12
                    BLASTX
 Method
 NCBI GI
                    g4056496
 BLAST score
                    283
 E value
                    8.0e-45
 Match length
                    142
 % identity
                    64
 NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    231384
 Seq. ID
                    LIB3197-027-Q1-M1-D2
 Method
                    BLASTX
 NCBI GI
                    g4103959
 BLAST score
                    594
 E value
                    1.0e-61
 Match length
                    116
 % identity
                    60
 NCBI Description (AF030033) calmodulin [Phaseolus vulgaris]
 Seq. No.
                    231385
 Seq. ID
                    LIB3197-027-Q1-M1-D3
 Method
                    BLASTX
 NCBI GI
                    g2369714
 BLAST score
                    468
 E value
                    6.0e-47
 Match length
                    101
 % identity
                    91
 NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]
 Seq. No.
                    231386
 Seq. ID
                    LIB3197-027-Q1-M1-D4
 Method
                    BLASTX
 NCBI GI
                    g3660467
 BLAST score
                    396
 E value
                    2.0e-38
 Match length
                    134
 % identity
                    64
 NCBI Description
                    (AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis
                    thaliana]
 Seq. No.
                    231387
```

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LIB3197-027-Q1-M1-D5

BLASTX

g832876



BLAST score E value 6.0e-60 Match length 128 88 % identity (L41345) ascorbate free radical reductase [Solanum NCBI Description lycopersicum] >gi 1097368 prf 2113407A ascorbate free radical reductase [Lycopersicon esculentum] 231388 Seq. No. Seq. ID LIB3197-027-Q1-M1-D7 Method BLASTX NCBI GI g267069 BLAST score 509 7.0e-52 E value 94 Match length 99 % identity TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594 NCBI Description tubulin alpha chain - Arabidopsis thaliana >gi\_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana] Seq. No. 231389 Seq. ID LIB3197-027-Q1-M1-D8 Method BLASTX NCBI GI g1399273 BLAST score 329 E value 1.0e-30 Match length 138 % identity 52 (U31834) calmodulin-domain protein kinase CDPK isoform 5 NCBI Description [Arabidopsis thaliana] >gi\_3080419\_emb\_CAA18738\_ (AL022604) calmodulin-domain protein kinase CDPK isoform 5 (CPK5) [Arabidopsis thaliana] Seq. No. 231390 Seq. ID LIB3197-027-Q1-M1-D9 BLASTX Method NCBI GI g1174592 BLAST score 670 E value 1.0e-70 133 Match length 100 % identity NCBI Description TUBULIN ALPHA-1 CHAIN >gi\_2119270\_pir\_\_S60233 alpha-tubulin - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum sativum] Seq. No. 231391

Seq. ID LIB3197-027-Q1-M1-E1

Method BLASTX
NCBI GI g2996012
BLAST score 267
E value 6.0e-33
Match length 103
% identity 71

NCBI Description (AF054455) cytosolic phosphoglucose isomerase; PgiC

[Leavenworthia crassa]



```
Seq. No.
                  231392
Seq. ID
                  LIB3197-027-Q1-M1-E10
Method
                  BLASTX
NCBI GI
                  g3738324
BLAST score
                  256
E value
                  4.0e-22
Match length
                  99
                  48
% identity
NCBI Description (AC005170) GMP synthase-like protein [Arabidopsis thaliana]
Seq. No.
                  231393
Seq. ID
                  LIB3197-027-Q1-M1-E4
Method
                  BLASTX
NCBI GI
                  q3158376
BLAST scoré
                  488
E value
                  3.0e-49
Match length
                  131
                  75
% identity
NCBI Description (AF035385) unknown [Arabidopsis thaliana]
                  231394
Seq. No.
Seq. ID
                  LIB3197-027-Q1-M1-E6
Method
                  BLASTX
NCBI GI
                  q3337356
BLAST score
                  593
E value
                  1.0e-61
Match length
                  119
                  97
% identity
                  (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                  subunit [Arabidopsis thaliana]
Seq. No.
                  231395
Seq. ID
                  LIB3197-027-Q1-M1-E8
Method
                  BLASTX
NCBI GI
                  g3834321
BLAST score
                  652
E value
                  2.0e-68
Match length
                  136
% identity
                  91
NCBI Description
                  (AC005679) Strong similarity to F13P17.9 gi 3337356
                  transport protein SEC61 alpha subunit homolog from
                  Arabidopsis thaliana BAC gb AC004481. [Arabidopsis
                  thaliana]
Seq. No.
                  231396
Seq. ID
                  LIB3197-027-Q1-M1-F10
Method
                  BLASTX
NCBI GI
                  g4559358
BLAST score
                  171
E value
```

4.0e-12 52 Match length

% identity

NCBI Description (AC006585) putative steroid binding protein [Arabidopsis

thaliana]

Seq. No. 231397

Seq. ID LIB3197-027-Q1-M1-F11



```
BLASTX
Method
NCBI GI
                  g1931639
BLAST score
                  234
                  9.0e-20
E value
                  126
Match length
                  39
% identity
NCBI Description (U95973) lysophospholipase isolog [Arabidopsis thaliana]
Seq. No.
                  231398
Seq. ID
                  LIB3197-027-Q1-M1-F3
Method
                  BLASTX
NCBI GI
                  q4008441
BLAST score
                  334
E value
                  2.0e-36
                  131
Match length
% identity
                  63
                  (AL034488) predicted using Genefinder; cDNA EST yk433c6.3
NCBI Description
                  comes from this gene; cDNA EST EMBL: D72601 comes from this
                  gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST
                  yk433c6.5 comes from this gene [Caenorhabditis elegans]
Seq. No.
                  231399
Seq. ID
                  LIB3197-027-Q1-M1-F4
Method
                  BLASTX
NCBI GI
                  g3402679
BLAST score
                  710
E value
                  3.0e-75
Match length
                  150
                  87
% identity
NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]
Seq. No.
                  231400
                  LIB3197-027-Q1-M1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3097321
BLAST score
                  226
E value
                  1.0e-18
Match length
                  116
% identity
                  41
NCBI Description (AB013289) Bd 30K [Glycine max]
                  231401
Seq. No.
Seq. ID
                  LIB3197-027-Q1-M1-F9
Method
                  BLASTX
NCBI GI
                  g1706403
BLAST score
                  338
E value
                  9.0e-32
                  69
Match length
                  94
% identity
NCBI Description GLUTAMATE DEHYDROGENASE (GDH) >gi 1085815 pir S54797
                  glutamate dehydrogenase (EC 1.4.1.2) - Vitis vinifera
                  >gi_806595_emb_CAA60507_ (X86924) glutamate dehydrogenase
                  [Vitis vinifera]
Seq. No.
                  231402
```

LIB3197-027-Q1-M1-G1 Seq. ID

Method BLASTX



```
NCBI GI
                   q2500399
BLAST score
                   283
E value
                   3.0e-29
Match length
                  87
% identity
                   85
NCBI Description
                  40S RIBOSOMAL PROTEIN S3 >gi 1836060 bbs 179561 (S83098)
                  ribosomal protein S3 [Ambystoma mexicanum=Mexican axolotls,
                  embryos, Peptide, 253 aa] [Ambystoma mexicanum]
                  231403
Seq. No.
Seq. ID
                  LIB3197-027-Q1-M1-G10
Method
                  BLASTX
NCBI GI
                  q2119353
BLAST score
                  197
E value
                   5.0e-27
Match length
                  125
                   28
% identity
NCBI Description calmodulin - moss (Physcomitrella patens)
Seq. No.
                  231404
                  LIB3197-027-Q1-M1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3169287
BLAST score
                   711
E value
                  2.0e-75
Match length
                  135
% identity
                   100
NCBI Description
                   (AF050673) vacuolar H+-ATPase catalytic subunit [Gossypium
                  hirsutum]
Seq. No.
                   231405
Seq. ID
                  LIB3197-027-Q1-M1-G4
Method
                  BLASTX
NCBI GI
                   q267082
BLAST score
                  513
E value
                   3.0e-52
Match length
                  100
% identity
                   93
                  TUBULIN BETA-8 CHAIN >gi 320189 pir JQ1592 tubulin beta-8
NCBI Description
                   chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8
                  tubulin [Arabidopsis thaliana]
Seq. No.
                  231406
Seq. ID
                  LIB3197-027-Q1-M1-G5
Method
                  BLASTX
NCBI GI
                  g2344894
BLAST score
                  415
E value
                  8.0e-41
                  125
Match length
% identity
NCBI Description (AC002388) hypothetical protein [Arabidopsis thaliana]
```

Seq. ID LIB3197-027-Q1-M1-G7

Method BLASTX
NCBI GI g3202000
BLAST score 638



E value 6.0e-67 Match length 128 % identity 97

NCBI Description (AF068846) scaffold attachment factor A [Homo sapiens]

Seq. No.

231408

Seq. ID

LIB3197-027-Q1-M1-G8

Method BLASTX
NCBI GI g1170949
BLAST score 484
E value 7.0e-49
Match length 130
% identity 68

NCBI Description SERINE/THREONINE-PROTEIN KINASE MHK >gi\_481207\_pir\_\_S38327

protein kinase - Arabidopsis thaliana  $>gi_1668\overline{1}1$  ( $\overline{L07249}$ )

protein kinase [Arabidopsis thaliana]

Seq. No.

231409

Seq. ID LIB3197-027-Q1-M1-G9

Method BLASTX
NCBI GI g3334661
BLAST score 290
E value 4.0e-26
Match length 91
% identity 58

NCBI Description (Y10490) putative cytochrome P450 [Glycine max]

Seq. No. 231410

Seq. ID LIB3197-027-Q1-M1-H1

Method BLASTX
NCBI GI g2130017
BLAST score 214
E value 3.0e-17
Match length 63
% identity 63

NCBI Description hypothetical protein - common sunflower

>gi\_1040729\_emb\_CAA60621\_ (X87143) cytochrome b5 containing

fusion protein [Helianthus annuus]

Seq. No. 231411

Seq. ID LIB3197-027-Q1-M1-H2

Method BLASTX
NCBI GI g267069
BLAST score 383
E value 3.0e-67
Match length 128
% identity 98

NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594

tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 231412

Seq. ID LIB3197-027-Q1-M1-H3

Method BLASTX NCBI GI g267069 BLAST score 670



```
E value
                  1.0e-70
Match length .
                  127
                  97
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                  231413
Seq. ID
                  LIB3197-027-Q1-M1-H5
Method
                  BLASTX
NCBI GI
                  g2501555
BLAST score
                  482
                  1.0e-48
E value
                  120
Match length
                  71
% identity
NCBI Description POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi 549984 (U13148)
                  possible apospory-associated protein [Pennisetum ciliare]
Seq. No.
                  231414
Seq. ID
                  LIB3197-027-Q1-M1-H6
Method
                  BLASTX
NCBI GI
                  q3342798
BLAST score
                  175
                  1.0e-12
E value
Match length
                  71
% identity
NCBI Description (AF061240) glutamine cyclotransferase precursor [Carica
                  papaya]
Seq. No.
                  231415
                  LIB3197-027-Q1-M1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130017
BLAST score
                  384
E value
                  4.0e-37
Match length
                  112
% identity
                  62
NCBI Description hypothetical protein - common sunflower
                  >gi 1040729 emb CAA60621_ (X87143) cytochrome b5 containing
                  fusion protein [Helianthus annuus]
Seq. No.
                  231416
Seq. ID
                  LIB3197-027-01-M1-H8
Method
                  BLASTX
NCBI GI
                  q3860277
BLAST score
                  400
E value
                  2.0e-45
Match length
                  123
% identity
                  78
```

NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi 4314394 gb AAD15604 (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 231417

LIB3197-027-Q1-M1-H9 Seq. ID

Method BLASTX



```
NCBI GI
                   q3157943
BLAST score
                   381
E value
                   8.0e-37
Match length
                   117
% identity
                   60
                  (AC002131) Contains similarity to BAP31 protein gb_X81816
NCBI Description
                   from Mus musculus. [Arabidopsis thaliana]
Seq. No.
                   231418
Seq. ID
                   LIB3197-028-Q1-M1-A10
Method
                   BLASTX
NCBI GI
                   g4544399
BLAST score
                   537
E value
                   5.0e-55
                   147
Match length
% identity
                   69
                  (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
                   231419
Seq. No.
                   LIB3197-028-Q1-M1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q464846
BLAST score
                   405
E value
                   1.0e-39
Match length
                   83
% identity
                   89
                   TUBULIN ALPHA-6 CHAIN >gi_322880_pir__S28983 tubulin alpha-6 chain - maize >gi_22158_emb_CAA44863_ (X63178)
NCBI Description
                   alpha-tubulin #6 [Zea mays]
                   231420
Seq. No.
Seq. ID
                   LIB3197-028-Q1-M1-A6
Method
                   BLASTX
NCBI GI
                   g2996012
BLAST score
                   525
E value
                   1.0e-53
Match length
                   128
                   77
% identity
NCBI Description (AF054455) cytosolic phosphoglucose isomerase; PgiC
                   [Leavenworthia crassa]
Seq. No.
                   231421
Seq. ID
                   LIB3197-028-Q1-M1-A8
Method
                   BLASTX
NCBI GI
                   q135406
BLAST score
                   396 -
E value
                   8.0e-39
Match length
                   76
% identity
                   93
NCBI Description TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi 99768 pir_A32712 tubulin
                   alpha-5 chain - Arabidopsis thaliana >gi 166912 (M17189)
                   alpha-tubulin [Arabidopsis thaliana] >gi 166918 (M84698)
                   alpha-5 tubulin [Arabidopsis thaliana]
```

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231422

LIB3197-028-Q1-M1-B10

Seq. No. Seq. ID



```
BLASTX
Method
NCBI GI
                  g2062167
BLAST score
                  462
E value
                  3.0e-46
                  99
Match length
% identity
                  87
                 (AC001645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  231423
Seq. ID
                  LIB3197-028-Q1-M1-B11
Method
                  BLASTX
NCBI GI
                  q4417289
BLAST score
                  149
E value
                  1.0e-09
Match length
                  84
                  54
% identity
NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]
Seq. No.
                  231424
                  LIB3197-028-Q1-M1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g135406
BLAST score
                  174
E value
                  2.0e-12
                  72
Match length
% identity
                  49
                  TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin
NCBI Description
                  alpha-5 chain - Arabidopsis thaliana >gi 166912 (M17189)
                  alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)
                  alpha-5 tubulin [Arabidopsis thaliana]
Seq. No.
                  231425
Seq. ID
                  LIB3197-028-Q1-M1-B6
Method
                  BLASTX
NCBI GI
                  g3892051
BLAST score
                  161
E value
                  3.0e-11
Match length
                  87
% identity
                  44
NCBI Description (AC002330) predicted NADH dehydrogenase 24 kD subunit
                  [Arabidopsis thaliana]
                  231426
Seq. No.
Seq. ID
                  LIB3197-028-Q1-M1-C12
                  BLASTX
Method
NCBI GI
                  g312179
BLAST score
                  524
E value
                  2.0e-53
Match length
                  105
% identity
                  93
NCBI Description
                 (X73151) glyceraldehyde 3-phosphate dehydrogenase
                  (phosphorylating) [Zea mays] >gi 1184772 (U45855) cytosolic
                  glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]
```

dehydrogenase [Zea mays]

>gi 1185554 (U45858) glyceraldehyde÷3-phosphate

Match length

% identity

71



```
Seq. No.
                   231427
Seq. ID
                   LIB3197-028-Q1-M1-C2
Method
                   BLASTX
NCBI GI
                   g2511529
BLAST score
                   305
E value
                   5.0e-28
Match length
                   78
% identity
                   77
NCBI Description (AF002697) E1B 19K/Bcl-2-binding protein Nip3 [Homo
                   sapiens]
                   231428
Seq. No.
Seq. ID
                   LIB3197-028-Q1-M1-C3
Method
                   BLASTX
NCBI GI
                   q3915826
BLAST score
                   399
E value
                   5.0e-39
                   99
Match length
% identity
                   77
NCBI Description 60S RIBOSOMAL PROTEIN L5
Seq. No.
                   231429
Seq. ID
                   LIB3197-028-Q1-M1-C5
Method
                   BLASTX
NCBI GI
                   q2119278
BLAST score
                   630
E value
                   6.0e-66
Match length
                   120
                   95
% identity
NCBI Description tubulin beta-1 chain - rice
                   231430
Seq. No.
Seq. ID
                   LIB3197-028-Q1-M1-C7
Method
                   BLASTX
NCBI GI
                   g730917
BLAST score
                   239
E value
                   2.0e-20
Match length
                   93
% identity
                   56
NCBI Description T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA)
                   >gi_626947_pir__S48232 TCP1 complex beta chain - yeast
                   (Saccharomyces cerevisiae) >gi_454887_emb_CAA54745_
                   (X77675) TCP1-related chaperonin [Saccharomyces cerevisiae]
                   >gi_557781_emb_CAA86136_ (Z38059) tcp1beta, len: 527, CAI:
0.19, chaperone protein [Saccharomyces cerevisiae]
                   >gi 571510 (U16761) Bin3p [Saccharomyces cerevisiae]
Seq. No.
                   231431
Seq. ID
                   LIB3197-028-Q1-M1-D10
Method
                   BLASTX
NCBI GI
                   g2911075
BLAST score
                   244
E value
                   9.0e-21
```

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NCBI Description (AL021960) putative protein [Arabidopsis thaliana]



Seq. No. 231432 Seq. ID LIB3197-028-Q1-M1-D11 Method BLASTX NCBI GI g135406 BLAST score 590 E value 3.0e-61 Match length 116 % identity 95 NCBI Description TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi\_99768\_pir\_\_A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi 166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi 166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana] Seq. No. 231433 Seq. ID LIB3197-028-Q1-M1-D12 Method BLASTX NCBI GI g303750 BLAST score 472 E value 2.0e-47 Match length 91 % identity 100 NCBI Description (D12548) GTP-binding protein [Pisum sativum] >gi 738940 prf 2001457H GTP-binding protein [Pisum sativum] Seq. No. 231434 Seq. ID LIB3197-028-Q1-M1-D2 Method BLASTX NCBI GI g113621 BLAST score 265 E value 1.0e-23 Match length 63 % identity 84 NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi 68196 pir ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi 168420 (M16220) aldolase [Zea mays] >gi\_295850\_emb\_CAA31366\_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi\_225624\_prf\_\_1307278A cytoplasmic aldolase [Zea mays] Seq. No. 231435 Seq. ID LIB3197-028-Q1-M1-D4 Method BLASTX NCBI GI g2982311 BLAST score 631 5.0e-66 E value 128 Match length % identity NCBI Description (AF051240) probable ubiquitin-conjugating enzyme E2 [Picea mariana]

Seq. No. 231436

Seq. ID LIB3197-028-Q1-M1-D5

Method BLASTX
NCBI GI g1332411
BLAST score 497
E value 2.0e-50



```
Match length
                   114
% identity
NCBI Description (D85102) dihydroflavonol 4-reductase [Rosa hybrida]
                   231437
Seq. No.
Seq. ID
                   LIB3197-028-Q1-M1-D7
Method
                   BLASTX
NCBI GI
                   g3152582
BLAST score
                   270
E value
                   8.0e-24
Match length
                   73
% identity
                   66
NCBI Description (AC002986) YUP8H12R.20 [Arabidopsis thaliana]
Seq. No.
                   231438
                   LIB3197-028-Q1-M1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3128176
BLAST score
                   262
E value
                   7.0e-23
                   87
Match length
% identity
                   54
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                   231439
Seq. ID
                  LIB3197-028-Q1-M1-E1
Method
                   BLASTX
NCBI GI
                   q2253010
BLAST score
                   577
                   8.0e-60
E value
Match length
                   122
                   89
% identity
NCBI Description
                  (Y14199) MAP3K delta-1 protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   231440
Seq. ID
                   LIB3197-028-Q1-M1-E10
Method
                   BLASTX
NCBI GI
                   q3776084
BLAST score
                   272
E value
                   6.0e-24
Match length
                  85
% identity
                   59
NCBI Description (Y18251) NtN2 [Medicago truncatula]
Seq. No.
                   231441
Seq. ID
                   LIB3197-028-Q1-M1-E11
Method
                   BLASTX
NCBI GI
                   g2651308
BLAST score
                   340
E value
                   6.0e-32
Match length
                   117
```

% identity 67

NCBI Description (AC002336) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.

231442

33289



BLASTX

LIB3197-028-Q1-M1-E4

Seq. ID

Method -

```
NCBI GI
                   q2129473
BLAST score
                   247
E value
                   5.0e-21
Match length
                  91
                   51
% identity
NCBI Description
                  arabinogalactan-like protein - loblolly pine >gi_607774
                   (U09556) arabinogalactan-like protein [Pinus taeda]
Seq. No.
                  231443
Seq. ID
                  LIB3197-028-Q1-M1-E5
Method
                  BLASTX
NCBI GI
                  q4033424
BLAST score
                   433
E value
                   8.0e-43
Match length
                  99
                  82
% identity
                  SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
NCBI Description
                  PHOSPHO-HYDROLASE) (PPASE) >gi 2668746 (AF034947) inorganic
                  pyrophosphatase [Zea mays]
Seq. No.
                  231444
Seq. ID
                  LIB3197-028-Q1-M1-E9
Method
                  BLASTX
NCBI GI
                  g2342735
BLAST score
                  233
E value
                  2.0e-19
Match length
                  52
% identity
                  87
NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]
Seq. No.
                  231445
Seq. ID
                  LIB3197-028-Q1-M1-F10
Method
                  BLASTX
NCBI GI
                  g82040
BLAST score
                  744
E value
                  3.0e-79
                  149
Match length
% identity
                  28
NCBI Description
                  ubiquitin precursor - flax (fragment) >qi 168304 (M57895)
                  ubiquitin [Linum usitatissimum]
Seq. No.
                  231446
Seq. ID
                  LIB3197-028-Q1-M1-F12
Method
                  BLASTX
NCBI GI
                  g2970051
BLAST score
                  441
E value
                  9.0e-44
Match length
                  109
% identity
                  77
NCBI Description (AB012110) ARG10 [Vigna radiata]
Seq. No.
                  231447
Seq. ID
                  LIB3197-028-Q1-M1-F2
Method
                  BLASTX
NCBI GI
                  g3420239
```

33290



207 BLAST score 1.0e-20 E value Match length 68 % identity 84 NCBI Description (AF059484) actin [Gossypium hirsutum] Seq. No. 231448 Seq. ID LIB3197-028-Q1-M1-F3 Method BLASTX NCBI GI q232024 BLAST score 744 E value 2.0e-79 Match length 139 100 % identity PROTEIN E6 >gi 421806 pir A46130 fiber protein - upland NCBI Description cotton >gi\_2129498\_pir\_\_S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi\_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi 1000084 (U30505) E6 [Gossypium hirsutum] 231449 Seq. No. Seq. ID LIB3197-028-Q1-M1-F4 Method BLASTX NCBI GI q3098571 BLAST score 232 E value 3.0e-19 Match length 134 37 % identity NCBI Description (AF049028) BURP domain containing protein [Brassica napus] Seq. No. 231450 LIB3197-028-Q1-M1-F5 Seq. ID Method BLASTX NCBI GI q2827550 BLAST score 193 E value 1.0e-14 57 Match length % identity 65 NCBI Description (AL021635) leucine rich repeat receptor kinase-like protein [Arabidopsis thaliana] Seq. No. 231451 Seq. ID LIB3197-028-Q1-M1-F8 BLASTX Method NCBI GI g2464905 BLAST score 275

2.0e-24 E value 110 Match length 54 % identity

NCBI Description (Z99708) minor allergen [Arabidopsis thaliana]

Seq. No. 231452

Seq. ID LIB3197-028-Q1-M1-F9

BLASTX Method NCBI GI g1009232 BLAST score 162 E value 4.0e-11



```
Match length
                    66
% identity
                    58
NCBI Description
                    (L38828) EF-1-alpha-related GTP-binding protein [Nicotiana
                    tabacum]
Seq. No.
                   231453
Seq. ID
                   LIB3197-028-Q1-M1-G10
Method
                   BLASTX
NCBI GI
                    q1256509
BLAST score
                    511
E value
                    5.0e-52
Match length
                   106
                    84
% identity
NCBI Description
                  (X92943) pectate lyase [Musa acuminata]
Seq. No.
                   231454
Seq. ID
                   LIB3197-028-Q1-M1-G11
Method
                   BLASTX
NCBI GI
                    g2811278
BLAST score
                   576
E value
                    6.0e-64
Match length
                   135
% identity
                    88
NCBI Description
                  (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                   231455
                   LIB3197-028-Q1-M1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g728938
BLAST score
                    692
E value
                   3.0e-73
Match length
                    148
% identity
                    91
NCBI Description
                   PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP
                    (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE)
                    (H+-PPASE) >gi_322841_pir__JC1466 inorganic pyrophosphatase (EC 3.6.1.1) - barley >gi_285638_dbj_BAA02717_ (D13472)
                    inorganic pyrophosphatse ase' [Hordeum vulgare]
Seq. No.
                    231456
Seq. ID
                   LIB3197-028-Q1-M1-G2
Method
                   BLASTX
NCBI GI
                   g1449179
BLAST score
                   161
E value
                   5.0e-11
Match length
                   54
% identity
                   54
NCBI Description
                   (D86506) N-ethylmaleimide sensitive fusion protein
                    [Nicotiana tabacum]
```

Seq. No. 231457

Seq. ID LIB3197-028-Q1-M1-G3

Method BLASTX
NCBI GI g1041706
BLAST score 524
E value 2.0e-53
Match length 111

NCBI Description



```
% identity
NCBI Description (U30480) expansin At-EXP6 [Arabidopsis thaliana]
Seq. No.
                   231458
Seq. ID
                  LIB3197-028-Q1-M1-G5
Method
                  BLASTX
NCBI GI
                  g2935298
BLAST score
                   400
E value
                   6.0e - 39
Match length
                  123
% identity
                   66
                  (AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase
NCBI Description
                   1 [Gossypium hirsutum]
Seq. No.
                   231459
                  LIB3197-028-Q1-M1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4545231
BLAST score
                   514
E value
                   2.0e-52
Match length
                   101
                   99
% identity
                  (AF116243) RAS-related GTP-binding protein [Gossypium
NCBI Description
                  hirsutum]
Seq. No.
                  231460
Seq. ID
                  LIB3197-028-Q1-M1-G7
Method
                  BLASTX
NCBI GI
                   g2811278
BLAST score
                   548
E value
                   3.0e-56
Match length
                  135
                   76
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                   231461
Seq. ID
                  LIB3197-028-Q1-M1-G8
Method
                  BLASTX
NCBI GI
                  q1361974
BLAST score
                   453
E value
                   3.0e-45
Match length
                  145
                   59
% identity
NCBI Description cysteine proteinase - clove pink (fragment) >gi 595986
                   (U17135) cysteine proteinase [Dianthus caryophyllus]
Seq. No.
                   231462
Seq. ID
                  LIB3197-028-Q1-M1-H1
Method
                  BLASTX
NCBI GI
                  g3885328
BLAST score
                  391
E value
                   5.0e-41
Match length
                  104
                   83
% identity
```

[Arabidopsis thaliana]

(AC005623) putative serine/threonine protein kinase



```
Seq. No.
                     231463
                     LIB3197-028-Q1-M1-H4
  Seq. ID
 Method
                     BLASTX
  NCBI GI
                     g120673
  BLAST score
                     626
 E value
                     2.0e-65
 Match length
                     146
  % identity
                     82
 NCBI Description
                    GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                     >gi_66013_pir__DEPJG glyceraldehyde-3-phosphate
                     dehydrogenase (EC 1.2.1.12) - garden petunia
                     >gi_20551_emb_CAA42904_ (X60346) glyceraldehyde
                     3-phosphate dehydrogenase [Petunia x hybrida]
  Seq. No.
                     231464
  Seq. ID
                     LIB3197-029-Q1-M1-A1
 Method
                     BLASTX
 NCBI GI
                     g4580455
 BLAST score
                     415
 E value
                     7.0e-41
 Match length
                     113
                     75
  % identity
 NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]
                     231465
  Seq. No.
  Seq. ID
                     LIB3197-029-Q1-M1-A10
 Method
                     BLASTX
 NCBI GI
                     q4056488
  BLAST score
                     189
 E value
                     6.0e-21
 Match length
                     67
                     76
  % identity
  NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]
                     231466
  Seq. No.
  Seq. ID
                     LIB3197-029-Q1-M1-A11
Method
                     BLASTX
  NCBI GI
                     q872116
 BLAST score
                     422
  E value
                     1.0e-41
  Match length
                     103
  % identity
                     80
  NCBI Description (X79770) sti (stress inducible protein) [Glycine max]
  Seq. No.
                     231467
  Seq. ID
                     LIB3197-029-Q1-M1-A2
  Method
                     BLASTX
  NCBI GI
                     g464849
  BLAST score
                     600
  E value
                     2.0e-62
                     129
 Match length
                     92
  % identity
  NCBI Description TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha
                     chain - almond >gi 20\overline{4}\overline{13} emb \overline{CAA47635} (X67162)
                     alpha-tubulin [Prunus dulcis]
```

Seq. No. 231468

% identity



Seq. ID LIB3197-029-Q1-M1-A3 BLASTX Method NCBI GI g3915031 BLAST score 177 E value 2.0e-16 69 Match length 74 % identity ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR NCBI Description (STEAROYL-ACP DESATURASE) >gi\_1217628\_emb\_CAA65232 (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase [Gossypium hirsutum] 231469 Seq. No. Seq. ID LIB3197-029-Q1-M1-A5 Method BLASTX NCBI GI g1771162 BLAST score 180 E value 2.0e-13 Match length 86 % identity 49 (X98930) SBT2 [Lycopersicon esculentum] NCBI Description >gi 3687307 emb CAA07000 (AJ006379) subtilisin-like protease [Lycopersicon esculentum] Seq. No. 231470 Seq. ID LIB3197-029-Q1-M1-A6 Method BLASTX NCBI GI g3858935 BLAST score 567 1.0e-58 E value 128 Match length 83 % identity NCBI Description (AL021636) synaptobrevin-like protein [Arabidopsis thaliana] >gi 4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana] 231471 Seq. No. Seq. ID LIB3197-029-Q1-M1-A7 Method BLASTX NCBI GI g2129499 BLAST score 663 E value 5.0e-70 Match length 133 % identity 92 NCBI Description fiber protein E6 (clone CKE6-4A) - upland cotton >gi 1000086 (U30506) E6 [Gossypium hirsutum] Seq. No. 231472 LIB3197-029-Q1-M1-B1 Seq. ID Method BLASTX NCBI GI g3426037 BLAST score 598 E value 3.0e-62 Match length 137

NCBI Description (AC005168) putative ABC transporter protein [Arabidopsis



## thaliana]

```
231473
Seq. No.
Seq. ID
                  LIB3197-029-Q1-M1-B12
Method
                  BLASTX
NCBI GI
                  g2252842
BLAST score
                  164
E value
                  2.0e-11
Match length
                  93
% identity
                  44
NCBI Description
                 (AF013293) No definition line found [Arabidopsis thaliana]
Seq. No.
                  231474
Seq. ID
                  LIB3197-029-Q1-M1-B2
Method
                  BLASTX
NCBI GI
                  g3914403
                  307
BLAST score
E value
                  3.0e-28
Match length
                  113
                  58
% identity
NCBI Description
                 PROTOPORPHYRINOGEN OXIDASE, MITOCHONDRIAL (PPO II)
                  (PROTOPORPHYRINOGEN IX OXIDASE ISOZYME II) (PPX II)
                  >gi_2370335_emb_CAA73866_ (Y13466) protoporphyrinogen
                  oxidase [Nicotiana tabacum] >gi_3929920_dbj_BAA34712_
                  (AB020500) mitochondrial protoporphyrinogen oxidase
                  [Nicotiana tabacum] >gi_4105188 (AF044129)
                  protoporphyrinogen oxidase PX-2 [Nicotiana tabacum]
Seq. No.
                  231475
Seq. ID
                  LIB3197-029-Q1-M1-B4
Method
                  BLASTX
NCBI GI
                  q3377797
BLAST score
                  501
E value
                  7.0e-51
Match length
                  125
% identity
NCBI Description
                  (AF075597) Similar to 60S ribosome protein L19; coded for
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
Seq. No.
                  231476
Seq. ID
                  LIB3197-029-Q1-M1-B5
Method
                  BLASTX
NCBI GI
                  g2062167
BLAST score
                  313
E value
                  5.0e-29
Match length
                  64
% identity
                  88
                  (AC001645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                  thaliana]
```

Seq. No.

231477 Seq. ID LIB3197-029-Q1-M1-B6

Method BLASTX NCBI GI g3142301

33296



```
BLAST score
E value
                  1.0e-17
Match length
                  113
% identity
                  49
                  (AC002411) Contains similarity to neural cell adhesion
NCBI Description
                  molecule 2, large isoform precursor gb_M76710 from Xenopus
                  laevis, and beta transducin from S. cerevisiae gb Q05946.
                  ESTs gb_N65081 gb_Z30910, gb_Z34190, gb_Z34611, gb_R30101,
                  gb_H3630
Seq. No.
                  231478
Seq. ID
                  LIB3197-029-Q1-M1-C1
Method
                  BLASTX
NCBI GI
                  q4128197
BLAST score
                  155
                  2.0e-10
E value
                  52
Match length
                  60
% identity
NCBI Description (U75273) acyl-CoA binding protein [Arabidopsis thaliana]
Seq. No.
                  231479
                  LIB3197-029-Q1-M1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1169534
BLAST score
                  593
E value
                  9.0e-62
Match length
                  122
% identity
                  94
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_542019_pir__S39203
                  phosphopyruvate hydratase (EC 4.2.1.11) - castor bean
                  >gi_433609_emb_CAA82232_ (Z28386) enolase [Ricinus
                  communis]
Seq. No.
                  231480
Seq. ID
                  LIB3197-029-Q1-M1-C11
Method
                  BLASTX
NCBI GI
                  q1173256
BLAST score
                  637
E value
                  9.0e-67
Match length
                  123
% identity
                  99
NCBI Description
                 40S RIBOSOMAL PROTEIN S4 >gi 629496 pir S45026 ribosomal
                  protein S4 - upland cotton >gi 488739 emb CAA55882
                  (X79300) ribosomal protein, small subunit 4e (RS4e)
                  [Gossypium hirsutum]
Seq. No.
                  231481
Seq. ID
                  LIB3197-029-Q1-M1-C12
Method
                  BLASTX
NCBI GI
                  g2499611
BLAST score
                  450
E value
                  8.0e-45
Match length
                  90
% identity
                  93
```

(ATMPK7) >gi 629548 pir S40473 mitogen-activated protein

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7)



kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana >gi 457406 dbj BAA04870 (D21843) MAP kinase [Arabidopsis thaliana]

231482 Seq. No. LIB3197-029-Q1-M1-C4 Seq. ID Method BLASTX NCBI GI g3421087 BLAST score 544 6.0e-56E value Match length 110

% identity (AF043524) 20S proteasome subunit PAE1 [Arabidopsis NCBI Description

thaliana]

231483 Seq. No.

LIB3197-029-Q1-M1-C5 Seq. ID

97

Method BLASTX NCBI GI g2414624 BLAST score 265 E value 4.0e-23 Match length 96 51 % identity

NCBI Description (Z99259) ATP synthase subunit [Schizosaccharomyces pombe]

231484 Seq. No.

LIB3197-029-Q1-M1-C7 Seq. ID

Method BLASTX q3337350 NCBI GI BLAST score 480 E value 1.0e-48 Match length 104

92 % identity

NCBI Description (AC004481) putative permease [Arabidopsis thaliana]

Seq. No. 231485

Seq. ID LIB3197-029-Q1-M1-D1

Method BLASTX NCBI GI q1707020 BLAST score 207 E value 1.0e-16 Match length 89 28 % identity

NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]

231486 Seq. No.

Seq. ID LIB3197-029-Q1-M1-D11

Method BLASTX NCBI GI q3860263 BLAST score 237 E value 6.0e-20 Match length 62 % identity

(AC005824) putative cytochrome p450 protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 231487



```
LIB3197-029-Q1-M1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2497543
BLAST score
                   163
                   2.0e-11
E value
                   39
Match length
                   77
 % identity
                   PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 542061 pir S41379
NCBI Description
                   pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_
                   (Z29492) pyruvate kinase [Nicotiana tabacum]
                   231488
 Seq. No.
                   LIB3197-029-Q1-M1-D3
 Seq. ID
Method
                   BLASTX
NCBI GI
                   a3097321
                   194
 BLAST score
                   7.0e-15
 E value
                   84
Match length
                   45
 % identity
 NCBI Description (AB013289) Bd 30K [Glycine max]
                   231489
 Seq. No.
                   LIB3197-029-Q1-M1-D4
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q4314378
 BLAST score
                   227
                   7.0e-19
. E value
 Match length
                   96
 % identity
                   46
 NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]
                   231490
 Seq. No.
                   LIB3197-029-Q1-M1-D6
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g3249081
 BLAST score
                   311
 E value
                   1.0e-28
 Match length
                   121
 % identity
                   18
                   (AC004473) Strong similarity to AROGP2 gene gb 1762634 from
 NCBI Description
                   Lycopersicon esculentum. [Arabidopsis thaliana]
 Seq. No.
                   231491
                   LIB3197-029-Q1-M1-D7
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2500192
 BLAST score
                   491
                   9.0e-50
 E value
                   95
 Match length
                   97
 % identity
                   RAC-LIKE GTP BINDING PROTEIN ARAC3 >gi 1304413 (U43501)
 NCBI Description
                   Rac-like protein [Arabidopsis thaliana] >gi 2645643
```

Rac-like protein [Arabidopsis thaliana] >g1\_2645643 (AF031427) Rho-like GTP binding protein [Arabidopsis thaliana] >g1\_2924513\_emb\_CAA17767.1\_ (AL022023) Rho1Ps

homolog/ Rac-like protein [Arabidopsis thaliana]

Seq. No. 231492



```
LIB3197-029-Q1-M1-E10
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                      g2244732
   BLAST score
                      551
   E value
                      1.0e-56
   Match length
                     105
   % identity
                      100
   NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
                     231493
   Seq. No.
   Seq. ID
                     LIB3197-029-Q1-M1-E11
   Method
                     BLASTX
   NCBI GI
                      q543905
   BLAST score
                      453
   E value
                      3.0e-45
   Match length
                      110
                      81
   % identity
   NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162)
                     brassinosteroid-regulated protein [Glycine max]
   Seq. No.
                      231494
   Seq. ID
                     LIB3197-029-Q1-M1-E12
   Method
                     BLASTX
   NCBI GI
                      g2702269
   BLAST score
                      146
   E value
                      2.0e-09
   Match length
                      34
                      79
   % identity
   NCBI Description (AC003033) hypothetical protein [Arabidopsis thaliana]
   Seq. No.
                      231495
                      LIB3197-029-Q1-M1-E2
   Seq. ID
   Method
                      BLASTX
   NCBI GI
                      g3461833
   BLAST score
                      247
   E value
                      3.0e-21
   Match length
                     52
% identity
   NCBI Description (AC004138) putative expansin [Arabidopsis thaliana]
   Seq. No.
                      231496
                      LIB3197-029-Q1-M1-E4
   Seq. ID
   Method
                      BLASTX
   NCBI GI
                      g4240385
   BLAST score
                      251
   E value
                      1.0e-21
                      96
   Match length
                      50
   % identity
   NCBI Description (AF061027) omega-3 fatty acid desaturase precursor
                      [Vernicia fordii]
   Seq. No.
                      231497
                      LIB3197-029-Q1-M1-E5
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                      q4006900
   BLAST score
```

33300

429

2.0e-42

E value



Match length 134 % identity 63 NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana] Seq. No. 231498 LIB3197-029-Q1-M1-E6 Seq. ID Method BLASTX NCBI GI q4406819 BLAST score 209 E value 1.0e-16 Match length 107 % identity 48 NCBI Description (AC006201) unknown protein [Arabidopsis thaliana] Seq. No. 231499 LIB3197-029-Q1-M1-E7 Seq. ID Method BLASTX NCBI GI g1708236 BLAST score 145 7.0e-11E value 59 Match length % identity 68 NCBI Description HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)  $\verb|>gi_2129617_pir\_JC4567| hydroxymethylglutaryl-CoA synthase|$ (EC 4.1.3.5) - Arabidopsis thaliana >gi\_1143390\_emb\_CAA58763\_ (X83882)
hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi 1586548 prf 2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana] Seq. No. 231500 Seq. ID LIB3197-029-Q1-M1-E8 Method BLASTX NCBI GI g2497366 275 BLAST score E value 3.0e-24Match length 109 51 % identity NCBI Description INTERFERON-GAMMA INDUCIBLE PROTEIN MG11 >gi\_2137851\_pir\_\_I49127 unknown intracellular protein - mouse >gi\_558903 (U15635) unknown intracellular protein [Mus musculus] Seq. No. 231501 Seq. ID LIB3197-029-Q1-M1-F10 Method BLASTX NCBI GI g1465770 BLAST score 146 E value 4.0e-09

129 Match length 34 % identity

NCBI Description (U61233) cofactor D [Bos taurus]

Seq. No. 231502

LIB3197-029-Q1-M1-F12 Seq. ID

Method BLASTX



```
NCBI GI
                   q2464905
BLAST score
                   195
E value
                   5.0e-15
Match length
                   85
                   51
% identity
NCBI Description
                  (Z99708) minor allergen [Arabidopsis thaliana]
Seq. No.
                   231503
Seq. ID
                   LIB3197-029-Q1-M1-F4
Method
                   BLASTX
NCBI GI
                   q2052383
BLAST score
                   581
E value
                   4.0e-60
Match length
                   121
% identity
NCBI Description (U66345) calreticulin [Arabidopsis thaliana]
Seq. No.
                   231504
                   LIB3197-029-Q1-M1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1352664
BLAST score
                   483
E value
                   1.0e-48
Match length
                   97
                   93
% identity
NCBI Description
                   SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC
                   SUBUNIT >gi_2117984_pir__S52660 phosphoprotein phosphatase (EC 3.1.3.16) 2A isoform 4 - Arabidopsis thaliana
                   >gi_473259 (U08047) Ser/Thr protein phosphatase
                   [Arabidopsis thaliana] >gi_4204949 (U60136)
                   serine/threonine protein phosphatase 2A-4 catalytic subunit
                   [Arabidopsis thaliana]
Seq. No.
                   231505
Seq. ID
                   LIB3197-029-Q1-M1-F6
Method
                   BLASTX
NCBI GI
                   q4544443
BLAST score
                   417
E value
                   4.0e-41
Match length
                   113
% identity
                   43
                   (AC006592) putative mitochondrial uncoupling protein
NCBI Description
                   [Arabidopsis thaliana]
                   231506
Seq. No.
Seq. ID
                   LIB3197-029-Q1-M1-F7
Method
                   BLASTX
NCBI GI
                   g3337352
BLAST score
                   413
```

E value 1.0e-40 Match length 102 81 % identity

(AC004481) putative chromatin structural protein Supt5hp NCBI Description

[Arabidopsis thaliana]

Seq. No. 231507

Seq. ID LIB3197-029-Q1-M1-F9



```
Method
                  BLASTX
NCBI GI
                  g4128133
BLAST score
                  240
E value
                  3.0e-20
Match length
                  106
% identity
                   46
NCBI Description (AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]
Seq. No.
                  231508
Seq. ID
                  LIB3197-029-Q1-M1-G10
Method
                  BLASTX
NCBI GI
                  q3341681
BLAST score
                  448
E value
                  1.0e-44
                  90
Match length
                  99
% identity
NCBI Description
                  (AC003672) small GTP-binding protein [Arabidopsis thaliana]
                  >gi 741994 prf 2008312A GTP-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  231509
Seq. ID
                  LIB3197-029-Q1-M1-G11
Method
                  BLASTX
NCBI GI
                  q2384758
BLAST score
                  478
E value
                  4.0e-48
Match length
                  96
% identity
                  94
                  (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza
NCBI Description
                  sativa]
                  231510
Seq. No.
Seq. ID
                  LIB3197-029-Q1-M1-G3
Method
                  BLASTX
NCBI GI
                  q2828702
BLAST score
                  748
E value
                  1.0e-79
Match length
                  144
                  99
% identity
NCBI Description (AF044414) alpha mannosidase 6A8B [Homo sapiens]
Seq. No.
                  231511
Seq. ID
                  LIB3197-029-Q1-M1-G4
Method
                  BLASTX
NCBI GI
                  g3548818
BLAST score
                  252
E value
                  1.0e-21
Match length
                  86
% identity
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
                  231512
Seq. No.
Seq. ID
                  LIB3197-029-Q1-M1-G5
```

Method BLASTX NCBI GI q3721864 BLAST score 176 E value 9.0e-13



```
Match length
                  37
% identity
NCBI Description (AB016068) Hs Ste24p [Homo sapiens]
                  231513
Seq. No.
Seq. ID
                  LIB3197-029-Q1-M1-G6
Method
                  BLASTX
NCBI GI
                  g1644427
BLAST score
                  226
                  1.0e-18
E value
Match length
                  45
% identity
                  89
NCBI Description (U74610) glyoxalase II [Arabidopsis thaliana]
                  231514
Seq. No.
                  LIB3197-029-Q1-M1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1737490
BLAST score
                  265
E value
                  3.0e-23
                  109
Match length
% identity
                  46
NCBI Description (U81006) p76 [Homo sapiens]
Seq. No.
                  231515
Seq. ID
                  LIB3197-029-Q1-M1-G8
Method
                  BLASTX
NCBI GI
                  q3548805
BLAST score
                  273
E value
                  4.0e-24
Match length
                  111
                  50
% identity
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
                  231516
Seq. No.
Seq. ID
                  LIB3197-029-Q1-M1-G9
Method
                  BLASTX
NCBI GI
                  q1009712
BLAST score
                  614
E value
                  4.0e-64
                  131
Match length
% identity
                  86
NCBI Description (U27698) calreticulin [Arabidopsis thaliana]
                  231517
Seq. No.
Seq. ID
                  LIB3197-029-Q1-M1-H1
Method
                  BLASTX
NCBI GI
                  g1706318
BLAST score
                  303
E value
                  1.0e-27
                  80
Match length
                  71
% identity
                  GLUTAMATE DECARBOXYLASE (GAD) (ERT D1)
NCBI Description
                  >gi 1362098 pir S56177 probable glutamate decarboxylase -
                  tomato >gi_995555_emb_CAA56812_ (X80840) homology to
```

putative start codon [Lycopersicon esculentum]

pyroxidal-5'-phosphate-dependant glutamate decarboxylases;

Match length

% identity

91

97



```
Seq. No.
                  231518
Seq. ID
                  LIB3197-029-Q1-M1-H10
Method
                  BLASTX
NCBI GI
                  g2431769
BLAST score
                  234
E value
                  1.0e-19
                  57
Match length
% identity
                  81
NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]
Seq. No.
                  231519
Seq. ID
                  LIB3197-029-Q1-M1-H12
Method
                  BLASTX
NCBI GI
                  g1408471
BLAST score
                  515
E value
                  2.0e-52
Match length
                  132
% identity
                  76
NCBI Description
                  (U48938) actin depolymerizing factor 1 [Arabidopsis
                  thaliana] >gi 3851707 (AF102173) actin depolymerizing
                  factor 1 [Arabidopsis thaliana]
Seq. No.
                  231520
Seq. ID
                  LIB3197-029-Q1-M1-H4
Method
                  BLASTX
NCBI GI
                  g1351030
BLAST score
                  574
E value
                  2.0e-59
Match length
                  138
                  84
% identity
NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60
                  KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >gi_289365
                  (M35599) 60-kDa chaperonin-60 alpha-polypeptide precursor
                  [Brassica napus]
Seq. No.
                  231521
Seq. ID
                  LIB3197-029-Q1-M1-H5
Method
                  BLASTX
NCBI GI
                  g267069
BLAST score
                  487
                  3.0e-49
E value
Match length
                  89
% identity
                  99
NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                  231522
Seq. ID
                  LIB3197-029-Q1-M1-H6
Method
                  BLASTX
NCBI GI
                  g2511574
BLAST score
                  431
E value
                  9.0e-43
```

33305



NCBI Description (Y13176) multicatalytic endopeptidase [Arabidopsis thaliana] >gi\_3421075 (AF043520) 20S proteasome subunit PAB1 [Arabidopsis thaliana]

Seq. No. 231523

Seq. ID LIB3197-029-Q1-M1-H7

Method BLASTX
NCBI GI g2129499
BLAST score 603
E value 7.0e-63
Match length 120
% identity 92

NCBI Description fiber protein E6 (clone CKE6-4A) - upland cotton

>gi\_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No. 231524

Seq. ID LIB3197-029-Q1-M1-H9

Method BLASTX
NCBI GI g1486472
BLAST score 441
E value 8.0e-44
Match length 101
% identity 84

NCBI Description (X99853) oxoglutarate malate translocator [Solanum

tuberosum]

Seq. No. 231525

Seq. ID LIB3197-030-Q1-M1-A10

Method BLASTX
NCBI GI g1778370
BLAST score 624
E value 3.0e-65
Match length 127
% identity 93

NCBI Description (U77678) asparagine synthetase 2 [Glycine max]

Seq. No. 231526

Seq. ID LIB3197-030-Q1-M1-A11

Method BLASTX
NCBI GI g2613143
BLAST score 189
E value 4.0e-16
Match length 79

% identity 55

NCBI Description (AF030548) tubulin [Oryza sativa]

Seq. No. 231527

Seq. ID LIB3197-030-Q1-M1-A12

Method BLASTX
NCBI GI g2651303
BLAST score 623
E value 4.0e-65
Match length 137
% identity 87

NCBI Description (AC002336) putative potassium transporter [Arabidopsis

thalianal

Seq. No.

Seq. ID

231533

LIB3197-030-Q1-M1-B10



```
Seq. No.
                   231528
Seq. ID
                   LIB3197-030-Q1-M1-A3
 Method
                   BLASTX
 NCBI GI
                   g3925363
 BLAST score
                   431
 E value
                   9.0e-43
 Match length
                   112
 % identity
                   68
 NCBI Description (AF067961) homeodomain protein [Malus domestica]
 Seq. No.
                   231529
 Seq. ID
                   LIB3197-030-Q1-M1-A4
 Method
                   BLASTX
 NCBI GI
                   q4558556
 BLAST score
                   307
 E value
                   4.0e-28
 Match length
                   126
 % identity
                   49
 NCBI Description (AC007138) predicted protein of unknown function
                   [Arabidopsis thaliana]
 Seq. No.
                   231530
 Seq. ID
                   LIB3197-030-Q1-M1-A8
 Method
                   BLASTX
 NCBI GI
                   q4138722
 BLAST score
                   239
 E value
                   3.0e-20
 Match length
                   81
 % identity
                   62
 NCBI Description (Y09590) hexose transporter [Vitis vinifera]
 Seq. No.
                   231531
 Seq. ID
                   LIB3197-030-Q1-M1-A9
 Method
                   BLASTX
 NCBI GI
                   g120669
 BLAST score
                   457
 E value
                   1.0e-45
 Match length
                   91
 % identity
                   92
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_66014 pir__DEJMG glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi 19566 emb_CAA42905_ (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
 Seq. No.
                   231532
 Seq. ID
                   LIB3197-030-Q1-M1-B1
 Method
                   BLASTX
 NCBI GI
                   g1587206
 BLAST score
                   153
 E value
                   1.0e-10
 Match length
                   39
 % identity
                   77
 NCBI Description T complex protein [Cucumis sativus]
```

33307



```
Method
                  BLASTX
NCBI GI
                  g2864624
BLAST score
                  335
E value
                  2.0e-31
                  137
Match length
% identity
                  53
NCBI Description (AL021811) putative protein [Arabidopsis thaliana]
Seq. No.
                  231534
Seq. ID
                  LIB3197-030-Q1-M1-B2
Method
                  BLASTX
NCBI GI
                  g1587206
BLAST score
                  421
                  2.0e-41
E value
                  110
Match length
                  79
% identity
NCBI Description T complex protein [Cucumis sativus]
                  231535
Seq. No.
Seq. ID
                  LIB3197-030-Q1-M1-B3
Method
                  BLASTX
NCBI GI
                  g1350956
BLAST score
                  490
E value
                  1.0e-49
Match length
                  105
                  92
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)
Seq. No.
                  231536
Seq. ID
                  LIB3197-030-Q1-M1-B5
                  BLASTX
Method
NCBI GI
                  g3097321
BLAST score
                  203
E value
                  7.0e-16
Match length
                  109
% identity
                  39
NCBI Description (AB013289) Bd 30K [Glycine max]
Seq. No.
                  231537
Seq. ID
                  LIB3197-030-Q1-M1-B6
Method
                  BLASTX
NCBI GI
                  g3123271
BLAST score
                  164
E value
                  7.0e-12
Match length
                  31
                  97
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S6 >qi 2224751 emb CAA74381 (Y14052)
                  ribosomal protein S6 [Arabidopsis thaliana]
Seq. No.
                  231538
Seq. ID
                  LIB3197-030-Q1-M1-B8
Method
                  BLASTX
NCBI GI
                  g3421109
```

Method BLASTX
NCBI GI g3421109
BLAST score 457
E value 1.0e-45
Match length 96
% identity 95



NCBI Description (AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis thaliana]

Seq. No. 231539

Seq. ID LIB3197-030-Q1-M1-C1 Method BLASTX NCBI GI g2811278 BLAST score 542 E value 1.0e-55 Match length % identity 76

NCBI Description (AF043284) expansin [Gossypium hirsutum]

Seq. No. 231540

Seq. ID LIB3197-030-Q1-M1-C11

Method BLASTX
NCBI GI g2811278
BLAST score 753
E value 2.0e-80
Match length 139
% identity 97

NCBI Description (AF043284) expansin [Gossypium hirsutum]

Seq. No. 231541

Seq. ID LIB3197-030-Q1-M1-C6

Method BLASTX
NCBI GI g2498565
BLAST score 175
E value 1.0e-12
Match length 94
% identity 37

NCBI Description C-MYC BINDING PROTEIN MM-1 >gi\_1731809\_dbj\_BAA14006\_

(D89667) c-myc binding protein [Homo sapiens] >gi 4505743 ref NP 002615.1 pPFDN5 prefoldin

Seq. No. 231542

Seq. ID LIB3197-030-Q1-M1-C7

Method BLASTX
NCBI GI . g3176690
BLAST score 169
E value 3.0e-12
Match length 91
% identity 46

NCBI Description (AC003671) Similar to ubiquitin ligase gb D63905 from S.

cerevisiae. EST gb\_R65295 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 231543

Seq. ID LIB3197-030-Q1-M1-C8

Method BLASTX
NCBI GI g3334115
BLAST score 715
E value 6.0e-76

E value 6.0e-76 Match length 137 % identity 43

NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)

(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi\_2463664



(AF006489) adenine nucleotide translocator 1 [Gossypium hirsutum]

 Seq. No.
 231544

 Seq. ID
 LIB3197-030-Q1-M1-C9

 Method
 BLASTX

Method BLASTX
NCBI GI g2811278
BLAST score 637
E value 9.0e-67
Match length 129
% identity 89

NCBI Description (AF043284) expansin [Gossypium hirsutum]

Seq. No. 231545

Seq. ID LIB3197-030-Q1-M1-D10

Method BLASTX
NCBI GI g2245136
BLAST score 476
E value 6.0e-48
Match length 135
% identity 67

NCBI Description (Z97344) trehalose-6-phosphate synthase homolog

[Arabidopsis thaliana]

Seq. No. 231546

Seq. ID LIB3197-030-Q1-M1-D11

Method BLASTX
NCBI GI g4249386
BLAST score 280
E value 6.0e-25
Match length 106
% identity 58

NCBI Description (AC005966) Strong similarity to gb\_AF061286 gamma-adaptin 1

from Arabidopsis thaliana. EST gb H37393 comes from this

gene. [Arabidopsis thaliana]

Seq. No. 231547

Seq. ID LIB3197-030-Q1-M1-D5

Method BLASTX
NCBI GI g3080450
BLAST score 363
E value 1.0e-34
Match length 109
% identity 60

NCBI Description (AL022605) hypothetical protein [Arabidopsis thaliana]

Seq. No. 231548

Seq. ID LIB3197-030-Q1-M1-D6

Method BLASTX
NCBI GI g4454012
BLAST score 175
E value 1.0e-12
Match length 49
% identity 65

NCBI Description (AL035396) Pollen-specific protein precursor like

[Arabidopsis thaliana]

Match length

NCBI Description

% identity

101

thaliana]

87



```
Seq. No.
                  231549
Seq. ID
                  LIB3197-030-Q1-M1-E10
Method
                  BLASTX
NCBI GI
                  q461987
BLAST score
                  638
E value
                  6.0e-67
Match length
                  133
% identity
                  92
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                  >gi_82042_pir__JS0719 translation elongation factor eEF-1
                  alpha chain - carrot >gi_217913_dbj_BAA02205_ (D12709)
                  elongation factor 1-alpha [Daucus carota]
                  231550
Seq. No.
Seq. ID
                  LIB3197-030-Q1-M1-E11
Method
                  BLASTX
NCBI GI
                  g4510430
BLAST score
                  514
E value
                  2.0e-52
Match length
                  106
                  87
% identity
NCBI Description
                 (AC006929) unknown protein, 3' partial [Arabidopsis
                  thaliana]
Seq. No.
                  231551
Seq. ID
                  LIB3197-030-Q1-M1-E4
Method
                  BLASTX
NCBI GI
                  g3522945
BLAST score
                  242
E value
                  2.0e-20
Match length
                  117
% identity
                  41
NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                  231552
Seq. ID
                  LIB3197-030-Q1-M1-E5
Method
                  BLASTX
NCBI GI
                  g2129929
BLAST score
                  660
E value
                  2.0e-69
Match length
                  132
% identity
                  96
NCBI Description
                 DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB2 -
                  tomato >gi 1049068 (U28403) RNA polymerase II subunit 2
                  [Solanum lycopersicum]
Seq. No.
                  231553
Seq. ID
                  LIB3197-030-Q1-M1-E6
Method
                  BLASTX
NCBI GI
                  g2062167
BLAST score
                  469
E value
                  4.0e-47
```

(AC001645) Proline-rich protein APG isolog [Arabidopsis



```
Seq. No.
Seq. ID
                   LIB3197-030-Q1-M1-F11
Method
                   BLASTX
NCBI GI
                   g1174592
BLAST score
                   598
E value
                   3.0e-62
Match length
                   111
% identity
                   99
NCBI Description TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
                   - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                   sativum]
                   231555
Seq. No.
Seq. ID
                   LIB3197-030-Q1-M1-F12
Method
                   BLASTX
NCBI GI
                   g549063
BLAST score
                   357
E value
                   6.0e - 34
Match length
                   110
% identity
                   65
NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
Seq. No.
                   231556
Seq. ID
                   LIB3197-030-Q1-M1-F5
Method
                   BLASTX
NCBI GI
                   g1174592
BLAST score
                   557
E value
                   2.0e-57
                   109
Match length
% identity
                   94
NCBI Description TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__$60233 alpha-tubulin
                   - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                   sativum]
Seq. No.
                   231557
Seq. ID
                   LIB3197-030-Q1-M1-G10
Method
                   BLASTX
NCBI GI
                   g267069
BLAST score
                   520
E value
                   4.0e-53
Match length
                   96
% identity
                   99
NCBI Description
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
                   tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] > gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                   231558
                   LIB3197-030-Q1-M1-G11
Seq. ID
Method
                   BLASTX
```

NCBI GI g2811278
BLAST score 523
E value 2.0e-53
Match length 128



% identity NCBI Description (AF043284) expansin [Gossypium hirsutum] Seq. No. 231559 Seq. ID LIB3197-030-Q1-M1-G4 Method BLASTX NCBI GI g1174470 BLAST score 348 E value 7.0e-33128 Match length 52 % identity NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi\_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi\_1588285\_prf\_\_2208301A integral membrane protein [Mus musculus] Seq. No. 231560 Seq. ID LIB3197-030-Q1-M1-G6 Method BLASTX NCBI GI g1332579 BLAST score 550 E value 1.0e-56 Match length 112 % identity 10 NCBI Description (X98063) polyubiquitin [Pinus sylvestris] Seq. No. 231561 Seq. ID LIB3197-030-Q1-M1-H10 Method BLASTX NCBI GI g2146797 BLAST score 353 E value 3.0e-39 114 Match length % identity 49 NCBI Description protein disulfide-isomerase (EC 5.3.4.1) - Castor bean >gi 1134968 (U41385) protein disulphide isomerase PDI [Ricinus communis] >gi\_1587210 prf 2206331A protein disulfide isomerase [Ricinus communis] 231562 Seq. No. Seq. ID LIB3197-030-Q1-M1-H5 Method BLASTX NCBI GI g2088654 BLAST score 398 E value 9.0e-39 Match length 120 % identity 71 (AF002109) 60S acidic ribosomal protein P0 isolog NCBI Description [Arabidopsis thaliana] Seq. No. 231563

Seq. ID LIB3197-031-Q1-M1-A5

Method BLASTX NCBI GI g2132184 BLAST score 173 E value 2.0e-12 Match length 44

33313



```
% identity
NCBI Description
                  hypothetical protein YPL093w - yeast (Saccharomyces
                   cerevisiae) >gi 1151233 (U43281) Lpg15p [Saccharomyces
                   cerevisiae]
                   231564
Seq. No.
Seq. ID
                   LIB3197-031-Q1-M1-A6
Method
                   BLASTX
NCBI GI
                   g3927825
BLAST score
                   239
E value
                   4.0e-20
Match length
                   56
                   77
% identity
NCBI Description
                  (AC005727) putative dTDP-glucose 4-6-dehydratase
                   [Arabidopsis thaliana]
Seq. No.
                   231565
                   LIB3197-031-Q1-M1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4007792
BLAST score
                   251
E value
                   2.0e-21
Match length
                   65
% identity
                   72
NCBI Description (AL034463) Xenopus 14s cohesin smc1 subunit homolog
                   [Schizosaccharomyces pombe]
Seq. No.
                   231566
                   LIB3197-031-Q1-M1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4165018
BLAST score
                   364
E value
                   9.0e-35
Match length
                   134
% identity
                   54
NCBI Description (D89053) Acyl-CoA synthetase 3 [Homo sapiens]
                   231567
Seq. No.
Seq. ID
                   LIB3197-031-Q1-M1-B4
                   BLASTX
Method
                   g2980793
NCBI GI
BLAST score
                   176
                   1.0e-12
E value
Match length
                   57
% identity
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]
                   231568
Seq. No.
Seq. ID
                   LIB3197-031-Q1-M1-B6
Method
                   BLASTX
NCBI GI
                   g2497753
BLAST score
                   190
                   2.0e-14
E value
Match length
                   49
% identity
                   63
```

>gi\_1321915\_emb\_CAA65477\_\_ (X96716) lipid transfer protein

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)

Seq. ID

Method

NCBI GI



## [Prunus dulcis]

```
231569
Seq. No.
Seq. ID
                  LIB3197-031-Q1-M1-C10
                  BLASTX
Method
NCBI GI
                  g2062167
BLAST score
                  402
E value
                  3.0e-39
Match length
                  85
% identity
                  88
NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis
                  thaliana]
                  231570
Seq. No.
Seq. ID
                  LIB3197-031-Q1-M1-C11
Method
                  BLASTX
                  q4098129
NCBI GI
BLAST score
                  707
E value
                  6.0e-75
Match length
                  143
                  94
% identity
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
                  231571
Seq. No.
                  LIB3197-031-Q1-M1-C12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1495251
BLAST score
                  466
E value
                  9.0e-47
                  97
Match length
                  91
% identity
NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]
                  231572
Seq. No.
Seq. ID
                  LIB3197-031-Q1-M1-C2
                  BLASTX
Method
                  q1899188
NCBI GI
BLAST score
                  187
E value
                  2.0e-14
                  46
Match length
                  74
% identity
NCBI Description (U90212) DNA binding protein ACBF [Nicotiana tabacum]
Seq. No.
                  231573
                  LIB3197-031-Q1-M1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2911052
BLAST score
                  563
E value
                   3.0e-58
Match length
                  124
% identity
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
Seq. No.
                  231574
```

33315

LIB3197-031-Q1-M1-C9

BLASTX

q1730502



```
BLAST score
E value
                  5.0e-13
Match length
                  80
                  51
% identity
NCBI Description TRANSMEMBRANE PROTEIN PFT27 >gi_110903_pir__A31351 probable
                  transmembrane protein FT27 - mouse >gi 535682 (M23568)
                  transmembrane protein [Mus musculus]
Seq. No.
                  231575
Seq. ID
                  LIB3197-031-Q1-M1-D10
                  BLASTX
Method
NCBI GI
                  q2811278
BLAST score
                  555
E value
                  4.0e-57
                  133
Match length
                  77
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                  231576
Seq. ID
                  LIB3197-031-Q1-M1-D11
Method
                  BLASTX
NCBI GI
                  g2924520
BLAST score
                  675
E value
                  3.0e-71
Match length
                  142
                  89
% identity
NCBI Description (AL022023) plasma membrane intrinsic protein (SIMIP)
                  [Arabidopsis thaliana]
Seq. No.
                  231577
Seq. ID
                  LIB3197-031-Q1-M1-D12
Method
                  BLASTX
NCBI GI
                  g2961300
BLAST score
                  520
E value
                  3.0e-53
                  118
Match length
                  92
% identity
NCBI Description (AJ225027) ribosomal protein L24 [Cicer arietinum]
                  231578
Seq. No.
Seq. ID
                  LIB3197-031-Q1-M1-D4
Method
                  BLASTX
NCBI GI
                  g2662341
BLAST score
                  717
E value
                  4.0e-76
Match length
                  145
% identity
                  95
NCBI Description
                 (D63580) EF-1 alpha [Oryza sativa]
                  >qi 2662345 dbj BAA23659 (D63582) EF-1 alpha [Oryza
                  satīva] >gi 2662347 dbj BAA23660 (D63583) EF-1 alpha
                  [Oryza sativa]
                  231579
Seq. No.
                  LIB3197-031-Q1-M1-D5
```

Seq. ID

Method BLASTX NCBI GI q728880 BLAST score 527



E value 7.0e-54Match length 144 71 % identity NCBI Description N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG >gi\_517485\_emb\_CAA54691\_ (X77588) ARD1 N-acetyl transferase
homologue [Homo sapiens] >gi\_1302661 (U52112) ARD1 N-acetyl
transferase related protein [Homo sapiens] Seq. No. 231580 Seq. ID LIB3197-031-Q1-M1-D6 Method BLASTX NCBI GI q2826884 BLAST score 155 E value 4.0e-10 Match length 41 71 % identity NCBI Description (AJ223635) transcription factor IIA large subunit [Arabidopsis thaliana] Seq. No. 231581 Seq. ID LIB3197-031-Q1-M1-D7 Method BLASTX NCBI GI g2493133 BLAST score 214 E value 3.0e-17 83 Match length % identity 49 NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT) >gi 2183244 (AF002134) Vma8p [Candida albicans] Seq. No. 231582 Seq. ID LIB3197-031-Q1-M1-D8 Method BLASTX NCBI GI g3413170 BLAST score 287 1.0e-25 E value 91 Match length % identity 68 NCBI Description (AJ010227) 40S ribosomal protein S6 [Cicer arietinum] Seq. No. 231583 Seq. ID LIB3197-031-Q1-M1-D9 Method BLASTX NCBI GI g3024020 BLAST score 655

E value 7.0e-69 Match length 131 % identity 93

NCBI Description INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)

>gi\_2225881\_dbj\_BAA20877 (AB004824) eukaryotic initiation

factor 5A3 [Solanum tuberosum]

Seq. No. 231584

Seq. ID LIB3197-031-Q1-M1-E10

Method BLASTX NCBI GI q282980 BLAST score 414



```
1.0e-40
E value
Match length
                   115
% identity
                   68
NCBI Description
                  helix-loop-helix protein DEL - garden snapdragon >gi 166428
                   (M84913) DEL [Antirrhinum majus]
Seq. No.
                   231585
Seq. ID
                  LIB3197-031-Q1-M1-E12
Method
                  BLASTX
NCBI GI
                   g4217999
BLAST score
                   577
E value
                   1.0e-59
Match length
                   130
% identity
NCBI Description
                  (AC006135) putative ubiquitin--protein ligase
                   (ubiquitin-conjugating enzyme) [Arabidopsis thaliana]
Seq. No.
                   231586
Seq. ID
                  LIB3197-031-Q1-M1-E6
Method
                  BLASTX
NCBI GI
                   g2117700
BLAST score
                   512
E value
                   4.0e-52
Match length
                   101
% identity
                   91
NCBI Description transketolase (EC 2.2.1.1) precursor - potato (fragment)
Seq. No.
                   231587
Seq. ID
                  LIB3197-031-Q1-M1-F10
Method
                  BLASTX
NCBI GI
                   g2811278
BLAST score
                   562
E value
                   6.0e-58
Match length
                   135
% identity
NCBI Description
                  (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                   231588
Seq. ID
                  LIB3197-031-Q1-M1-F12
Method
                  BLASTX
NCBI GI
                   g464986
BLAST score
                   370
E value
                   1.0e-35
Match length
                   69
% identity
                   97
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
                  LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                  >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana
                  >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                  enzyme homolog [Arabidopsis thaliana] >gi 349211 (L00639)
                  ubiquitin conjugating enzyme [Arabidopsis thaliana]
                  >gi 600391 emb CAA51201 (X72626) ubiquitin conjugating
                  enzyme E2 [Arabidopsis Thaliana]
```

ligase UBC9 [Arabidopsis thaliana]

>gi\_4455355 emb CAB36765.1 (AL035524) ubiquitin-protein



231589

Seq. No.

```
Seq. ID
                    LIB3197-031-Q1-M1-F4
 Method
                    BLASTX
 NCBI GI
                    g231503
 BLAST score
                    704
 E value
                    1.0e-74
 Match length
                    152
 % identity
                    96
                    ACTIN 97 >gi_100417_pir__S20098 actin - potato
 NCBI Description
                    >gi 21544 emb CAA39\overline{2}80 (X55751) actin [Solanum tuberosum]
 Seq. No.
                    231590
 Seq. ID
                    LIB3197-031-Q1-M1-F5
 Method
                    BLASTX
 NCBI GI
                    g3249081
 BLAST score
                    323
 E value
                    5.0e-30
 Match length
                    124
 % identity
                    27
 NCBI Description
                   (AC004473) Strong similarity to AR0GP2 gene gb 1762634 from
                    Lycopersicon esculentum. [Arabidopsis thaliana]
 Seq. No.
                    231591
 Seq. ID
                    LIB3197-031-Q1-M1-F8
 Method
                    BLASTX
 NCBI GI
                    q2244734
 BLAST score
                    534
 E value
                    7.0e-55
                    106
 Match length
 % identity
                    98
 NCBI Description (D88414) actin [Gossypium hirsutum]
 Seq. No.
                    231592
 Seq. ID
                    LIB3197-031-Q1-M1-F9
 Method
                    BLASTX
 NCBI GI
                    g1170373
 BLAST score
                    637
 E value
                    8.0e-67
 Match length
                    133
 % identity
                    92
                   HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi 1072473 pir S46302
 NCBI Description
                    heat shock cognate protein 70-1 - Arabidopsis thaliana
                    >gi_397482_emb_CAA52684 (X74604) heat shock protein 70
                    cognate [Arabidopsis thaliana]
 Seq. No.
                    231593
 Seq. ID
                    LIB3197-031-Q1-M1-G1
 Method
                    BLASTX
 NCBI GI
                    g2662343
 BLAST score
                    647
 E value
                    7.0e-68
 Match length
                    124
 % identity
                    100
 NCBI Description (D63581) EF-1 alpha [Oryza sativa]
 Seq. No.
                    231594
 Seq. ID
                    LIB3197-031-Q1-M1-G10
```

BLAST score

E value

150

5.0e-10



```
Method
                  BLASTX
NCBI GI
                  g2984709
BLAST score
                  326
                  2.0e-30
E value
Match length
                  68
% identity
                  88
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                  231595
Seq. ID
                  LIB3197-031-Q1-M1-G11
Method
                  BLASTX
NCBI GI
                  g2706450
BLAST score
                  481
E value
                  2.0e-48
Match length
                  111
% identity
                  84
                 (AJ225172) magnesium dependent soluble inorganic
NCBI Description
                  pyrophosphatase [Solanum tuberosum]
Seq. No.
                  231596
Seq. ID
                  LIB3197-031-Q1-M1-G2
Method
                  BLASTX
NCBI GI
                  g3860272
BLAST score
                  373
E value
                  8.0e-36
Match length
                  74
% identity
                  97
NCBI Description
                  (AC005824) putative suppressor protein [Arabidopsis
                  thaliana] >gi 4314399 gb AAD15609 (AC006232) putative skd1
                  protein [Arabidopsis thaliana]
                  231597
Seq. No.
                  LIB3197-031-Q1-M1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4538911
BLAST score
                  186
                  3.0e-16
E value
                  114
Match length
% identity
                  43
NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]
                  231598
Seq. No.
Seq. ID
                  LIB3197-031-Q1-M1-G5
Method
                  BLASTX
NCBI GI
                  g3258576
BLAST score
                  375
E value
                  5.0e-36
Match length
                  121
% identity
                  60
NCBI Description (U89959) Unknown protein [Arabidopsis thaliana]
                  231599
Seq. No.
Seq. ID
                  LIB3197-031-Q1-M1-G6
Method
                  BLASTX
NCBI GI
                  q108513
```



```
Match length
                  57
% identity
NCBI Description aldehyde reductase (EC 1.1.1.21) - bovine
Seq. No.
                  231600
Seq. ID
                  LIB3197-031-Q1-M1-G8
Method
                  BLASTX
NCBI GI
                  g2244749
BLAST score
                  628
E value
                  1.0e-65
Match length
                  127
                  92
% identity
NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
Seq. No.
                  231601
Seq. ID
                  LIB3197-031-Q1-M1-H1
Method
                  BLASTX
NCBI GI
                  g2462744
BLAST score
                  175
E value
                  9.0e-13
                  92
Match length
                  51
% identity
NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  231602
Seq. ID
                  LIB3197-031-Q1-M1-H2
Method
                  BLASTX
NCBI GI
                  g1173198
BLAST score
                  401
                  1.0e-41
E value
Match length
                  97
% identity
                  89
NCBI Description 40S RIBOSOMAL PROTEIN S13 >gi 480095 pir S36423 ribosomal
                  protein S13.e - garden pea >gi 396639 emb CAA80974
                  (Z25509) ribosomal protein S13 [Pisum sativum]
Seq. No.
                  231603
Seq. ID
                  LIB3197-031-Q1-M1-H5
                  BLASTX
Method
NCBI GI
                  g2654385
BLAST score
                  177
E value
                  2.0e-13
Match length
                  49
% identity
                  76
NCBI Description (Z49852) alpha-tubulin [Loxodes striatus]
Seq. No.
                  231604
Seq. ID
                  LIB3197-031-Q1-M1-H7
Method
                  BLASTX
NCBI GI
                  g3702368
BLAST score
                  341
E value
                  3.0e - 32
Match length
                  87
% identity
                  74
```

NCBI Description (AJ001855) alpha subunit of F-actin capping protein

[Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                  LIB3197-031-Q1-M1-H8
Method
                  BLASTX
NCBI GI
                  g1351722
BLAST score
                  275
E value
                  3.0e-24
Match length
                  136
% identity
                  42
                  HYPOTHETICAL 29.7 KD PROTEIN C18G6.06 IN CHROMOSOME I
NCBI Description
                  >gi 1122371 emb CAA92386 (Z68198) hypothetical protein
                  [Schizosaccharomyces pombe]
Seq. No.
                  231606
Seq. ID
                  LIB3197-033-Q1-M1-A10
Method
                  BLASTX
NCBI GI
                  g2493146
BLAST score
                  404
E value
                  2.0e-39
Match length
                  115
% identity
                  52
NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi 755148
                  (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit
                  [Gossypium hirsutum] >gi_4519415_dbj_BAA75542.1_ (AB024275)
                  vacuolar H+-ATPase c subunit [Citrus unshiu]
Seq. No.
                  231607
Seq. ID
                  LIB3197-033-Q1-M1-A11
Method
                  BLASTX
NCBI GI
                  g3874228
BLAST score
                  182
E value
                  2.0e-13
Match length
                  123
                  21
% identity
NCBI Description
                  (Z49909) cDNA EST CEMSF21F comes from this gene; cDNA EST
                  EMBL: D73546 comes from this gene; cDNA EST EMBL: D73669
                  comes from this gene; cDNA EST EMBL:D70979 comes from this
                  gene; cDNA EST EMBL:D71075 comes from this gene; cDNA E
Seq. No.
                  231608
Seq. ID
                  LIB3197-033-Q1-M1-A5
Method
                  BLASTX
NCBI GI
                  q2244732
BLAST score
                  307
E value
                  3.0e-28
                  89
Match length
% identity
NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
Seq. No.
                  231609
Seq. ID
                  LIB3197-033-Q1-M1-A6
Method
                  BLASTX
```

NCBI GI q1710521 BLAST score 148 E value 2.0e-13 Match length 46 % identity 89

NCBI Description 60S RIBOSOMAL PROTEIN L24 >gi 1154859 emb CAA63960





## (X94296) L24 ribosomal protein [Hordeum vulgare]

```
Seq. No.
                   231610
Seq. ID
                  LIB3197-033-Q1-M1-A8
Method
                  BLASTX
NCBI GI
                   g2586127
BLAST score
                  237
E value
                   5.0e-20
Match length
                  95
% identity
                   51
NCBI Description (U89510) b-keto acyl reductase [Hordeum vulgare]
Seq. No.
                  231611
Seq. ID
                  LIB3197-033-Q1-M1-A9
Method
                  BLASTX
NCBI GI
                  g542052
BLAST score
                  375
E value
                  3.0e-36
Match length
                  85
% identity
                  79
NCBI Description
                  ethylene-forming enzyme EFE - common tobacco
                  >gi_450357_emb_CAA82646_ (Z29529) ethylene forming enzyme
                   (EFE) [Nicotiana tabacum]
Seq. No.
                  231612
Seq. ID
                  LIB3197-033-Q1-M1-B10
Method
                  BLASTX
NCBI GI
                  g100535
BLAST score
                  205
E value
                  3.0e-16
                  44
Match length
                  91
% identity
NCBI Description hypothetical protein - swollen duckweed
                  >gi 1929057_emb_CAA32236 (X14075) longest ORF (1) [Lemna
                  gibba]
Seq. No.
                  231613
Seq. ID
                  LIB3197-033-Q1-M1-B2
Method
                  BLASTX
NCBI GI
                  g3914999
BLAST score
                  278
E value
                  1.0e-24
Match length
                  75
% identity
                  80
NCBI Description SUPEROXIDE DISMUTASE, CHLOROPLAST [CU-ZN] PRECURSOR
                  >gi_1944326_dbj_BAA19675_ (D49486) copper/zinc-superoxide
                  dismutase precursor [Solidago canadensis]
Seq. No.
                  231614
                  LIB3197-033-Q1-M1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q267069
BLAST score
                  336
E value
                  4.0e-45
Match length
                  95
% identity
NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
```



tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916 ·(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 231615 Seq. ID LIB3197-033-Q1-M1-B7 Method BLASTX NCBI GI g3599491 BLAST score 228 8.0e-19 E value 57 Match length 75 % identity

231616

NCBI Description (AF085149) putative aminotransferase [Capsicum chinense]

Seq. ID LIB3197-033-Q1-M1-B8 Method BLASTX NCBI GI g543905 BLAST score 464 E value 2.0e-46 Match length 110 % identity 82

Seq. No.

NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi 347459 (L22162)

brassinosteroid-regulated protein [Glycine max]

Seq. No. 231617 Seq. ID LIB3197-033-Q1-M1-C1 Method BLASTX

NCBI GI g1762144 BLAST score 291 E value 3.0e-26 108 Match length % identity

NCBI Description (U48435) putative cytochrome P450 [Solanum chacoense]

Seq. No. 231618

Seq. ID LIB3197-033-Q1-M1-C10

BLASTX Method NCBI GI g4544399 BLAST score 564 E value 3.0e-58 Match length 128 % identity

NCBI Description (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana]

Seq. No. 231619

LIB3197-033-Q1-M1-C2 Seq. ID

Method BLASTX g125887 NCBI GI BLAST score 207 E value 2.0e-16 115 Match length % identity 42

NCBI Description ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR

>qi 82092 pir S04765 LAT52 protein precursor - tomato >gi 295812 emb CAA33854 (X15855) LAT52 [Lycopersicon



## esculentum]

Seq. No. 231620

Seq. ID LIB3197-033-Q1-M1-C4

Method BLASTX
NCBI GI g2499535
BLAST score 360
E value 3.0e-38
Match length 111
% identity 65

NCBI Description 2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi\_595681

(U13238) 2-oxoglutarate/malate translocator [Spinacia

oleracea]

Seq. No. 231621

Seq. ID LIB3197-033-Q1-M1-C5

Method BLASTX
NCBI GI g2739382
BLAST score 540
E value 2.0e-55
Match length 148
% identity 31

NCBI Description (AC002505) myosin heavy chain-like protein [Arabidopsis

thaliana]

Seq. No. 231622

Seq. ID LIB3197-033-Q1-M1-C6

Method BLASTX
NCBI GI g1172977
BLAST score 514
E value 2.0e-52
Match length 120
% identity 83

NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic

ribosomal protein L18 [Arabidopsis thaliana]

Seq. No. 231623

Seq. ID LIB3197-033-Q1-M1-C8

Method BLASTX
NCBI GI g2384758
BLAST score 498
E value 2.0e-50
Match length 101
% identity 93

NCBI Description (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza

sativa]

Seq. No. 231624

Seq. ID LIB3197-033-Q1-M1-C9

Method BLASTX
NCBI GI g4098128
BLAST score 556
E value 3.0e-57
Match length 123
% identity 89

NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]

Match length

% identity

45 73



```
231625
Seq. No.
Seq. ID
                  LIB3197-033-Q1-M1-D11 ~
Method
                  BLASTX
NCBI GI
                  g3738257
BLAST score
                  500
E value
                  1.0e-50
Match length
                  105
% identity
                  93
                  (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
NCBI Description
                  nigra]
                  231626
Seq. No.
Seq. ID
                  LIB3197-033-Q1-M1-D2
Method
                  BLASTX
NCBI GI
                  g2267567
BLAST score
                  336
E value
                  1.0e-31
Match length
                  81
% identity
NCBI Description
                  (AF009003) glycine-rich RNA binding protein 1 [Pelargonium
                  x hortorum] >gi 2267569 (AF009004) glycine-rich RNA binding
                  protein 2 [Pelargonium x hortorum]
Seq. No.
                  231627
Seq. ID
                  LIB3197-033-Q1-M1-D5
Method
                  BLASTX
NCBI GI
                  g120669
BLAST score
                  260
E value
                  4.0e-30
Match length
                  73
% identity
                  81
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                  >gi 19566 emb_CAA42905_ (X60347) glyceraldehyde
                  3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                  231628
Seq. ID
                  LIB3197-033-Q1-M1-D8
Method
                  BLASTX
NCBI GI
                  q1814403
BLAST score
                  536
E value
                  6.0e-55
Match length
                  133
% identity
NCBI Description
                  (U84889) methionine synthase [Mesembryanthemum
                  crystallinum]
Seq. No.
                  231629
Seq. ID
                  LIB3197-033-Q1-M1-D9
Method
                  BLASTX
                  g4469023
NCBI GI
BLAST score
                  175
E value
                  6.0e-13
```

NCBI Description (AL035602) putative protein [Arabidopsis thaliana]



```
Seq. No.
                  231630
Seq. ID
                  LIB3197-033-Q1-M1-E1
Method
                  BLASTX
NCBI GI
                  g126041
BLAST score
                  344
E value
                  5.0e-33
Match length
                  71
% identity
                  99
NCBI Description
                  L-LACTATE DEHYDROGENASE H CHAIN (LDH-B)
                  >gi 1070432 pir DEHULH L-lactate dehydrogenase (EC
                  1.1.1.27) chain H - human >gi_34329_emb_CAA68701_ (Y00711)
                  lactate dehydrogenase B (AA 1 - 334) [Homo sapiens]
                  >gi 1200083 emb CAA32033 (X13794) lactate dehydrogenase B
                  [Homo sapiens] >gi 4557032 ref NP 002291.1 pLDHB lactate
                  dehydrogenase B
Seq. No.
                  231631
Seq. ID
                  LIB3197-033-Q1-M1-E2
Method
                  BLASTX
NCBI GI
                  g3202042
BLAST score
                  192
                  9.0e-15
E value
Match length
                  112
% identity
                  43
NCBI Description
                 (AF069324) 26S proteasome regulatory subunit S5A
                  [Mesembryanthemum crystallinum]
Seq. No.
                  231632
Seq. ID
                  LIB3197-033-Q1-M1-E4
Method
                  BLASTX
NCBI GI
                  g1071913
BLAST score
                  527
E value
                  6.0e-54
Match length
                  126
% identity
NCBI Description cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial
                  - spinach >gi 1066153 dbj BAA07177 (D37963) cysteine
                  synthase [Spinacia oleracea]
Seq. No.
                  231633
Seq. ID
                  LIB3197-033-Q1-M1-E7
Method
                  BLASTX
NCBI GI
                  q1174867
BLAST score
                  163
E value
                  3.0e-17
Match length
                  68
% identity
                  69
NCBI Description
                  PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2
```

UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING

KD PROTEIN) >gi 633687 emb CAA55862 (X79275)

ubiquinol--cytochrome c reductase [Solanum tuberosum]

>gi 1094912 prf 2107179A cytochrome c oxidase:SUBUNIT=8.2kD [Solanum tuberosum]

231634 Seq. No.

Seq. ID LIB3197-033-Q1-M1-E9

Seq. ID

Method



```
Method
                  BLASTX
NCBI GI
                  g1245343
BLAST score
                  269
E value
                  1.0e-23
Match length
                  92
                  55
% identity
NCBI Description
                 (U50194) tripeptidylpeptidase II [Rattus norvegicus]
Seq. No.
                  231635
Seq. ID
                  LIB3197-033-Q1-M1-F10
Method
                  BLASTX
NCBI GI
                  q4454056
BLAST score
                  143
E value
                  7.0e-09
Match length
                  40
                  70
% identity
NCBI Description (AJ000930) ClpP [Arabidopsis thaliana]
Seq. No.
                  231636
Seq. ID
                  LIB3197-033-Q1-M1-F5
Method
                  BLASTX
NCBI GI
                  g2078350
BLAST score
                  223
E value
                  3.0e-18
Match length
                  50
% identity
                  82
NCBI Description (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                  231637
Seq. ID
                  LIB3197-033-Q1-M1-F6
Method
                  BLASTX
NCBI GI
                  g3831444
BLAST score
                  149
E value
                  2.0e-09
Match length
                  105
% identity
                  51
                 (AC005819) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  231638
Seq. ID
                  LIB3197-033-Q1-M1-G1
                  BLASTX
Method
NCBI GI
                  g117501
BLAST score
                  624
E value
                  3.0e-65
Match length
                  115
% identity
                  100
NCBI Description CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60)
                  (52 KD RIBONUCLEOPROTEIN AUTOANTIGEN RO/SS-A)
                  >gi 87015 pir A37047 calreticulin precursor - human
                  >gi_179882 (M84739) calreticulin [Homo sapiens] >gi_337487
                  (M32294) Ro ribonucleoprotein autoantigen (Ro/SS-A)
                  precursor [Homo sapiens] >gi 1905911 (AD000092)
                  calreticulin [Homo sapiens]
Seq. No.
                  231639
```

33328

LIB3197-033-Q1-M1-G3

BLASTX



```
NCBI GI
                    q2827082
 BLAST score
                   220
 E value
                   6.0e-18
                   51
 Match length
                   80
 % identity
 NCBI Description (AF020272) malate dehydrogenase [Medicago sativa]
 Seq. No.
                   231640
 Seq. ID
                   LIB3197-033-Q1-M1-G4
 Method
                   BLASTX
 NCBI GI
                   q119350
 BLAST score
                   253
                   4.0e-37
 E value
 Match length
                   102
                   79
 % identity
NCBI Description
                   ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                    (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi 81608 pir JQ1187
                   phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                   thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
                    [Arabidopsis thaliana]
                   231641
 Seq. No.
 Seq. ID
                   LIB3197-033-Q1-M1-G5
 Method
                   BLASTX
 NCBI GI
                   q4539335
 BLAST score
                   547
 E value
                   3.0e-56
 Match length
                   151
 % identity
                    68
 NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
 Seq. No.
                   231642
 Seq. ID
                   LIB3197-033-Q1-M1-G6
 Method
                   BLASTX
 NCBI GI
                   q267073
 BLAST score
                   452
 E value
                    3.0e-52
 Match length
                   108
 % identity
                    93
                   TUBULIN BETA-2/BETA-3 CHAIN >gi 320184 pir JQ1587 tubulin
 NCBI Description
                   beta chain - Arabidopsis thaliana >gi 166898 (M84700)
                   beta-2 tubulin [Arabidopsis thaliana] >gi 166900 (M84701)
                   beta-3 tubulin [Arabidopsis thaliana]
 Seq. No.
                   231643
                   LIB3197-033-Q1-M1-G7
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2961300
 BLAST score
                   572
                    3.0e-59
 E value
 Match length
                   120
 % identity
                   93
 NCBI Description (AJ225027) ribosomal protein L24 [Cicer arietinum]
```

Seq. No. 231644

Seq. ID LIB3197-033-Q1-M1-G9

Method BLASTX

NCBI GI

BLAST score



```
q2654559
NCBI GI
BLAST score
                  253
E value
                  1.0e-21
                  140
Match length
% identity
                  36
                 (AF006621) embryonic lung protein [Homo sapiens]
NCBI Description
Seq. No.
                  231645
Seq. ID
                  LIB3197-033-Q1-M1-H1
Method
                  BLASTX
NCBI GI
                  q3236237
                  270
BLAST score
                  8.0e-24
E value
Match length
                  91
% identity
                  (AC004684) putative ribotol dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  231646
                  LIB3197-033-Q1-M1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3915031
                  693
BLAST score
                  2.0e-73
E value
Match length
                  137
% identity
                  96
NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
                  (STEAROYL-ACP DESATURASE) >gi 1217628 emb CAA65232
                   (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase
                  [Gossypium hirsutum]
                  231647
Seq. No.
Seq. ID
                  LIB3197-033-Q1-M1-H12
Method
                  BLASTX
NCBI GI
                  g1419088
BLAST score
                  668
                  2.0e-70
E value
Match length
                  127
                  94
% identity
NCBI Description (Z71395) calreticulin [Nicotiana plumbaginifolia]
                  231648
Seq. No.
                  LIB3197-033-Q1-M1-H7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4406780
BLAST score
                  512
                  4.0e-52
E value
Match length
                  130
                  74
% identity
NCBI Description (AC006532) putative multispanning membrane protein
                  [Arabidopsis thaliana]
Seq. No.
                  231649
Seq. ID
                  LIB3197-033-Q1-M1-H8
Method
                  BLASTX
```

g3461833

Method

NCBI GI BLAST score

E value

BLASTX g3420239

236 2.0e-20



```
3.0e-45
E value
Match length
                   108
                   74
% identity
                  (AC004138) putative expansin [Arabidopsis thaliana]
NCBI Description
                   231650
Seq. No.
                   LIB3197-034-Q1-M1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1841464
BLAST score
                   165
E value
                   2.0e-11
Match length
                   38
% identity
                   45
                  (Y11002) LIM-domain SF3 protein [Nicotiana tabacum]
NCBI Description
Seq. No.
                   231651
                   LIB3197-034-Q1-M1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1841464
BLAST score
                   223
                   3.0e-18
E value
Match length
                   41
                   51
% identity
NCBI Description (Y11002) LIM-domain SF3 protein [Nicotiana tabacum]
                   231652
Seq. No.
                   LIB3197-034-Q1-M1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1408471
BLAST score
                   426
E value
                   5.0e-42
Match length
                   97
                   77
% identity
                   (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                   thaliana] >gi 3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
                   231653
Seq. No.
Seq. ID
                   LIB3197-034-Q1-M1-A5
                   BLASTX
Method
NCBI GI
                   g3377797
BLAST score
                   305
E value
                   2.0e-50
Match length
                   132
% identity
                   76
NCBI Description
                   (AF075597) Similar to 60S ribosome protein L19; coded for
                   by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                   H36046; coded for by A. thaliana cDNA T44067; coded for by
                   A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                   R90691 [Ara
 Seq. No.
                   231654
                   LIB3197-034-Q1-M1-A7
 Seq. ID
```



```
Match length
                  46
                  96
% identity
NCBI Description (AF059484) actin [Gossypium hirsutum]
Seq. No.
                  231655
                  LIB3197-034-Q1-M1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2286153
BLAST score
                  554
E value
                  4.0e-57
                  112
Match length
                  99
% identity
                 (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
                  231656
Seq. No.
Seq. ID
                  LIB3197-034-Q1-M1-B11
Method
                  BLASTX
NCBI GI
                  q3395432
BLAST score
                  179
                  4.0e-13
E value
Match length
                  74
                  55
% identity
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                  231657
Seq. No.
                  LIB3197-034-Q1-M1-B12
Seq. ID
Method
                  BLASTX
                  g3668089
NCBI GI
BLAST score
                  262
                  8.0e-23
E value
Match length
                  98
% identity
                  49
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.
                  231658
Seq. ID
                  LIB3197-034-Q1-M1-B2
Method
                  BLASTX
NCBI GI
                  q1890281
BLAST score
                  365
E value
                  6.0e-35
Match length
                  117
% identity
NCBI Description
                  (U89984) transformation-sensitive protein homolog
                   [Acanthamoeba castellanii]
Seq. No.
                  231659
Seq. ID
                  LIB3197-034-Q1-M1-B4
Method
                  BLASTX
NCBI GI
                  g3021348
BLAST score
                  183
E value
                  8.0e-14
Match length
                  38
% identity
                  87
NCBI Description (AJ004961) ribosomal protein L18 [Cicer arietinum]
```

Seq. No. 231660

Seq. ID LIB3197-034-Q1-M1-B5

Match length

% identity

66

92



```
Method
                  BLASTX
NCBI GI
                  g267069
BLAST score
                  658
E value
                  3.0e-69
Match length
                  122
                  99
% identity
NCBI Description
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                  231661
Seq. ID
                  LIB3197-034-Q1-M1-B6
Method
                  BLASTX
NCBI GI
                  g2911050
BLAST score
                  141
E value
                  1.0e-08
Match length
                  97
                  40
% identity
NCBI Description
                  (AL021961) putative protein [Arabidopsis thaliana]
Seq. No.
                  231662
                  LIB3197-034-Q1-M1-B9
Seq. ID
Method
                  BLASTX
                  g133959
NCBI GI
BLAST score
                  242
E value
                  2.0e-20
Match length
                  50
                  94
% identity
                 CHLOROPLAST 30S RIBOSOMAL PROTEIN S4 >gi_81526_pir__A30833
NCBI Description
                  ribosomal protein S4 - spinach chloroplast >gi 343377
                  (M16878) ribosomal protein S4 [Spinacia oleracea]
                  >gi_225464_prf__1303355A ribosomal protein S4 [Spinacia
                  oleracea}
                       231663
Seq. No.
                  LIBNIS 134-01-M1-C1
BLASTX
Seq. ID
Méthod
NCBI GI
                  a464981
BLAST score
                  274
E value
                  2.0e-24
Match length
                  55
                  93
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762)
                  ubiquitin carrier protein [Lycopersicon esculentum]
Seq. No.
                  231664
Seq. ID
                  LIB3197-034-Q1-M1-C10
Method
                  BLASTX
NCBI GI
                  q4544384
BLAST score
                  243
E value
                  4.0e-21
```

NCBI Description (AC007047) unknown protein [Arabidopsis thaliana]

Match length

NCBI Description

% identity

144 90



```
Seq. No.
                  231665
                  LIB3197-034-Q1-M1-C11
Seq. ID
Method
                  BLASTX
                  q2739046
NCBI GI
                  194
BLAST score
                  8.0e-15
E value
Match length
                  102
                  38
% identity
                  (AF024652) polyphosphoinositide binding protein Ssh2p
NCBI Description
                  [Glycine max]
Seq. No.
                  231666
                  LIB3197-034-Q1-M1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3157932
BLAST score
                  150
                  1.0e-09
E value
Match length
                  131
                  33
% identity
                  (AC002131) Similar to hypothetical protein HYP1 gb Z97338
NCBI Description
                  from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                  231667
                  LIB3197-034-Q1-M1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334115
BLAST score
                  438
E value
                  2.0e-44
Match length
                  117
                  81
% identity
                  ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                  hirsutum]
                  231668
Seq. No.
                  LIB3197-034-Q1-M1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q135406
BLAST score
                   647
                   7.0e-68
E value
                  126
Match length
% identity
                   96
                  TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin
NCBI Description
                   alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189)
                   alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)
                   alpha-5 tubulin [Arabidopsis thaliana]
Seq. No.
                   231669
                  LIB3197-034-Q1-M1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3819164
BLAST score
                   660
                   2.0e-69
E value
```

(AJ012318) cytosolic chaperonin, delta-subunit [Glycine



## max]

```
Seq. No.
                  231670
                  LIB3197-034-Q1-M1-C8
Seq. ID
Method
                  BLASTX
                  g3023190
NCBI GI
BLAST score
                  521
                  4.0e-53
E value
                  129
Match length
                  79
% identity
                  14-3-3-LIKE PROTEIN 16R >gi 1888459 emb_CAA72381_ (Y11685)
NCBI Description
                  14-3-3 protein [Solanum tuberosum]
                  231671
Seq. No.
Seq. ID
                  LIB3197-034-Q1-M1-D1
Method
                  BLASTX
                  q1922251
NCBI GI
BLAST score
                  496
                  3.0e-50
E value
Match length
                  97
                   98
% identity
                  (Y12072) farnesyl pyrophosphate synthase [Gossypium
NCBI Description
                  arboreum]
                   231672
Seq. No.
                  LIB3197-034-Q1-M1-D10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2129758
BLAST score
                   535
                   8.0e-55
E value
                  112
Match length
                   82
% identity
                  ubiquitin conjugating enzyme E2 protein - Arabidopsis
NCBI Description
                   thaliana >gi_992704 (U33757) UBC7 [Arabidopsis thaliana]
                   231673
Seq. No.
                  LIB3197-034-Q1-M1-D6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2688830
                   574
BLAST score
                   2.0e-59
E value
                   150
Match length
                   76
% identity
                  (AF000952) putative sugar transporter [Prunus armeniaca]
NCBI Description
Seq. No.
                   231674
                   LIB3197-034-Q1-M1-D8
Seq. ID
                   BLASTX
Method
                   q475048
NCBI GI
BLAST score
                   630
E value
                   6.0e-66
                   134
Match length
                   64
% identity
                  (X72581) tonoplast intrinsic protein gamma (gamma-TIP)
NCBI Description
                   [Arabidopsis thaliana]
```

33335

231675

Seq. No.

NCBI GI

BLAST score



```
Seq. ID
                  LIB3197-034-Q1-M1-D9
                  BLASTX
Method
NCBI GI
                  q2894592
BLAST score
                  329
                  1.0e-30
E value
Match length
                  87
                  71
% identity
                  (AL021889) predicted protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  231676
                  LIB3197-034-Q1-M1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2894612
BLAST score
                  302
                  1.0e-27
E value
Match length
                  94
% identity
                   63
                  (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  231677
                  LIB3197-034-Q1-M1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2791834
BLAST score
                   527
                  7.0e-54
E value
Match length
                  103
                   98
% identity
NCBI Description
                  (AF041463) elongation factor 1-alpha [Manihot esculenta]
                  231678
Seq. No.
                  LIB3197-034-Q1-M1-E8
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1620898
                   333
BLAST score
                   4.0e-31
E value
                   88
Match length
                   73
% identity
NCBI Description
                   (D87957) protein involved in sexual development [Homo
                   sapiens]
                   231679
Seq. No.
                   LIB3197-034-Q1-M1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1945611
                   265
BLAST score
                   3.0e-23
E value
                   120
Match length
                   44
% identity
                   (AB003103) 26S proteasome subunit p55 [Homo sapiens]
NCBI Description
                   >gi_4506221_ref_NP_002807.1_pPSMD12_ proteasome (prosome,
                   macropain) 26S subunit, non-ATPase,
                   231680
Seq. No.
                   LIB3197-034-Q1-M1-F10
Seq. ID
Method
                   BLASTX
```

g2497543 536



4.0e-55 E value Match length 117 % identity 91 NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi\_542061\_pir\_\_\$41379 pyruvate kinase - common tobacco >gi 444023 emb CAA82628 (Z29492) pyruvate kinase [Nicotiana tabacum] Seq. No. 231681 LIB3197-034-Q1-M1-F12 Seq. ID Method BLASTX NCBI GI g479386 BLAST score 407 E value 9.0e-40Match length 89 90 % identity NCBI Description isocitrate dehydrogenase - soybean

231682 Seq. No.

LIB3197-034-Q1-M1-F2 Seq. ID

Method BLASTX NCBI GI q464849 BLAST score 804 E value 3.0e-86 Match length 152 99 % identity

NCBI Description TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha

chain - almond  $>gi_20413$  emb\_CAA47635\_ (X67162)

alpha-tubulin [Prunus dulcis]

Seq. No. 231683

LIB3197-034-Q1-M1-F3 Seq. ID

BLASTX Method NCBI GI q4193388 BLAST score 424 E value 9.0e-42 Match length 125 % identity 70

NCBI Description (AF091455) translationally controlled tumor protein [Hevea

brasiliensis]

Seq. No. 231684

Seq. ID LIB3197-034-Q1-M1-F4

Method BLASTX NCBI GI q81857 BLAST score 340 E value 6.0e-32 Match length 71 % identity 90

NCBI Description IgE-dependent histamine-releasing factor homolog - alfalfa

(fragment) >qi 19658 emb CAA45349 (X63872) translationally

controlled tumor protein [Medicago sativa]

Seq. No. 231685

Seq. ID LIB3197-034-Q1-M1-F5

Method BLASTX NCBI GI q4193388 BLAST score 259



```
E value
                    1.0e-22
 Match length
                    69
                    72
 % identity
NCBI Description
                    (AF091455) translationally controlled tumor protein [Hevea
                    brasiliensis]
                    231686
  Seq. No.
                    LIB3197-034-Q1-M1-F6
  Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g312179
  BLAST score
                    558
                    2.0e-57
 E value
                    130
 Match length
                    82
  % identity
  NCBI Description
                    (X73151) glyceraldehyde 3-phosphate dehydrogenase
                     (phosphorylating) [Zea mays] >gi 1184772 (U45855) cytosolic
                    glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]
                    >gi 1185554 (U45858) glyceraldehyde-3-phosphate
                    dehydrogenase [Zea mays]
  Seq. No.
                    231687
  Seq. ID
                    LIB3197-034-Q1-M1-F9
 Method
                    BLASTX
 NCBI GI
                    g4193388 .
                    <u>2</u>92
  BLAST score
                    2.0e-26
  E value
 Match length
                    82
 % identity
                    74
                    (AF091455) translationally controlled tumor protein [Hevea
 NCBI Description
                    brasiliensis]
  Seq. No.
                    231688
  Seq. ID
                    LIB3197-034-Q1-M1-G11
  Method
                    BLASTX
  NCBI GI
                    g4049349
  BLAST score
                    423
  E value
                    1.0e-41
  Match length
                    122
  % identity
                    67
                    (AL034567) ubiquinol-cytochrome c reductase-like protein
  NCBI Description
                     [Arabidopsis thaliana]
  Seq. No.
                    231689
                    LIB3197-034-Q1-M1-G2
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q3334299
  BLAST score
                    584
  E value
                    1.0e-60
 Match length
                    122
  % identity
                    93
```

NCBI Description PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE

COMPLEX ALPHA SUBUNIT) >gi\_2315211\_emb\_CAA74725\_ (Y14339)

proteasome alpha subunit [Lycopersicon esculentum]

Seq. No. 231690

Seq. ID LIB3197-034-Q1-M1-G3

Method BLASTX



```
NCBI GI
                  g2661840
BLAST score
                  147
                  2.0e-09
E value
                  51
Match length
                   55
% identity
                  (Y15430) adenosine kinase [Physcomitrella patens]
NCBI Description
Seq. No.
                  231691
Seq. ID
                  LIB3197-034-Q1-M1-G5
Method
                  BLASTX
NCBI GI
                  g4006924
BLAST score
                   482
                   1.0e-48
E value
Match length
                   108
                   79
% identity
NCBI Description
                   (Z99708) beta-galactosidase like protein [Arabidopsis
                   thaliana]
Seq. No.
                   231692
                   LIB3197-034-Q1-M1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3219766
BLAST score
                   737
                   2.0e-78
E value
Match length
                   150
                   97
% identity
                  ACTIN 82 >gi 1498370 (U60483) actin [Solanum tuberosum]
NCBI Description
Seq. No.
                   231693
                   LIB3197-034-Q1-M1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3913366
BLAST score
                   202
E value
                   8.0e-16
Match length
                   120
% identity
                   36
                   PUTATIVE RECEPTOR PROTEIN KINASE CRINKLY4 PRECURSOR
NCBI Description
                   >gi 1597723 (U67422) CRINKLY4 precursor [Zea mays]
                   231694
Seq. No.
                   LIB3197-034-Q1-M1-G9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2811278
BLAST score
                   567
                   1.0e-58
E value
Match length
                   135
                   77
% identity
                  (AF043284) expansin [Gossypium hirsutum]
NCBI Description
                   231695
Seq. No.
                   LIB3197-034-Q1-M1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3122673
BLAST score
                   521
E value
                   4.0e-53
Match length
                   129
```

79

% identity



```
60S RIBOSOMAL PROTEIN L15 >gi 2245027_emb_CAB10447_
NCBI Description
                  (Z97341) ribosomal protein [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB3197-034-Q1-M1-H2
                  BLASTX
Method
                  q3860247
NCBI GI
BLAST score
                  539
                  3.0e-55
E value
                  112
Match length
                  87
% identity
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                  231697
Seq. No.
                  LIB3197-034-Q1-M1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2760326
BLAST score
                  250
E value
                  3.0e-21
Match length
                  81
                  56
% identity
                  (AC002130) F1N21.11 [Arabidopsis thaliana]
NCBI Description
                  231698
Seq. No.
Seq. ID
                  LIB3197-035-Q1-M1-A11
                  BLASTX
Method
                  q2118231
NCBI GI
BLAST score
                   582
E value
                   2.0e-60
Match length
                   130
                   85
% identity
                  H+-transporting ATPase (EC 3.6.1.35) AHA10 - Arabidopsis
NCBI Description
                   thaliana >gi_765354_bbs_157347 (S74033) plasma membrane
                   H(+)-ATPase isoform AHA10=P-type ATPase [Arabidopsis
                   thaliana, cv. Columbia, Peptide, 946 aa] [Arabidopsis
                   thaliana]
                   231699
Seq. No.
Seq. ID
                   LIB3197-035-Q1-M1-A12
Method
                   BLASTX
NCBI GI
                   g4559322
BLAST score
                   303
                   9.0e-28
E value
Match length
                   107
                   62
% identity
                  (AC007087) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   231700
                   LIB3197-035-Q1-M1-A3
Seq. ID
Method
                   BLASTX
                   g2642450
NCBI GI
```

NCBI GI g2642450 BLAST score 328 E value 1.0e-30

E value 1.0e Match length 102 % identity 63

NCBI Description (AC002391) putative metal ion transporter (Nramp) [Arabidopsis thaliana] >gi\_3169188 (AC004401) putative



## metal ion transporter (Nramp) [Arabidopsis thaliana]

```
231701
Seq. No.
Seq. ID
                  LIB3197-035-Q1-M1-A5
Method
                  BLASTX
                  q2129753
NCBI GI
                  381
BLAST score
                  1.0e-36
E value
                  95
Match length
                  67
% identity
                  threonine synthase (EC 4.2.99.2) precursor - Arabidopsis
NCBI Description
                  thaliana (fragment) >gi_1448917 (L41666) threonine synthase
                  [Arabidopsis thaliana]
                  231702
Seq. No.
                  LIB3197-035-Q1-M1-A6
Seq. ID
Method
                  BLASTX
                  q1076282
NCBI GI
BLAST score
                  542
                  6.0e-59
E value
                  130
Match length
                  87
% identity
                  aconitate hydratase (EC 4.2.1.3) - Arabidopsis thaliana
NCBI Description
                   (fragment) >gi 599625 emb CAA58046 (X82839) aconitase
                   [Arabidopsis thaliana]
                   231703
Seq. No.
Seq. ID
                  LIB3197-035-Q1-M1-B1
                  BLASTX
Method
NCBI GI
                  q3450889
                   350
BLAST score
                   4.0e-33
E value
                   102
Match length
                   73
% identity
                  (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
NCBI Description
                   231704
Seq. No.
                   LIB3197-035-Q1-M1-B10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3834310
BLAST score
                   473
                   1.0e-47
E value
                   91
Match length
                   99
% identity
                   (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
NCBI Description
                   gb D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464,
                   gb_N37265, gb_H36151, gb_Z34711, gb_AAO40983, and gb_T22122
                   come from this gene. [Arabidopsis thaliana]
Seq. No.
                   231705
                   LIB3197-035-Q1-M1-B11
Seq. ID
Method
                   BLASTX
                   g3608171
NCBI GI
                   303
BLAST score
                   8.0e-28
E value
                   81
Match length
```

75

% identity



NCBI Description

```
[Cucurbita moschata]
                  231706
Seq. No.
                  LIB3197-035-Q1-M1-B12
Seq. ID
                  BLASTX
Method
                  q42356
NCBI GI
BLAST score
                  270
                  9.0e-24
E value
                  132
Match length
                  45
% identity
                  (X03709) aminopeptidase N (aa 1-176) [Escherichia coli]
NCBI Description
                  231707
Seq. No.
                  LIB3197-035-Q1-M1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                   q462137
BLAST score
                   308
                   3.0e-53
E value
                   126
Match length
                   81
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
Seq. No.
                   231708
                   LIB3197-035-Q1-M1-B3
Seq. ID
                   BLASTX
Method
                   q3420055
NCBI GI
BLAST score
                   426
E value
                   5.0e-42
Match length
                   106
                   76
% identity
                  (AC004680) cyclophilin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   231709
                   LIB3197-035-Q1-M1-B4
Seq. ID
                   BLASTX
Method
                   g1710521
NCBI GI
                   583
BLAST score
                   2.0e-60
E value
Match length
                   125
                   91
% identity
                  60S RIBOSOMAL PROTEIN L24 >gi 1154859 emb CAA63960_
NCBI Description
                   (X94296) L24 ribosomal protein [Hordeum vulgare]
                   231710
Seq. No.
                   LIB3197-035-Q1-M1-B6
Seq. ID
                   BLASTX
Method
                   g1617274
NCBI GI
                   668
BLAST score
                   2.0e-70
E value
                   145
Match length
% identity
                   83
NCBI Description (Z72152) AMP-binding protein [Brassica napus]
                   231711
Seq. No.
                   LIB3197-035-Q1-M1-B8
Seq. ID
                   BLASTX
Method
```

(D86306) proton-translocating inorganic pyrophosphatase

NCBI Description



```
NCBI GI
                  q4490737
BLAST score
                  281
E value
                  4.0e-25
Match length
                  123
% identity
                  53
NCBI Description
                 (AL035708) putative protein [Arabidopsis thaliana]
Seq. No.
                  231712
Seq. ID
                  LIB3197-035-Q1-M1-B9
Method
                  BLASTX
                  g1350944
NCBI GI
BLAST score
                  391
                  5.0e-38
E value
Match length
                  80
% identity
                  96
NCBI Description 40S RIBOSOMAL PROTEIN S17
Seq. No.
                  231713
                  LIB3197-035-Q1-M1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4469025
BLAST score
                  222
E value
                  3.0e-18
Match length
                  49
% identity
                  80
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                  231714
                  LIB3197-035-Q1-M1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q467698
BLAST score
                  185
E value
                   9.0e-14
Match length
                  125
% identity
                  34
NCBI Description (X78326) SUR4 [Saccharomyces cerevisiae]
Seq. No.
                  231715
Seq. ID
                  LIB3197-035-Q1-M1-C12
Method
                  BLASTX
NCBI GI
                  g2341034
BLAST score
                  547
E value
                  3.0e-56
Match length
                  111
                  97
% identity
NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]
Seq. No.
                  231716
Seq. ID
                  LIB3197-035-Q1-M1-C2
Method
                  BLASTX
NCBI GI
                  q2088651
BLAST score
                  217
E value
                  1.0e-17
                  87
Match length
% identity
                  44
```

33343

[Arabidopsis thaliana]

(AF002109) hypersensitivity-related gene 201 isolog

Seq. No.

Seq. ID Method



```
Seq. No.
                  231717
                  LIB3197-035-Q1-M1-C4
Seq. ID
                  BLASTX
Method
                  g2388689
NCBI GI
BLAST score
                  271
                  7.0e-24
E value
                  92
Match length
                   65
% identity
                  (AF016633) GH1 protein [Glycine max]
NCBI Description
Seq. No.
                  231718
                  LIB3197-035-Q1-M1-C8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1843527
BLAST score
                   569
                  7.0e-59
E value
Match length
                  116
                   56
% identity
                  (U73747) annexin [Gossypium hirsutum]
NCBI Description
                  231719
Seq. No.
                  LIB3197-035-Q1-M1-D1
Seq. ID
                  BLASTX
Method
                   g4206210
NCBI GI
BLAST score
                   256
                   8.0e-40
E value
Match length
                   136
                   69
% identity
                  (AF071527) putative calcium channel [Arabidopsis thaliana]
NCBI Description
                   >gi_4263043_gb_AAD15312_ (AC005142) putative calcium
                   channel [Arabidopsis thaliana]
                   231720
Seq. No.
                   LIB3197-035-Q1-M1-D11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4544399
BLAST score
                   478
                   4.0e-48
E value
                   140
Match length
                   63
% identity
NCBI Description
                   (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
                   thaliana]
Seq. No.
                   231721
                   LIB3197-035-Q1-M1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2815246
BLAST score
                   144
                   2.0e-14
E value
                   55
Match length
                   69
% identity
NCBI Description
                  (X95709) class I type 2 metallothionein [Cicer arietinum]
                   231722
```

LIB3197-035-Q1-M1-D3

BLASTX



NCBI GI q1174470 BLAST score 254 E value 6.0e-22Match length 72 61 % identity NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi\_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi\_1588285\_prf\_\_2208301A integral membrane protein [Mus musculus] Seq. No. 231723 Seq. ID LIB3197-035-Q1-M1-D4 Method BLASTX NCBI GI q4454051 BLAST score 353 E value 2.0e-33 Match length 74 % identity (AL035394) putative polygalacturonase [Arabidopsis NCBI Description thaliana] 231724 Seq. No. Seq. ID LIB3197-035-Q1-M1-D5 Method BLASTX NCBI GI q1335862 BLAST score 659 E value 2.0e-69 Match length 141 % identity NCBI Description (U42608) clathrin heavy chain [Glycine max] Seq. No. 231725 Seq. ID LIB3197-035-Q1-M1-D6 Method BLASTX NCBI GI q2662341 BLAST score 752 E value 3.0e-80 Match length 145 97 % identity (D63580) EF-1 alpha [Oryza sativa] NCBI Description >gi\_2662345\_dbj\_BAA23659\_ (D63582) EF-1 alpha [Oryza
sativa] >gi\_2662347\_dbj\_BAA23660\_ (D63583) EF-1 alpha [Oryza sativa] Seq. No. 231726 Seq. ID LIB3197-035-Q1-M1-D8 Method BLASTX NCBI GI g3914394 BLAST score 360 2.0e-34 E value

Match length 80 % identity 82

2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE NCBI Description

(PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi\_2118335\_pir\_\_S60473 phosphoglycerate mutase (EC 5.4.2.1) - common ice plant >gi 602426 (U16021) phosphoglyceromutase [Mesembryanthemum crystallinum]

Method

NCBI GI

BLASTX

g2444178



```
231727
Seq. No.
                  LIB3197-035-Q1-M1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3123745
BLAST score
                  232
E value
                  3.0e-19
                  115
Match length
                  43
% identity
NCBI Description
                  (AB013447) aluminum-induced [Brassica napus]
                  231728
Seq. No.
                  LIB3197-035-Q1-M1-E11
Seq. ID
Method
                  BLASTX
                  q3757514
NCBI GI
BLAST score
                  583
E value
                  2.0e-60
Match length
                  128
                  88
% identity
                  (AC005167) putative plasma membrane intrinsic protein
NCBI Description
                  [Arabidopsis thaliana]
                  231729
Seq. No.
                  LIB3197-035-Q1-M1-E6
Seq. ID
Method
                  BLASTX
                  g2570047
NCBI GI
BLAST score
                  174
                  2.0e-12
E value
                  118
Match length
                  28
% identity
                  (Y09234) MSTK2S kinase-like protein [Mus musculus]
NCBI Description
                  231730
Seq. No.
                  LIB3197-035-Q1-M1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q547753
BLAST score
                  196
                  4.0e-15
E value
                  67
Match length
                   61
% identity
NCBI Description KERATIN, TYPE II CYTOSKELETAL 4 (CYTOKERATIN 4) (K4) (CK4)
Seq. No.
                  231731
                  LIB3197-035-Q1-M1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1710551
BLAST score
                   281
E value
                   5.0e-25
Match length
                  51
                   100
% identity
                  60S RIBOSOMAL PROTEIN L39 >qi 1177369 emb CAA64728
NCBI Description
                   (X95458) ribosomal protein L39 [Zea mays]
Seq. No.
                   231732
                  LIB3197-035-Q1-M1-F7
Seq. ID
```



```
BLAST score
                  265
                  2.0e-25
E value
                  82
Match length
                  72
% identity
                  (U94784) unconventional myosin [Helianthus annuus]
NCBI Description
                  231733
Seq. No.
                  LIB3197-035-Q1-M1-F9
Seq. ID
                  BLASTX
Method
                  g2827753
NCBI GI
                  364
BLAST score
                  1.0e-44
E value
                  102
Match length
                  93
% identity
                  TUBULIN BETA CHAIN >gi 1490665 (U64029) beta-tubulin 1
NCBI Description
                  [Daucus carota]
Seq. No.
                  231734
                  LIB3197-035-Q1-M1-G2
Seq. ID
                  BLASTX
Method
                  g120669
NCBI GI
                  458
BLAST score
E value
                  7.0e-46
                  92
Match length
                  91
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 66014 pir DEJMG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                  >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
                  231735
Seq. No.
                  LIB3197-035-Q1-M1-G3
Seq. ID
Method
                  BLASTX
                  g120669
NCBI GI
                   225
BLAST score
                   1.0e-18
E value
Match length
                  77
                   57
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi 19566 emb CAA42905 (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
                   231736
Seq. No.
                   LIB3197-035-Q1-M1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g135406
BLAST score
                   507
                   1.0e-51
E value
                   99
Match length
                   96
% identity
NCBI Description TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi 99768 pir A32712 tubulin
                   alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189)
```

alpha-5 tubulin [Arabidopsis thaliana]

alpha-tubulin [Arabidopsis thaliana] >gi-166918 (M84698)

BLAST score

Match length

E value

225

49

1.0e-18



```
231737
Seq. No.
                   LIB3197-035-Q1-M1-H1
Seq. ID
                   BLASTX
Method
                   g1172872
NCBI GI
                   261
BLAST score
                   7.0e-23
E value
                   102
Match length
                   59
% identity
                  CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
NCBI Description
                   precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_
                   (D13042) thiol protease [Arabidopsis thaliana]
                   >gi 4539328_emb_CAB38829.1_ (AL035679) drought-inducible
                   cysteine proteinase RD19A precursor [Arabidopsis thaliana]
                   231738
Seq. No.
                   LIB3197-035-Q1-M1-H2
Seq. ID
Method
                   BLASTX
                   q70644
NCBI GI
BLAST score
                   410
                   4.0e-40
E value
Match length
                   82
% identity
                   18
                   ubiquitin precursor - common sunflower (fragment)
NCBI Description
Seq. No.
                   231739
Seq. ID
                   LIB3197-035-Q1-M1-H3
Method
                   BLASTX
                   g2500341
NCBI GI
                   166
BLAST score
                   2.0e-11
E value
Match length
                   38
                   76
% identity
                   50S RIBOSOMAL PROTEIN L36 >gi_1652406_dbj_BAA17328
NCBI Description
                   (D90905) 50S ribosomal protein L36 [Synechocystis sp.]
Seq. No.
                   231740
                   LIB3197-035-Q1-M1-H7
Seq. ID
                   BLASTX
Method
                   g267069
NCBI GI
                   416
BLAST score
                   4.0e-41
E value
                   76
Match length
                   100
% identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi_166914
                    (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                    (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                   231741
Seq. No.
                   LIB3197-035-Q1-M1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2529677
```

NCBI Description



```
% identity
                  (AC002535) kinesin-like protein, heavy chain [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  231742
                  LIB3197-037-Q1-M1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3122326
BLAST score
                  230
E value
                  1.0e-19
                  56
Match length
                  77
% identity
                  LEC14B PROTEIN >gi_1181604_dbj_BAA11768 (D83074) LEC14B
NCBI Description
                  protein [Lithospermum erythrorhizon]
                  231743
Seq. No.
                  LIB3197-037-Q1-M1-A3
Seq. ID
                  BLASTX
Method
                  g3420239
NCBI GI
                  309
BLAST score
                  1.0e-28
E value
Match length
                  61
                  95
% identity
                  (AF059484) actin [Gossypium hirsutum]
NCBI Description
Seq. No.
                  231744
Seq. ID
                  LIB3197-037-Q1-M1-A4
Method
                  BLASTX
                  g2088651
NCBI GI
BLAST score
                  164
                  1.0e-11
E value
Match length
                  80
                   40
% identity
NCBI Description
                  (AF002109) hypersensitivity-related gene 201 isolog
                   [Arabidopsis thaliana]
Seq. No.
                   231745
                  LIB3197-037-Q1-M1-A9
Seq. ID
Method
                  BLASTX
                  g4006848
NCBI GI
                  184
BLAST score
E value
                   1.0e-23
Match length
                   77
                   74
% identity
                  (AJ131433) selenocysteine methyltransferase [Astragalus
NCBI Description
                  bisulcatus]
Seq. No.
                   231746
Seq. ID
                   LIB3197-037-Q1-M1-B12
Method
                   BLASTX
NCBI GI
                   q2435522
BLAST score
                   267
E value
                   2.0e-23
Match length
                   105
                   59
% identity
```

33349

[Arabidopsis thaliana]

(AF024504) contains similarity to other AMP-binding enzymes



```
231747
Seq. No.
                  LIB3197-037-Q1-M1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3097321
BLAST score
                  164
                  2.0e-11
E value
Match length
                  83
                  41
% identity
                  (AB013289) Bd 30K [Glycine max]
NCBI Description
                  231748
Seq. No.
                  LIB3197-037-Q1-M1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4512651
                  198
BLAST score
E value
                   2.0e-15
Match length
                  95
                   39
% identity
                  (AC007048) putative tyrosine transaminase [Arabidopsis
NCBI Description
                  thaliana]
                   231749
Seq. No.
                  LIB3197-037-Q1-M1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4539010
BLAST score
                   228
E value
                   7.0e-19
                   134
Match length
                   18
% identity
                   (AL049481) putative DNA-directed RNA polymerase
NCBI Description
                   [Arabidopsis thaliana]
                   231750
Seq. No.
Seq. ID
                   LIB3197-037-Q1-M1-C4
Method
                   BLASTX
NCBI GI
                   q730583
BLAST score
                   247
E value
                   4.0e-21
Match length
                   113
% identity
                   50
                   60S ACIDIC RIBOSOMAL PROTEIN P2 >gi_551267_emb_CAA55047_
NCBI Description
                   (X78213) 60s acidic ribosomal protein P2 [Parthenium
                   argentatum]
                   231751
Seq. No.
Seq. ID
                   LIB3197-037-Q1-M1-C5
Method
                   BLASTX
NCBI GI
                   g3128176
BLAST score
                   123
E value
                   3.0e-10
Match length
                   103
                   39
% identity
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
```

231752

LIB3197-037-Q1-M1-C7

Seq. No. Seq. ID

BLAST score

251



```
BLASTX
Method
                  g3549669
NCBI GI
                  348
BLAST score
                  7.0e-33
E value
Match length
                  81
                  84
% identity
NCBI Description (AL031394) putative protein [Arabidopsis thaliana]
                  231753
Seq. No.
                  LIB3197-037-Q1-M1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4115377
                  383
BLAST score
                  6.0e-37
E value
                  111
Match length
                  71
% identity
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
                  231754
Seq. No.
                  LIB3197-037-Q1-M1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4249388
                  153
BLAST score
                  3.0e-10
E value
                  74
Match length
% identity
                  46
                  (AC005966) Similar to gb_AF025438 Opa-interacting protein
NCBI Description
                  (OIP2) from Homo sapiens. [Arabidopsis thaliana]
                  231755
Seq. No.
                  LIB3197-037-Q1-M1-D8
Seq. ID
Method
                  BLASTX
                  g1174718
NCBI GI
BLAST score
                  146
E value
                  2.0e-09
                  99
Match length
% identity
                  37
                  PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR
NCBI Description
                  >gi_322579_pir__JQ1674 receptor protein kinase TMK1 (EC
                  2.7.1.-) precursor - Arabidopsis thaliana >gi 166888
                  (L00670) protein kinase [Arabidopsis thaliana]
                  231756
Seq. No.
                  LIB3197-037-Q1-M1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1335862
BLAST score
                  175
E value
                  6.0e-13
Match length
                  73
                  49
% identity
NCBI Description (U42608) clathrin heavy chain [Glycine max]
Seq. No.
                  231757
                  LIB3197-037-Q1-M1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129471
```



```
2.0e-21
E value
                    72
Match Length
                    64
% identity
                    glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
NCBI Description
                    precursor - Scotch pine >gi_1100223 (L32560)
                    glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
                    231758
Seq. No.
                    LIB3197-037-Q1-M1-E8
Seq. ID
                    BLASTX
Method
                    g3128176
NCBI GI
BLAST score
                    146
                    2.0e-09
E value
                    113
Match length
                    31
% identity
                    (AC004521) unknown protein [Arabidopsis thaliana]
NCBI Description
                    231759
Seq. No.
                    LIB3197-037-Q1-M1-E9
Seq. ID
                    BLASTX
Method
NCBI GI
                    g120470
                    189
BLAST score
                    1.0e-14
E value
                    51
Match length
                    71
% identity
                    P55-C-FOS PROTO-ONCOGENE PROTEIN (G0S7 PROTEIN)
NCBI Déscription
                    >gi_68869_pir__TVHUF1 transforming protein fos - human
>gi_29904_emb_CAA24756_ (V01512) c-fos [Homo sapiens]
                    >gi_18273\overline{5} (\overline{K00650}) c-\overline{f}os protein [Homo sapiens]
                    >gi 4063509_gb_AAC98315.1_ (AF111167) cfos [Homo sapiens]
Seq. No.
                    231760
                    LIB3197-037-Q1-M1-F1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q4512711
BLAST score
                    383
E value
                     5.0e-37
                    138
Match length
% identity
                    (AC006569) unknown protein [Arabidopsis thaliana]
NCBI Description
                    231761
Seq. No.
                    LIB3197-037-Q1-M1-F3
Seq. ID
                    BLASTX
Method
                     g3046731
NCBI GI
                    227
BLAST score
E value
                     1.0e-34
Match length
                     86
% identity
                     93
                    (AJ005373) protein kinase [Craterostigma plantagineum]
NCBI Description
                     231762
Seq. No.
                    LIB3197-037-Q1-M1-F7
Seq. ID
Method
                     BLASTX
                     g2789660
NCBI GI
```

2.0e-35

BLAST score

E value

Match length

% identity

123

50



```
Match length
                   96
% identity
                   74
NCBI Description (AF040102) p105 [Arabidopsis thaliana]
                   231763
Seq. No.
                   LIB3197-037-Q1-M1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4567273
BLAST score
                   238
                   3.0e-23
E value
Match length
                   69
% identity
                    (AC006841) putative vacuolar proton ATPase subunit
NCBI Description
                    [Arabidopsis thaliana]
                   231764
Seq. No.
                   LIB3197-037-Q1-M1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2811278
BLAST score
                   409
                   4.0e-40
E value
                   115
Match length
% identity
                   69
NCBI Description
                   (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                   231765
                   LIB3197-037-01-M1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                    q462013
BLAST score
                    316
E value
                    3.0e-29
Match length
                   108
                    61
% identity
NCBI Description
                   ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
                   >gi_542022_pir__S39558 HSP90 homolog - Madagascar periwinkle >gi_348696 (L14594) heat shock protein 90
                    [Catharanthus roseus]
Seq. No.
                    231766
                   LIB3197-037-Q1-M1-H2
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3869088
BLAST score
                    625
E value
                    2.0e-65
                    120
Match length
% identity
                    100
NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
Seq. No.
                    231767
Seq. ID
                    LIB3197-038-Q1-M1-H11
Method
                    BLASTX
NCBI GI
                    g730241
                    316
BLAST score
                    4.0e-29
E value
```

33353

NCBI Description DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN



GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) >gi\_473947\_dbj\_BAA06126\_ (D29643) similar to Canis oligosaccharyltransferase 48 kDa subunit (M98392). [Homo sapiens]

```
231768
Seq. No.
                    LIB3197-038-Q1-M1-H12
Seq. ID
Method
                    BLASTX
NCBI GI
                    q2829902
BLAST score
                    505
E value
                    2.0e-51
Match length
                    110
                    88
% identity
                    (AC002311) Putative sulphate transporter protein#protein
NCBI Description
                    [Arabidopsis thaliana]
                    231769
Seq. No.
                    LIB3197-038-Q1-M1-H6
Seq. ID
Method
                    BLASTX
NCBI GI
                    q401322
BLAST score
                    230
                    4.0e-19
E value
                    58
Match length
% identity
                    79
                    VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
NCBI Description
                    SUBUNIT) >gi 167313 (L03186) vacuolar H+-ATPase catalytic
                    subunit [Gossypium hirsutum]
                    231770
Seq. No.
Seq. ID
                    LIB3197-039-Q1-M1-A1
Method
                    BLASTX
NCBI GI
                    q464734
                    608
BLAST score
                    2.0e-63
E value
Match length
                    126
% identity
                    94
NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
                    HYDROLASE) (ADOHCYASE) >gi_481237_pir__S38379 adenosylhomocysteinase (EC 3.3.1.1) - Madagascar periwinkle
                    >gi_407412_emb_CAA81527_ (Z26881) S-adenosyl-L-homocysteine hydrolase [Catharanthus roseus]
                    231771
Seq. No.
                    LIB3197-039-Q1-M1-A12
Seq. ID
Method
                    BLASTX
NCBI GI
                    g119350
BLAST score
                    611
E value
                    1.0e-63
Match length
                    136
% identity
                    88
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
```

[Arabidopsis thaliana]

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi\_81608\_pir\_\_JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi\_16271\_emb\_CAA41114\_ (X58107) enolase



```
231772
Seq. No.
                  LIB3197-039-Q1-M1-A8
Seq. ID
                  BLASTX
Method
                  g4217999
NCBI GI
                  391
BLAST score
                  4.0e-38
E value
                  95
Match length
                  80
% identity
                  (AC006135) putative ubiquitin--protein ligase
NCBI Description
                  (ubiquitin-conjugating enzyme) [Arabidopsis thaliana]
                  231773
Seq. No.
                  LIB3197-039-Q1-M1-B1
Seq. ID
                  BLASTX
Method
                  q3608137
NCBI GI
                  192
BLAST score
                  1.0e-14
E value
                  100
Match length
                  44
% identity
NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]
                  231774
Seq. No.
                  LIB3197-039-Q1-M1-B11
Seq. ID
                  BLASTX
Method
                  g1737492
NCBI GI
                  393
BLAST score
                  4.0e-38
E value
Match length
                  111
                  19
% identity
NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]
                  231775
Seq. No.
                  LIB3197-039-Q1-M1-B2
Seq. ID
                   BLASTX
Method
                   q114682
NCBI GI
BLAST score
                   345
E value
                   2.0e-32
                   113
Match length
                   65
% identity
NCBI Description ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
                   (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)
                   >gi_100471_pir__A35227 H+-transporting ATP synthase (EC
                   3.6.1.34) gamma chain precursor, mitochondrial - sweet
                   potato >gi_168270 (J05397) F-1-ATPase delta subunit
                   precursor (EC 3.6.1.3) [Ipomoea batatas]
Seq. No.
                   231776
                   LIB3197-039-Q1-M1-B3
Seq. ID
Method
                   BLASTX
                   g3319682
NCBI GI
BLAST score
                   545
E value
                   6.0e-56
                   114
Match length
                   85
 % identity
NCBI Description (Y17720) SPINDLY protein [Petunia x hybrida]
```

231777

Seq. No.



```
LIB3197-039-Q1-M1-B5
Seq. ID
Method
                  BLASTX
                  g3360289
NCBI GI
BLAST score
                  180
                  3.0e-13
E value
                  50
Match length
% identity
                  62
                  (AF023164) leucine-rich repeat transmembrane protein kinase
NCBI Description
                  1 [Zea mays]
                  231778
Seq. No.
                  LIB3197-039-Q1-M1-C1
Seq. ID
Method
                  BLASTX
                  g267069
NCBI GI
                   649
BLAST score
                   3.0e-68
E value
Match length
                   120
                   99
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                   231779
Seq. No.
                   LIB3197-039-Q1-M1-C12
Seq. ID
                   BLASTX
Method
                   q4490308
NCBI GI
BLAST score
                   232
                   3.0e-19
E value
                   56
Match length
                   86
% identity
                  (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                   231780
Seq. No.
                   LIB3197-039-Q1-M1-C3
Seq. ID
                   BLASTX
Method
                   g2827537
NCBI GI
                   437
BLAST score
                   2.0e-43
E value
Match length
                   120
                   69
% identity
                   (AL021633) putative zinc finger protein [Arabidopsis
NCBI Description
                   thaliana]
                   231781
Seq. No.
                   LIB3197-039-Q1-M1-C6
Seq. ID
                   BLASTX
Method
                   g2499710
NCBI GI
                   535
BLAST score
                   9.0e-55
E value
Match length
                   125
                   77
 % identity
                  PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
NCBI Description
                    (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                   >gi 1438075 (L33686) phospholipase D [Ricinus communis]
```

Seq. No.



```
LIB3197-039-Q1-M1-C7
Seq. ID
                  BLASTX
Method
                  g267069
NCBI GI
BLAST score
                  668
                  2.0e-70
E value
                  124
Match length
% identity
                  99
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  231783
Seq. No.
                  LIB3197-039-Q1-M1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2507281
BLAST score
                  666
                  3.0e-70
E value
                  119
Match length
                  100
% identity
                  GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_
NCBI Description
                  (X97380) atran2 [Arabidopsis thaliana]
                  231784
Seq. No.
                  LIB3197-039-Q1-M1-C9
Seq. ID
Method
                  BLASTX
                  g120669
NCBI GI
BLAST score
                  556
                  2.0e-57
E value
Match length
                  107
                  95
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                  >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
                  3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                  231785
                  LIB3197-039-Q1-M1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3776578
BLAST score
                  300
E value
                   3.0e-27
                  118
Match length
                   46
% identity
                  (AC005388) ESTs gb F13915 and gb_F13916 come from this
NCBI Description
                  gene. [Arabidopsis thaliana]
                  231786
Seq. No.
                  LIB3197-039-Q1-M1-D11
Seq. ID
                  BLASTX
Method
                   q2130442
NCBI GI
BLAST score
                   315
                   5.0e-29
E value
Match length
                  142
                   47
% identity
NCBI Description hypothetical protein SPAC8A4.01c - fission yeast
```

Match length

NCBI Description

% identity

110

thaliana]



(Schizosaccharomyces pombe) (fragment) >gi\_1052534\_emb\_CAA91511\_ (Z66569) unknown [Schizosaccharomyces pombe]

231787 Seq. No. LIB3197-039-Q1-M1-D12 Seq. ID Method BLASTX g2281649 NCBI GI 165 BLAST score 2.0e-11 E value 82 Match length % identity 51 (AF003105) AP2 domain containing protein RAP2.12 NCBI Description [Arabidopsis thaliana] Seq. No. 231788 LIB3197-039-Q1-M1-D4 Seq. ID Method BLASTX q2809232 NCBI GI 399 BLAST score 7.0e-39 E value 121 Match length % identity 67 (AC002560) F21B7.1 [Arabidopsis thaliana] NCBI Description 231789 Seq. No. LIB3197-039-Q1-M1-D5 Seq. ID Method BLASTX NCBI GI g2065019 333 BLAST score 4.0e-31 E value Match length 121 27 % identity (Y09823) hypothetical protein [Arabidopsis thaliana] NCBI Description 231790 Seq. No. LIB3197-039-Q1-M1-D6 Seq. ID BLASTX Method g231496 NCBI GI 633 BLAST score 3.0e-66 E value 143 Match length 87 % identity ACTIN 58 >gi\_100421\_pir\_\_\_\$20094 actin - potato NCBI Description >gi 21536 emb CAA39278 (X55749) actin [Solanum tuberosum] 231791 Seq. No. Seq. ID LIB3197-039-Q1-M1-D7 Method BLASTX NCBI GI g4220474 496 BLAST score 2.0e-50 E value

33358

(AC006069) putative myosin heavy chain [Arabidopsis



```
231792
Seq. No.
                  LIB3197-039-Q1-M1-D8
Seq. ID
Method
                  BLASTX
                  g2281092
NCBI GI
BLAST score
                  216
                  2.0e-17
E value
                  66
Match length
                  70
% identity
                  (AC002333) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  231793
Seq. No.
                  LIB3197-039-Q1-M1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173218
BLAST score
                  622
                  6.0e-65
E value
                  124
Match length
                  97
% identity
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                  231794
Seq. No.
                  LIB3197-039-Q1-M1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2494626
BLAST score
                  169
E value
                  7.0e-12
                  121
Match length
                  35
% identity
                  HYPOTHETICAL 47.6 KD PROTEIN F49C12.8 IN CHROMOSOME IV
NCBI Description
                  >gi_3877366_emb_CAA92512_ (Z68227) cDNA EST EMBL:Z14827
                  comes from this gene; cDNA EST EMBL:C13370 comes from this
                   gene; cDNA EST EMBL:C11280 comes from this gene; cDNA EST
                   yk336d8.3 comes from this gene; cDNA EST yk336d8.5 comes
                   from this gene; cDNA ES
                   231795
Seq. No.
                  LIB3197-039-Q1-M1-E5
Seq. ID
                  BLASTX
Method
NCBI GI
                   q2642443
BLAST score
                   307
                   5.0e-28
E value
Match length
                   150
% identity
                   36
NCBI Description
                  (AC002391) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                   231796
                   LIB3197-039-Q1-M1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2982463
```

Method BLASTX
NCBI GI g2982463
BLAST score 316
E value 6.0e-32
Match length 109
% identity 72

NCBI Description (AL022223) putative protein [Arabidopsis thaliana]

Seq. No.

231802



```
231797
Seq. No.
                  LIB3197-039-Q1-M1-F10
Seq. ID
                  BLASTX
Method
                  g232024
NCBI GI
BLAST score
                  350
                  4.0e-33
E value
                  120
Match length
                  61
% identity
                  PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland
NCBI Description
                  cotton >gi_2129498_pir__S65061 fiber protein E6 (clone
                  CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site
                  is putative; putative [Gossypium hirsutum] >gi_1000084
                   (U30505) E6 [Gossypium hirsutum]
                  231798
Seq. No.
Seq. ID
                  LIB3197-039-Q1-M1-F11
Method
                  BLASTX
                  g4406780
NCBI GI
                  361
BLAST score
                   2.0e-41
E value
                  118
Match length
                   73
% identity
                  (AC006532) putative multispanning membrane protein
NCBI Description
                   [Arabidopsis thaliana]
                   231799
Seq. No.
Seq. ID
                  LIB3197-039-Q1-M1-F12
Method
                   BLASTX
                   g4490332
NCBI GI
                   268
BLAST score
                   2.0e-23
E value
Match length
                   99
                   56
% identity
NCBI Description (AL035656) putative protein [Arabidopsis thaliana]
                   231800
Seq. No.
Seq. ID
                   LIB3197-039-Q1-M1-F4
Method
                   BLASTX
                   q3738257
NCBI GI
                   464
BLAST score
                   1.0e-46
E value
Match length
                   97
                   94
% identity
                  (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
NCBI Description
                   nigra]
Seq. No.
                   231801
                   LIB3197-039-Q1-M1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g495866
BLAST score
                   588
E value
                   4.0e-61
Match length
                   107
% identity
                  (L23982) collagen type VII [Homo sapiens]
NCBI Description
```

% identity

NCBI Description

89

[Arabidopsis thaliana]



```
LIB3197-039-Q1-M1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2633727
BLAST score
                   170
E value
                   5.0e-12
Match length
                   93
% identity
                   44
NCBI Description (Z99111) ykrT [Bacillus subtilis]
Seq. No.
                   231803
Seq. ID
                   LIB3197-039-Q1-M1-G11
Method
                   BLASTX
NCBI GI
                   q3914996
BLAST score
                   258
E value
                   2.0e-22
Match length
                   95
% identity
                   60
NCBI Description
                  PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT)
                   >gi_1665831_dbj_BAA13640 (D88541) phosphoserine
                   aminotransferase [Arabidopsis thaliana]
                   >gi_2804260_dbj_BAA24441_ (AB010408) phosphoserine
                   aminotransferase [Arabidopsis thaliana]
                   >gi_3367581_emb_CAA20033_ (AL031135) phosphoserine
                   aminotransferase [Arabidopsis thaliana]
Seq. No.
                  231804
Seq. ID
                  LIB3197-039-Q1-M1-G5
Method
                  BLASTX
NCBI GI
                  q3249084
BLAST score
                   466
E value
                   1.0e-46
Match length
                  127
% identity
NCBI Description
                  (AC004473) Similar to red-1 (related to thioredoxin) gene
                  gb_X92750 from Mus musculus. ESTs gb AA712687 and
                  gb Z37223 come from this gene [Arabidopsis thaliana]
Seq. No.
                  231805
Seq. ID
                  LIB3197-039-Q1-M1-G6
Method
                  BLASTX
NCBI GI
                  q4454014
BLAST score
                  278
E value
                  1.0e-24
Match length
                  141
% identity
                  45
NCBI Description (AL035396) putative protein [Arabidopsis thaliana]
Seq. No.
                  231806
Seq. ID
                  LIB3197-039-Q1-M1-H10
Method
                  BLASTX
NCBI GI
                  q2829902
BLAST score
                  538
E value
                  3.0e-55
Match length
                  116
```

33361

(AC002311) Putative sulphate transporter protein#protein

```
Seq. No.
                   231807
Seq. ID
                   LIB3197-039-01-M1-H12
Method
                   BLASTX
NCBI GI
                   g1706377
BLAST score
                   495
E value
                   3.0e-50
Match length
                   117
% identity
                   78
NCBI Description
                  DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL
                   4-REDUCTASE) >gi_499018_emb_CAA53578 (X75964)
                   dihydroflavonol reductase [Vitis vinifera]
Seq. No.
                   231808
Seq. ID
                   LIB3197-039-Q1-M1-H5
Method
                   BLASTX
NCBI GI
                   g4098129
BLAST score
                   582
E value
                   2.0e-60
Match length
                  129
% identity
                   88
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
Seq. No.
                   231809
Seq. ID
                  LIB3197-039-Q1-M1-H9
Method
                  BLASTX
NCBI GI
                  g2340050
BLAST score
                  226
E value
                  9.0e-19
Match length
                  66
% identity
                  71
NCBI Description (L48989) troponin T [Mus musculus]
Seq. No.
                  231810
Seq. ID
                  LIB3197-040-Q1-M1-A10
Method
                  BLASTX
NCBI GI
                  g1911166
BLAST score
                  607
E value
                  3.0e-63
Match length
                  142
% identity
                  74
NCBI Description (X94400) soluble-starch-synthase [Solanum tuberosum]
Seq. No.
                  231811
                  LIB3197-040-Q1-M1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
```

Method BLASTX
NCBI GI g3292830
BLAST score 278
E value 1.0e-24
Match length 139
% identity 50

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 231812

Seq. ID LIB3197-040-Q1-M1-A12

Method BLASTX NCBI GI g2129499

E value

1.0e-39



```
BLAST score
E value
                   4.0e-13
Match length
                   72
% identity
                   57
NCBI Description fiber protein E6 (clone CKE6-4A) - upland cotton
                   >gi_1000086 (U30506) E6 [Gossypium hirsutum]
Seq. No.
                   231813
Seq. ID
                   LIB3197-040-Q1-M1-A2
Method
                   BLASTX
NCBI GI
                   g1800147
BLAST score
                   362
E value
                   1.0e-34
Match length
                   106
% identity
                   69
NCBI Description (U83655) membrane associated protein [Arabidopsis thaliana]
Seq. No.
                   231814
Seq. ID
                   LIB3197-040-Q1-M1-A3
Method
                   BLASTX
NCBI GI
                   g1724102
BLAST score
                   471
E value
                   2.0e-47
Match length
                   94
% identity
                   96
NCBI Description
                  (U79766) S-adenosyl-L-homocystein hydrolase; SAH
                   [Mesembryanthemum crystallinum]
Seq. No.
                   231815
Seq. ID
                   LIB3197-040-Q1-M1-A6
Method
                   BLASTX
NCBI GI
                   g3786001
BLAST score
                   302
E value
                   2.0e-27
Match length
                   74
% identity
                   74
NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.
                   231816
Seq. ID
                  LIB3197-040-Q1-M1-A8
Method
                  BLASTX
NCBI GI
                   g267069
BLAST score
                   441
E value
                   5.0e-44
Match length
                   81
% identity
                   100
NCBI Description
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
                   tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                  231817
Seq. ID
                  LIB3197-040-Q1-M1-B10
Method
                  BLASTX
                  g4204695
NCBI GI
BLAST score
                  405
```



Match length 143 % identity NCBI Description (AF117062) putative inositol polyphosphate 5-phosphatase At5P1 [Arabidopsis thaliana] Seq. No. 231818 LIB3197-040-Q1-M1-B3 Seq. ID Method BLASTX NCBI GI q2811278 BLAST score 491 E value 1.0e-49 Match length 124 75 % identity NCBI Description (AF043284) expansin [Gossypium hirsutum] Seq. No. 231819 LIB3197-040-Q1-M1-B4 Seq. ID Method BLASTX NCBI GI g4567260 BLAST score 520 E value 4.0e-53 Match length 131 % identity 73 NCBI Description (AC006841) putative NADPH dependent mannose 6-phosphate reductase [Arabidopsis thaliana] 231820 Seq. No. Seq. ID LIB3197-040-Q1-M1-B5 Method BLASTX NCBI GI q4204695 BLAST score 423 E value 1.0e-41 Match length 152 % identity 59 NCBI Description (AF117062) putative inositol polyphosphate 5-phosphatase At5P1 [Arabidopsis thaliana] Seq. No. 231821 Seq. ID LIB3197-040-Q1-M1-B6 Method BLASTX NCBI GI g2642448

BLAST score 602 E value 1.0e-62 Match length 142 36 % identity

NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana]

>gi\_3169187 (AC004401) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 231822

Seq. ID LIB3197-040-Q1-M1-B7

Method BLASTX NCBI GI g2147165 BLAST score 487 E value 3.0e-49Match length 96 % identity 55



NCBI Description calmodulin - Bidens pilosa >gi 939860 emb CAA61980 (X89890) Calmodulin [Bidens pilosa] Seq. No. 231823 Seq. ID LIB3197-040-Q1-M1-B8 Method BLASTX NCBI GI g2687726 BLAST score 142

39 % identity (AJ003246) 2'-hydroxydihydrodaidzein reductase [Glycine NCBI Description

Seq. No. 231824

E value

Match length

Seq. ID LIB3197-040-Q1-M1-B9

85

7.0e-09

Method BLASTX NCBI GI g3212869 BLAST score 481 E value 1.0e-48 Match length 106 % identity 84

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 231825

Seq. ID LIB3197-040-Q1-M1-C10

Method BLASTX NCBI GI g3360289 BLAST score 285 E value 2.0e-25 Match length 103 % identity 27

NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase

1 [Zea mays]

Seq. No. 231826

Seq. ID LIB3197-040-Q1-M1-C12

Method BLASTX NCBI GI g120669 BLAST score 457 E value 1.0e-4591 Match length % identity 92

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_66014\_pir DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 231827

Seq. ID LIB3197-040-Q1-M1-C2

Method BLASTX NCBI GI q4417283 BLAST score 196 E value 3.0e-15 Match length 104 % identity 40



NCBI Description (AC007019) putative cytochrome p450 [Arabidopsis thaliana] Seq. No. 231828

Seq. ID LIB3197-040-Q1-M1-C6

Method BLASTX
NCBI GI g1839188
BLAST score 264
E value 5.0e-23
Match length 65
% identity 77

NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No. 231829

Seq. ID LIB3197-040-Q1-M1-C8

Method BLASTX
NCBI GI 94103324
BLAST score 601
E value 1.0e-62
Match length 129
% identity 91

NCBI Description (AF022716) GDP-mannose pyrophosphorylase [Solanum

tuberosum]

Seq. No. 231830

Seq. ID LIB3197-040-Q1-M1-C9

Method BLASTX
NCBI GI g2706450
BLAST score 287
E value 1.0e-25
Match length 85
% identity 71

NCBI Description (AJ225172) magnesium dependent soluble inorganic

pyrophosphatase [Solanum tuberosum]

Seq. No. 231831

Seq. ID LIB3197-040-Q1-M1-D11

Method BLASTX
NCBI GI g1945611
BLAST score 352
E value 2.0e-33
Match length 134
% identity 52

NCBI Description (AB003103) 26S proteasome subunit p55 [Homo sapiens]

>gi\_4506221\_ref\_NP\_002807.1\_pPSMD12\_ proteasome (prosome,

macropain) 26S subunit, non-ATPase,

Seq. No. 231832

Seq. ID LIB3197-040-Q1-M1-D12

Method BLASTX
NCBI GI g4469023
BLAST score 558
E value 2.0e-57
Match length 124
% identity 85

NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 231833

E value

Match length

9.0e-40

119



```
Seq. ID
                   LIB3197-040-Q1-M1-D2
Method
                   BLASTX
NCBI GI
                   g3068705
BLAST score
                   183
E value
                   2.0e-13
Match length
                   116
% identity
                   39
NCBI Description (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                   231834
Seq. ID
                   LIB3197-040-Q1-M1-D3
Method
                   BLASTX
NCBI GI
                   g2190992
BLAST score
                   340
E value
                   4.0e-32
Match length
                   103
% identity
                   64
NCBI Description
                  (AF004358) glutathione S-transferase TSI-1 [Aegilops
                   tauschii]
Seq. No.
                   231835
Seq. ID
                   LIB3197-040-Q1-M1-D5
Method
                   BLASTX
NCBI GI
                   g2791834
BLAST score
                   643
E value
                   2.0e-67
Match length
                   125
% identity
                   98
NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta]
Seq. No.
                   231836
Seq. ID
                   LIB3197-040-Q1-M1-D7
Method
                   BLASTX
NCBI GI
                   g4056503
BLAST score
                   151
E value
                   5.0e-10
                  36
Match length
% identity
                   81
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]
Seq. No.
                  231837
Seq. ID
                  LIB3197-040-Q1-M1-D9
Method
                  BLASTX
NCBI GI
                  g4538897
BLAST score
                  375
E value
                  4.0e-36
                  101
Match length
% identity
                  68
NCBI Description (AL049482) AX110P-like protein [Arabidopsis thaliana]
Seq. No.
                  231838
Seq. ID
                  LIB3197-040-Q1-M1-E1
Method
                  BLASTX
NCBI GI
                  g2677828
BLAST score
                  407
```



```
% identity
NCBI Description (U93166) cysteine protease [Prunus armeniaca]
Seq. No.
                  231839
Seq. ID
                  LIB3197-040-Q1-M1-E11
Method
                  BLASTX
                  g2662343
NCBI GI
BLAST score
                  667
E value
                  3.0e-70
Match length
                  128
% identity
                  100
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  231840
Seq. No.
Seq. ID
                  LIB3197-040-Q1-M1-E12
Method
                  BLASTX
NCBI GI
                  q4314370
BLAST score
                  344
E value
                  2.0e-39
Match length
                  122
% identity
                  62
NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  231841
Seq. ID
                  LIB3197-040-Q1-M1-E2
Method
                  BLASTX
NCBI GI
                  g2564112
BLAST score
                  278
E value
                  1.0e-24
Match length
                  140
% identity
                  39
NCBI Description (AF000371) UDP glucose:flavonoid 3-o-glucosyltransferase
                  [Vitis vinifera]
Seq. No.
                  231842
Seq. ID
                  LIB3197-040-Q1-M1-E3
Method
                  BLASTX
NCBI GI
                  g2832623
BLAST score
                  309
E value
                  3.0e-28
Match length
                  76
% identity
                  74
NCBI Description (AL021711) protein kinase - like protein [Arabidopsis
                  thaliana]
Seq. No.
                  231843
Seq. ID
                  LIB3197-040-Q1-M1-E4
Method
                  BLASTX
NCBI GI
                  g3080427
BLAST score
                  672
E value
                  7.0e-71
```

Seq. No. 231844

Match length

NCBI Description

% identity

Seq. ID LIB3197-040-Q1-M1-E5

139

90

(AL022604) putative protein [Arabidopsis thaliana]



```
Method
                  BLASTX
NCBI GI
                  g1220196
BLAST score
                  682
E value
                  5.0e-72
Match length
                  146
% identity
                  87
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.
                  231845
Seq. ID
                  LIB3197-040-Q1-M1-E6
Method
                  BLASTX
NCBI GI
                  g2501578
BLAST score
                  465
E value
                  1.0e-46
Match length
                  104
                  93
% identity
NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913 pir S60047
                  ethylene-responsive protein 1 - Para rubber tree
                  >gi 1209317 (M88254) ethylene-inducible protein [Hevea
                  brasiliensis]
                  231846
Seq. No.
Seq. ID
                  LIB3197-040-Q1-M1-E7
Method
                  BLASTX
NCBI GI
                  g2832625
BLAST score
                  560
E value
                  9.0e-58
Match length
                  142
% identity
                  74
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                  231847
Seq. ID
                  LIB3197-040-Q1-M1-E8
Method
                  BLASTX
NCBI GI
                  q2832623
BLAST score
                  156
E value
                  2.0e-10
Match length
                  56
% identity
NCBI Description (AL021711) protein kinase - like protein [Arabidopsis
                  thaliana]
Seq. No.
                  231848
Seq. ID
                  LIB3197-040-Q1-M1-E9
Method
                  BLASTX
NCBI GI
                  q2501578
BLAST score
                  487
                 4.0e-49
E value
Match length
                  109
% identity
NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi 2129913 pir S60047
                  ethylene-responsive protein 1 - Para rubber tree
                  >gi_1209317 (M88254) ethylene-inducible protein [Hevea
                  brasiliensis]
```

Seq. No. 231849

Seq. ID LIB3197-040-Q1-M1-F1



Method BLASTX NCBI GI g1304227 BLAST score 30-7 E value 5.0e-28 Match length 69 % identity 75 (D63781) Epoxide hydrolase [Glycine max] NCBI Description >gi\_2764804\_emb\_CAA55293\_ (X78547) epoxide hydrolase [Glycine max] Seq. No. 231850 Seq. ID LIB3197-040-Q1-M1-F5 Method BLASTX NCBI GI g417060 BLAST score 551 E value 1.0e-56 Match length 108 % identity 94 NCBI Description GLUTAMINE SYNTHETASE NODULE ISOZYME (GLUTAMATE--AMMONIA LIGASE) (GS) >gi 170637 (M94765) glutamine synthetase [Vigna aconitifolia] >gi\_1094850\_prf\_\_2106409A Gln synthetase [Vigna aconitifolia] Seq. No. 231851 Seq. ID LIB3197-040-Q1-M1-F6 Method BLASTX NCBI GI g464734 BLAST score 366 E value 3.0e - 35Match length 79 % identity 92 NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi\_481237\_pir\_\_S38379 adenosylhomocysteinase (EC 3.3.1.1) - Madagascar periwinkle >gi\_407412\_emb\_CAA81527 (Z26881) S-adenosyl-L-homocysteine hydrolase [Catharanthus roseus] Seq. No. 231852 Seq. ID LIB3197-040-Q1-M1-F7 Method BLASTX NCBI GI g1707857 BLAST score 574 E value 2.0e-59 Match length 134 % identity NCBI Description (Y09291) obtusifoliol 14-alpha-demethylase [Triticum aestivum]

Seq. No. 231853

Seq. ID LIB3197-040-Q1-M1-F9

Method BLASTX NCBI GI g2827529 BLAST score 255 E value 6.0e-22 Match length 125 % identity

NCBI Description (AL021633) putative protein [Arabidopsis thaliana]

% identity

NCBI Description

91

[Arabidopsis thaliana]



```
Seq. No.
                   231854
Seq. ID
                  LIB3197-040-Q1-M1-G10
Method
                  BLASTX
NCBI GI
                  q3334138
BLAST score
                  151
E value
                  1.0e-14
Match length
                  82
% identity
NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin
                  [Glycine max]
Seq. No.
                   231855
                  LIB3197-040-Q1-M1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q464849
BLAST score
                  590
                  2.0e-61
E value
Match length
                  118
% identity
                   99
NCBI Description TUBULIN ALPHA CHAIN >gi_486847 pir S36232 tubulin alpha
                  chain - almond >gi_20413_emb_CAA47635_ (X67162)
                  alpha-tubulin [Prunus dulcis]
Seq. No.
                  231856
Seq. ID
                  LIB3197-040-Q1-M1-G12
Method
                  BLASTX
NCBI GI
                  g4539543
BLAST score
                  638
E value
                  6.0e-67
Match length
                  130
% identity
                  97
NCBI Description (AJ133422) glyceraldehyde-3-phosphate dehydrogenase
                  [Nicotiana tabacum]
Seq. No.
                  231857
Seq. ID
                  LIB3197-040-Q1-M1-G3
Method
                  BLASTX
NCBI GI
                  g4063751
BLAST score
                  284
E value
                  2.0e-25
Match length
                  152
% identity
                  39
NCBI Description (AC005851) putative white protein [Arabidopsis thaliana]
                  >gi 4510409 gb AAD21495.1_ (AC006929) putative white
                  protein [Arabidopsis thaliana]
Seq. No.
                  231858
Seq. ID
                  LIB3197-040-Q1-M1-G5
Method
                  BLASTX
NCBI GI
                  g3927825
BLAST score
                  346
E value
                  1.0e-32
Match length
                  70
```

33371

(AC005727) putative dTDP-glucose 4-6-dehydratase

NCBI Description

Seq. No.

thaliana]

231864



```
Seq. No.
                  231859
Seq. ID
                  LIB3197-040-Q1-M1-G8
Method
                  BLASTX
NCBI GI
                  g1345882
BLAST score
                  561
E value
                  8.0e-58
Match length
                  134
                  77
% identity
NCBI Description CYTOCHROME B5
Seq. No.
                  231860
Seq. ID
                  LIB3197-040-Q1-M1-H1
Method
                  BLASTX
NCBI GI
                  g322750
BLAST score
                  502
E value
                  1.0e-62
Match length
                  128
% identity
                  89
NCBI Description
                  ubiquitin / ribosomal protein CEP52 - wood tobacco
                  >gi_170217 (M74100) ubiquitin fusion protein [Nicotiana
                  sylvestris]
Seq. No.
                  231861
Seq. ID
                  LIB3197-040-Q1-M1-H10
Method
                  BLASTX
NCBI GI
                  q2462746
BLAST score
                  539
E value
                  2.0e-55
Match length
                  119
% identity
                  84
NCBI Description (AC002292) Similar to ATP-citrate-lyase [Arabidopsis
                  thaliana]
Seq. No.
                  231862
Seq. ID
                  LIB3197-040-Q1-M1-H11
Method
                  BLASTX
NCBI GI
                  g2583125
BLAST score
                  627
E value
                  1.0e-65
Match length
                  134
                  90
% identity
NCBI Description (AC002387) putative transketolase precursor [Arabidopsis
                  thaliana]
Seq. No.
                  231863
                  LIB3197-040-Q1-M1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2262170
BLAST score
                  183
E value
                  1.0e-13
Match length
                  62
% identity
```

33372

(ACO02329) predicted glycosyl hydrolase [Arabidopsis

NCBI GI

E value

BLAST score

g541847

1.0e-36

379



```
Seq. ID
                   LIB3197-040-Q1-M1-H2
 Method
                    BLASTX
 NCBI GI
                    q2811278
 BLAST score
                    654
 E value
                    9.0e-69
 Match length
                   132
 % identity
 NCBI Description (AF043284) expansin [Gossypium hirsutum]
 Seq. No.
                   231865
 Seq. ID
                   LIB3197-040-Q1-M1-H3
 Method
                   BLASTX
 NCBI GI
                   q1703375
 BLAST score
                   578
 E value
                   7.0e-60
 Match length
                   117
 % identity
                   96
 NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 965483 dbj BAA08259 (D45420)
                   DcARF1 [Daucus carota]
 Seq. No.
                   231866
Seq. ID
                   LIB3197-040-Q1-M1-H6
 Method
                   BLASTX
 NCBI GI
                   g3451075
 BLAST score
                   221
 E value
                   3.0e-18
 Match length
                   62
 % identity
                   65
 NCBI Description (AL031326) putative protein [Arabidopsis thaliana]
 Seq. No.
                   231867
 Seq. ID
                   LIB3197-040-Q1-M1-H7
Method
                   BLASTX
NCBI GI
                   g2347198
 BLAST score
                   368
 E value
                   3.0e-35
                   86
Match length
 % identity
                   80
NCBI Description (AC002338) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                   231868
 Seq. ID
                   LIB3197-040-Q1-M1-H9
Method
                   BLASTX
NCBI GI
                   g1486472
BLAST score
                   344
E value
                   1.0e-32
                   78
Match length
 % identity
                   85
NCBI Description (X99853) oxoglutarate malate translocator [Solanum
                   tuberosum]
Seq. No.
                   231869
Seq. ID
                   LIB3197-041-Q1-M1-A1
Method
                   BLASTX
```



```
Match length
                   111
% identity
                   65
NCBI Description alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana
Seq. No.
                   231870 ~
Seq. ID
                   LIB3197-041-Q1-M1-A10
Method
                   BLASTX
NCBI GI
                   q4455209
BLAST score
                   581
E value
                   3.0e-60
Match length
                   145
                   77
% identity
NCBI Description
                   (AL035440) putative Proline synthetase associated protein
                   [Arabidopsis thaliana]
Seq. No.
                   231871
Seq. ID
                   LIB3197-041-Q1-M1-A12
Method
                   BLASTX
NCBI GI
                   g132944
BLAST score
                   542
E value
                   1.0e-55
Match length
                   137
                   74
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ07,72 ribosomal
                   protein L3 (ARP2) - Arabidopsis thaliana >qi 806279
                   (M32655) ribosomal protein [Arabidopsis thaliana]
Seq. No. ..
                   231872
Seq. ID
                   LIB3197-041-Q1-M1-A3
Method
                   BLASTX
NCBI GI
                   g231587
BLAST score
                   145
E value
                   4.0e-12
Match length
                   70
% identity
                   61
NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
                   >gi_283001_pir__S25304 H+-transporting ATP synthase (EC
3.6.1.34) beta chain precursor, mitochondrial - rice
                   >gi 218147 dbj BAA01372 (D10491) mitochondrial F1-ATPase
                   [Oryza sativa]
Seq. No.
                   231873
Seq. ID
                   LIB3197-041-Q1-M1-A4
Method
                   BLASTX
NCBI GI
                   g1703108
BLAST score
                   339
E value
                   5.0e-49
Match length
                   95
% identity
```

ACTIN 2/7 >gi\_2129525\_pir\_\_S71210 actin 2 - Arabidopsis thaliana >gi\_2129528\_pir\_\_S68107 actin 7 - Arabidopsis NCBI Description

thaliana >gi\_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi\_1943863 (U27811) actin7 [Arabidopsis

thaliana]

Seq. No. 231874

Seq. ID LIB3197-041-Q1-M1-A5

Method

NCBI GI

BLASTX

q2738.949



```
Method
                  BLASTX
NCBI GI
                  g4263507
BLAST score
                  211
E value
                  1.0e-19
                  97
Match length
% identity
                  49
NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  231875
Seq. ID
                  LIB3197-041-Q1-M1-A7
Method
                  BLASTX
NCBI GI
                  g2501490
BLAST score
                  331
E value
                  7.0e-31
Match length
                  124
% identity
                  51
NCBI Description FLAVONOL 3-0-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVONOID
                  3-O-GLUCOSYLTRANSFERASE) >gi_1620013_dbj_BAA12737 (D85186)
                  UDP-glucose:flavonoid-3-glucosyltransferase [Gentiana
                  triflora]
Seq. No.
                  231876
Seq. ID
                  LIB3197-041-Q1-M1-A8
Method
                  BLASTX
NCBI GI
                  g2827559
BLAST score
                  205
E value
                  3.0e-16
                  70
Match length
% identity
                  59
NCBI Description
                  (AL021635) predicted protein [Arabidopsis thaliana]
                  >gi_3292808_emb_CAA19798 (AL031018) putative protein
                  [Arabidopsis thaliana]
Seq. No.
                  231877
Seq. ID
                  LIB3197-041-Q1-M1-B12
Method
                  BLASTX
NCBI GI
                  g3201627
BLAST score
                  152
E value
                  7.0e-10
Match length
                  44
% identity
                  61
NCBI Description (AC004669) putative SWH1 protein [Arabidopsis thaliana]
Seq. No.
                  231878
Seq. ID
                  LIB3197-041-Q1-M1-B3
Method
                  BLASTX
NCBI GI
                  q2811278
BLAST score
                  561
E value
                  8.0e-58
Match length
                  134
% identity
                  77
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                  231879
Seq. ID
                  LIB3197-041-Q1-M1-B5
```



```
BLAST score
E value
                   2.0e-53
Match length
                   109
% identity
                   90
NCBI Description
                   (AF022213) cytosolic ascorbate peroxidase [Fragaria x
                  ananassa]
                   231880
Seq. No.
Seq. ID
                  LIB3197-041-Q1-M1-B7
Method
                  BLASTX
NCBI GI
                   q3309243
BLAST score
                   704
E value
                   1.0e-74
Match length
                   147
% identity
                   90
NCBI Description
                   (AF073507) aconitase-iron regulated protein 1 [Citrus
                  limon]
                  231881
Seq. No.
Seq. ID
                  LIB3197-041-Q1-M1-B8
Method
                  BLASTX
NCBI GI
                  q3834321
BLAST score
                   632
E value
                   3.0e-66
Match length
                   135
% identity
                   92
                  (AC005679) Strong similarity to F13P17.9 gi 3337356
NCBI Description
                   transport protein SEC61 alpha subunit homolog from
                  Arabidopsis thaliana BAC gb AC004481. [Arabidopsis
                  thaliana]
Seq. No.
                   231882
                  LIB3197-041-Q1-M1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4325282
BLAST score
                   604
E value
                   7.0e-63
Match length
                  135
                   81
% identity
                   (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
NCBI Description
                   >gi 4325286 gb AAD17314 (AF123311) NAC domain protein NAM
                   [Arabidopsis thaliana]
                   231883
Seq. No.
Seq. ID
                  LIB3197-041-Q1-M1-C1
Method
                  BLASTX
NCBI GI
                   g4544399
BLAST score
                   380
```

E value 1.0e-36 Match length 146 50 % identity

NCBI Description (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana]

Seq. No. 231884

Seq. ID LIB3197-041-Q1-M1-C10

Method BLASTX

Match length

% identity

80

88



```
NCBI GI
                   g2058456
BLAST score
                   577
E value
                   1.0e-59
Match length
                   115
                   97
% identity
NCBI Description
                   (U66408) GTP-binding protein [Arabidopsis thaliana]
                   >gi_2345150_gb_AAB67830_ (AF014822) developmentally
                   regulated GTP binding protein [Arabidopsis thaliana]
Seq. No.
                   231885
Seq. ID
                   LIB3197-041-Q1-M1-C11
Method
                  BLASTX
NCBI GI
                   q4107343
BLAST score
                   173
E value
                   2.0e-12
Match length
                  97
% identity
                   38
NCBI Description (AJ224922) ATP citrate lyase [Sordaria macrospora]
Seq. No.
                  231886
Seq. ID
                  LIB3197-041-Q1-M1-C12
Method
                  BLASTX
NCBI GI
                  g2078350
BLAST score
                  275
E value
                  3.0e-24
Match length
                  120
% identity
                   51
NCBI Description (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                  231887
Seq. ID
                  LIB3197-041-Q1-M1-C2
Method
                  BLASTX
NCBI GI
                  g2160166
BLAST score
                  352
E value
                  2.0e-33
Match length
                  142
                  57
% identity
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.
                  231888
Seq. ID
                  LIB3197-041-Q1-M1-C5
Method
                  BLASTX
NCBI GI
                  g4455293
BLAST score
                  378
E value
                  2.0e-36
Match length
                  87
% identity
NCBI Description (AL035528) putative protein [Arabidopsis thaliana]
Seq. No.
                  231889
Seq. ID
                  LIB3197-041-Q1-M1-C6
Method
                  BLASTX
NCBI GI
                  g3080400
BLAST score
                  373
E value
                  8.0e-36
```

E value

Match length

1.0e-37

119





```
NCBI Description
                   (AL022603) putative protein [Arabidopsis thaliana]
                   >gi_4455264_emb_CAB36800.1 (AL035527) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                   231890
Seq. ID
                   LIB3197-041-Q1-M1-C7
Method
                   BLASTX
NCBI GI
                   q3334115
BLAST score
                   301
E value
                   2.0e-27
Match length
                   80
                   75
% identity
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                  hirsutum]
Seq. No.
                   231891
Seq. ID
                  LIB3197-041-Q1-M1-C9
Method
                  BLASTX
NCBI GI
                  g1724102
BLAST score
                   443
E value
                   4.0e-44
Match length
                  89
% identity
                   96
NCBI Description
                  (U79766) S-adenosyl-L-homocystein hydrolase; SAH
                   [Mesembryanthemum crystallinum]
Seq. No.
                  231892
Seq. ID
                  LIB3197-041-Q1-M1-D1
Method
                  BLASTX
NCBI GI
                  g3182981
BLAST score
                  525
E value
                  1.0e-53
Match length
                  127
% identity
                  78
NCBI Description CELL ELONGATION PROTEIN DIMINUTO >gi_1695692_dbj_BAA13096_
                   (D86494) diminuto [Pisum sativum]
Seq. No.
                  231893
Seq. ID
                  LIB3197-041-01-M1-D10
Method
                  BLASTX
NCBI GI
                  g1724102
BLAST score
                  519
E value
                  6.0e-53
Match length
                  117
% identity
                  85
NCBI Description
                  (U79766) S-adenosyl-L-homocystein hydrolase; SAH
                   [Mesembryanthemum crystallinum]
Seq. No.
                  231894
Seq. ID
                  LIB3197-041-Q1-M1-D12
Method
                  BLASTX
NCBI GI
                  g729475
BLAST score
                  389
```



```
% identity
NCBI Description FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1)
                    >gi_1362788_pir__A56531 DNA structure-specific endonuclease
FEN1 - human >gi_704377_bbs_157592 DNase IV=nuclear 42 kda
5' -> 3' exonuclease [human, HeLa cells, Peptide, 380 aa]
                    >gi_642090 (L37374) endonuclease [Homo sapiens] >gi 3169155
                    (ACO04770) FEN1 HUMAN; MATURATION FACTOR 1 (MF1); DNase IV;
                    RAD2_HUMAN [Homo sapiens] >gi_3980293_emb_CAA54166_
                    (X76771) flap endonuclease-1 [Homo sapiens]
Seq. No.
                    231895
Seq. ID
                    LIB3197-041-Q1-M1-D5
Method
                    BLASTX
NCBI GI
                    q3790102
BLAST score
                    732
E value
                    7.0e-78
Match length
                    146
% identity
                    88
NCBI Description (AF095521) pyrophosphate-dependent phosphofructokinase
                    alpha subunit [Citrus X paradisi]
Seq. No.
                    231896
Seq. ID
                    LIB3197-041-Q1-M1-D8
Method
                    BLASTX
NCBI GI
                    g3122386
BLAST score
                    506
E value
                    2.0e-51
Match length
                    113
% identity
                    82
NCBI Description WD-40 REPEAT PROTEIN MSI1 >gi 2394227 (AF016845) WD-40
                    repeat protein [Lycopersicon esculentum]
Seq. No.
                    231897
Seq. ID
                    LIB3197-041-Q1-M1-E1
Method
                    BLASTX
NCBI GI
                    g2407790
BLAST score
                    422
E value
                    1.0e-41
Match length
                    139
% identity
                    18
NCBI Description (AF019910) grr1 [Glycine max]
Seq. No.
                    231898
Seq. ID
                    LIB3197-041-Q1-M1-E11
Method
                    BLASTX
NCBI GI
                    g2655008
BLAST score
                    319
                    2.0e-29
E value
Match length
                    112
% identity
                    54
NCBI Description (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon
                    esculentum]
```

Seq. No. 231899 Seq. ID LIB3197-041-Q1-M1-E12

Method BLASTX

NCBI GI g3108053

```
BLAST score
E value
                   3.0e-80
Match length
                   150
% identity
                   96
NCBI Description
                  (AF056326) myo-inositol 1-phosphate synthase; INO1 [Zea
                   mays]
Seq. No.
                   231900
Seq. ID
                   LIB3197-041-Q1-M1-E2
Method
                   BLASTX
NCBI GI
                   q2493046
BLAST score
                   404
E value
                   2.0e-39
Match length
                   112
% identity
                   72
NCBI Description ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR
                   >gi_82297_pir__A41740 H+-transporting ATP synthase (EC
3.6.1.34) delta' chain precursor - sweet potato
                   >gi_217938_dbj_BAA01511_ (D10660) mitochondrial F1-ATPase
                   delta subunit [Ipomoea batatas]
Seq. No.
                   231901
Seq. ID
                   LIB3197-041-Q1-M1-E5
Method
                   BLASTX
NCBI GI
                   q401322
BLAST score
                   384
E value
                   4.0e-37
Match length
                   88
% identity
                   86
NCBI Description
                   VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
                   SUBUNIT) >gi 167313 (L03186) vacuolar H+-ATPase catalytic
                   subunit [Gossypium hirsutum]
Seq. No.
                   231902
Seq. ID
                   LIB3197-041-Q1-M1-E6
Method
                   BLASTX
NCBI GI
                   q1082766
BLAST score
                   212
E value
                   6.0e-17
Match length
                   52
                   73
% identity
NCBI Description ribosomal protein L29 - human >gi 793843 emb CAA89008
                   (Z49148) ribosomal protein L29 [Homo sapiens]
Seq. No.
                   231903
Seq. ID
                   LIB3197-041-Q1-M1-F1
Method
                   BLASTX
NCBI GI
                   q4335750
```

Method BLASTX
NCBI GI g4335750
BLAST score 271
E value 7.0e-24
Match length 84
% identity 54

NCBI Description (AC006284) putative beta-1,3-endoglucanase [Arabidopsis

thaliana]

Seq. No. 231904

Seq. ID LIB3197-041-Q1-M1-F10



Method BLASTX NCBI GI g232024 BLAST score 768 E value 4.0e-82 Match length 144 % identity 100

PROTEIN E6 >gi\_421806\_pir\_\_A46130 fiber protein - upland NCBI Description cotton >gi\_2129498\_pir\_\_S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi\_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi\_1000084

(U30505) E6 [Gossypium hirsutum]

Seq. No. 231905

Seq. ID LIB3197-041-Q1-M1-F11

Method BLASTX NCBI GI g2252824 BLAST score 340 E value 6.0e-32 Match length 126 % identity

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 231906

Seq. ID LIB3197-041-Q1-M1-F12

Method BLASTX NCBI GI q1703129 BLAST score 524 E value 1.0e-53 Match length 97 % identity 99

ACTIN 11 >gi\_2129522\_pir\_\_S68109 actin 11 - Arabidopsis thaliana >gi\_1002533 (U27981) actin-11 [Arabidopsis NCBI Description

thaliana]

Seq. No. 231907

Seq. ID LIB3197-041-Q1-M1-F2

Method BLASTX NCBI GI q3183454 BLAST score 207 E value 2.0e-16 Match length 94 % identity 43

NCBI Description HYPOTHETICAL 30.7 KD PROTEIN IN MCPC-KINA INTERGENIC REGION

>gi\_2632217\_emb\_CAA10859\_ (AJ222587) YkwC protein [Bacillus subtilis] >gi\_2633767\_emb\_CAB13269\_ (Z99111) similar to 3-hydroxyisobutyrate dehydrogenase [Bacillus subtilis]

231908 Seq. No.

Seq. ID LIB3197-041-Q1-M1-F4

Method BLASTX NCBI GI g3360289 BLAST score 439 E value 2.0e-43 Match length 102 % identity 83

NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase

1 [Zea mays]



```
Seq. No.
                   231909
Seq. ID
                  LIB3197-041-Q1-M1-F5
Method
                  BLASTX
NCBI GI
                   q1041706
BLAST score
                   448
E value
                   1.0e-44
Match length
                   103
% identity
                   75
NCBI Description
                  (U30480) expansin At-EXP6 [Arabidopsis thaliana]
                  231910
Seq. No.
Seq. ID
                  LIB3197-041-Q1-M1-F7
Method
                  BLASTX
NCBI GI
                   a543905
BLAST score
                   357
E value
                   9.0e-51
Match length
                  127
% identity
                   83
NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi 347459 (L22162)
                  brassinosteroid-regulated protein [Glycine max]
Seq. No.
                   231911
Seq. ID
                  LIB3197-041-Q1-M1-F8
Method
                  BLASTX
NCBI GI
                   q2275210
BLAST score
                   156
E value
                   2.0e-10
Match length
                  81
                   43
% identity
NCBI Description
                   (AC002337) peptidyl-prolyl cis-trans isomerase isolog
                   [Arabidopsis thaliana]
Seq. No.
                   231912
Seq. ID
                  LIB3197-041-Q1-M1-G1
Method
                  BLASTX
NCBI GI
                   q3395427
BLAST score
                   205
E value
                   4.0e-16
Match length
                   110
% identity
                   45
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                   231913
Seq. ID
                  LIB3197-041-Q1-M1-G10
Method
                  BLASTX
NCBI GI
                   q2833380
BLAST score
                  299
E value
                   3.0e-27
Match length
                  120
% identity
                   56
                  RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 2 (PHOSPHORIBOSYL
NCBI Description
                  PYROPHOSPHATE SYNTHETASE 2) (PRS II)
                  >gi_2146772_pir__S71262 ribose-phosphate pyrophosphokinase
                   (EC 2.7.6.1) II - Arabidopsis thaliana (fragment)
```

>gi\_1064885\_emb\_CAA63552\_ (X92974) phosphoribosyl
pyrophosphate synthetase II [Arabidopsis thaliana]

NCBI GI

BLAST score



```
Seq. No.
                   231914
Seq. ID
                   LIB3197-041-Q1-M1-G12
Method
                   BLASTX
NCBI GI
                   g1220196
BLAST score
                   807
E value
                   1.0e-86
Match length
                   150
% identity
                   100
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.
                   231915
Seq. ID
                   LIB3197-041-Q1-M1-G2
Method
                   BLASTX
NCBI GI
                   g2558654
BLAST score
                   391
E value
                   6.0e-38
Match length
                   141
% identity
                   56
NCBI Description
                 (AC002354) No definition line found [Arabidopsis thaliana]
Seq. No.
                   231916
Seq. ID
                  LIB3197-041-Q1-M1-G3
Method
                  BLASTX
NCBI GI
                   g2119937
BLAST score
                   378
E value
                   2.0e-36
Match length
                   79
% identity
                   91
NCBI Description
                  translation initiation factor eIF-4A.13 - common tobacco
                   (fragment)
Seq. No.
                   231917
Seq. ID
                  LIB3197-041-Q1-M1-G4
Method
                  BLASTX
NCBI GI
                  g2213610
BLAST score
                  165
E value
                   3.0e-20
Match length
                  81
% identity
                   50
NCBI Description
                  (AC000103) F21J9.4 [Arabidopsis thaliana]
Seq. No.
                   231918
Seq. ID
                  LIB3197-041-Q1-M1-G5
Method
                  BLASTX
NCBI GI
                  g2980788
BLAST score
                  257
E value
                  3.0e-22
Match length
                  136
% identity
                  46
NCBI Description
                 (AL022197) putative protein [Arabidopsis thaliana]
Seq. No.
                  231919
Seq. ID
                  LIB3197-041-Q1-M1-G7
Method
                  BLASTX
```

33383

g2827713 376



```
E value
                   3.0e-36
Match length
                   126
% identity
                   63
                   (AL021684) pyridoxal-phosphate-dependent aminotransferase -
NCBI Description
                  like protein [Arabidopsis thaliana]
Seq. No.
                   231920
Seq. ID
                  LIB3197-041-Q1-M1-G9
Method
                  BLASTX
NCBI GI
                   g1170898
BLAST score
                  507
E value
                   1.0e-51
Match length
                   122
% identity
NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
                  >gi_629659_pir__S44167 malate dehydrogenase, mitochondrial
                   - cider tree >gi_473206_emb_CAA55383 (X78800)
                  mitochondrial malate dehydrogenase [Eucalyptus gunnii]
Seq. No.
                  231921
Seq. ID
                  LIB3197-041-Q1-M1-H1
Method
                  BLASTX
NCBI GI
                  g1617036
BLAST score
                  370
E value
                  2.0e-35
Match length
                  89
% identity
                  75
NCBI Description (Y08624) Ted2 [Vigna unguiculata]
Seq. No.
                  231922
Seq. ID
                  LIB3197-041-Q1-M1-H10
Method
                  BLASTX
NCBI GI
                  g3128175
BLAST score
                  181
E value
                  3.0e-13
Match length
                  100
% identity
                  39
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                  231923
Seq. ID
                  LIB3197-041-Q1-M1-H11
Method
                  BLASTX
NCBI GI
                  g1848212
BLAST score
                  536
E value
                  4.0e-55
Match length
                  116
% identity
                  49
NCBI Description
                  (Y11209) protein disulfide-isomerase precursor [Nicotiana
                  tabacum]
Seq. No.
                  231924
Seq. ID
                  LIB3197-041-Q1-M1-H12
Method
                  BLASTX
```

Method BLASTX
NCBI GI g541950
BLAST score 245
E value 2.0e-21
Match length 52



```
% identity
NCBI Description SPCP1 protein - soybean >gi_310576 (L12257) nodulin-26
                  [Glycine max]
Seq. No.
                  231925
Seq. ID
                  LIB3197-041-Q1-M1-H3
Method
                  BLASTX
NCBI GI
                  g729623
BLAST score
                  454
E value
                  3.0e-45
Match length
                  106
                  85
% identity
NCBI Description
                  78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 5 PRECURSOR (GRP
                  78-5) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG
                  5) (BIP 5) >gi_100340_pir__S21880 heat shock protein BiP
                  homolog blp5 - common tobacco >gi_19813_emb_CAA42660
                  (X60058) luminal binding protein (BiP) [Nicotiana tabacum]
Seq. No.
                  231926
Seq. ID
                  LIB3197-041-Q1-M1-H5
Method
                  BLASTX
NCBI GI
                  g1170507
BLAST score
                  727
E value
                  3.0e-77
Match length
                  144
                  97
% identity
NCBI Description EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3)
                  >gi 100276 pir S22579 translation initiation factor eIF-4A
                  - curled-leaved tobacco >gi_19699_emb_CAA43514_ (X61206)
                  nicotiana eukaryotic translation initiation factor 4A
                  [Nicotiana plumbaginifolia]
Seq. No.
                  231927
Seq. ID
                  LIB3197-041-Q1-M1-H8
Method
                  BLASTX
NCBI GI
                  g3650037
BLAST score
                  433
E value
                  7.0e-43
Match length
                  103
% identity
                  82
                 (AC005396) auxin-responsive GH3-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  231928
Seq. ID
                  LIB3197-041-Q1-M1-H9
Method
                  BLASTX
                  g2811278
                  479
                  3.0e-48
                  102
% identity
                  86
```

NCBI GI BLAST score E value Match length

NCBI Description (AF043284) expansin [Gossypium hirsutum]

Seq. No. 231929

LIB3197-042-Q1-M1-A7 Seq. ID

Method BLASTX NCBI GI g416758



```
BLAST score
                  166
E value
                  9.0e-12
                  77
Match length
                  45
% identity
                  SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130)
NCBI Description
                  carboxypeptidase Y-like protein [Arabidopsis thaliana]
                  >gi 445120 prf 1908426A carboxypeptidase Y [Arabidopsis
                  thaliana]
                  231930
Seq. No.
Seq. ID
                  LIB3197-042-Q1-M1-A9
Method
                  BLASTX
NCBI GI
                  q2984709
BLAST score
                  357
E value
                  3.0e - 34
Match length
                  71
                  96
% identity
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                  231931
Seq. ID
                  LIB3197-042-Q1-M1-B1
Method
                  BLASTX
NCBI GI
                  g4432830
BLAST score
                  482
E value
                  1.0e-48
Match length
                  121
% identity
                  71
NCBI Description
                  (AC006283) similar to pheromone receptor deficient mutant
                  [Arabidopsis thaliana]
Seq. No.
                  231932
Seq. ID
                  LIB3197-042-Q1-M1-B2
Method
                  BLASTX
NCBI GI
                  g1483150
BLAST score
                  371
E value
                  1.0e-35
Match length
                  84
% identity
                  80
NCBI Description
                  (D84417) monodehydroascorbate reductase [Arabidopsis
                  thaliana]
                  231933
Seq. No.
Seq. ID
                  LIB3197-042-Q1-M1-B3
Method
                  BLASTX
NCBI GI
                  g112972
BLAST score
                  568
E value
                  1.0e-58
Match length
                  128
% identity
                  85
NCBI Description
                  ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
                  >gi 167546 (M92660) aspartate aminotransferase [Daucus
                  carota] >gi_445587_prf__1909339A Asp aminotransferase
                  [Daucus carota]
```

Seq. No. 231934

Seq. ID LIB3197-042-Q1-M1-B9

Method BLASTX

NCBI GI

E value

BLAST score

g267069

2.0e-65

626



```
g2194118
NCBI GI
BLAST score
                  195
E value
                  6.0e-15
Match length
                  68
% identity
NCBI Description (AC002062) F20P5.4 gene product [Arabidopsis thaliana]
Seq. No.
                  231935
Seq. ID
                  LIB3197-042-Q1-M1-C1
Method
                  BLASTX
NCBI GI
                  q4097579
BLAST score
                  583
E value
                  2.0e-60
Match length
                  121
% identity
                  88
NCBI Description
                 (U64922) NTGP1 [Nicotiana tabacum]
                  231936
Seq. No.
                  LIB3197-042-Q1-M1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2507422
BLAST score
                  446
E value
                  2.0e-44
Match length
                  107
                  86
% identity
NCBI Description
                  CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS)
                   (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi_3293261 (AF039206)
                  cystathionine gamma-synthase precursor [Arabidopsis
                  thaliana]
Seq. No.
                  231937
Seq. ID
                  LIB3197-042-Q1-M1-C7
Method
                  BLASTX
NCBI GI
                  g2246442
BLAST score
                  166
E value
                  2.0e-11
Match length
                  70
% identity
                  46
NCBI Description (U63298) farnesyltransferase alpha subunit [Pisum sativum]
Seq. No.
                  231938
Seq. ID
                  LIB3197-042-Q1-M1-F10
Method
                  BLASTX
NCBI GI
                  g2749939
BLAST score
                  169
                  7.0e-12
E value
Match length
                  55
% identity
NCBI Description
                  (U70999) CCS1 [Chlamydomonas reinhardtii] >gi 2749941
                   (U71000) CCS1 [Chlamydomonas reinhardtii]
Seq. No.
                  231939
Seq. ID
                  LIB3197-042-Q1-M1-F11
Method
                  BLASTX
```

BLAST score

E value Match length 340 2.0e-32



```
Match length
% identity
                  99
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  231940
Seq. No.
Seq. ID
                  LIB3197-042-Q1-M1-F4
Method
                  BLASTX
NCBI GI
                  q4490736
BLAST score
                  459
                  7.0e-46
E value
Match length
                  140
% identity
                  39
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]
Seq. No.
                  231941
                  LIB3197-042-Q1-M1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3121853
BLAST score
                  159
E value
                  1.0e-10
Match length
                  132
                  32
% identity
NCBI Description
                  CHLORIDE INTRACELLULAR CHANNEL PROTEIN 2 (XAP121)
                  >gi_2584785_emb_CAA73228_ (Y12696) p64 bovine chloride
                  channel-like protein [Homo sapiens]
                  231942
Seq. No.
                  LIB3197-042-Q1-M1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4512671
BLAST score
                  189
E value
                  6.0e-15
                  59
Match length
                  73
% identity
NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]
                  231943
Seq. No.
Seq. ID
                  LIB3197-042-Q1-M1-G12
Method
                  BLASTX
NCBI GI
                  g4406372
BLAST score
                  278
E value
                  1.0e-24
                  99
Match length
                   57
% identity
NCBI Description (AF109156) thiosulfate sulfurtransferase [Datisca
                  glomerata]
Seq. No.
                   231944
Seq. ID
                  LIB3197-042-Q1-M1-G5
Method
                  BLASTX
NCBI GI
                  g3646373
```

% identity

NCBI Description

90



```
% identity
NCBI Description (AJ011078) RGP1 protein [Oryza sativa]
                  231945
Seq. No.
Seq. ID
                  LIB3197-042-Q1-M1-H10
Method
                  BLASTX
NCBI GI
                  g2146731
BLAST score
                  568
                  1.0e-58
E value
Match length
                  141
                  31
% identity
NCBI Description FK506-binding protein - Arabidopsis thaliana >gi 1354207
                  (U49453) rof1 [Arabidopsis thaliana]
Seq. No.
                  231946
Seq. ID
                  LIB3197-042-Q1-M1-H11
Method
                  BLASTX
NCBI GI
                  g2623300
BLAST score
                  167
E value
                  1.0e-11
                  74
Match length
% identity
                  66
                  (AC002409) putative protein phosphatase 2C [Arabidopsis
NCBI Description
                  thaliana]
                  231947
Seq. No.
Seq. ID
                  LIB3197-042-Q1-M1-H12
Method
                  BLASTX
NCBI GI
                  g2911047
BLAST score
                  400
E value
                  5.0e-39
Match length
                  113
% identity
                  70
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
                  231948
Seq. No.
Seq. ID
                  LIB3197-042-Q1-M1-H4
Method
                  BLASTX
NCBI GI
                  g3249105
BLAST score
                  265
E value
                  4.0e-23
Match length
                  146
% identity
                  40
NCBI Description
                  (AC003114) Contains similarity to protein phosphatase 2C
                   (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                  231949
Seq. ID
                  LIB3197-042-Q1-M1-H5
Method
                  BLASTX
NCBI GI
                  g169989
BLAST score
                  515
E value
                  2.0e-52
Match length
                  111
```

(L12157) NADPH-specific isocitrate dehydrogenase [Glycine



```
Seq. No.
                  231950
Seq. ID
                  LIB3197-043-Q1-M1-A10
Method
                  BLASTX
NCBI GI
                  g2244839
BLAST score
                  355
E value
                  1.0e-33
Match length
                  153
% identity
                  15
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  231951
Seq. ID
                  LIB3197-043-Q1-M1-A5
Method
                  BLASTX
NCBI GI
                  g1657617
BLAST score
                  486
E value
                  5.0e-49
Match length
                  110
% identity
                  85
NCBI Description
                  (U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236)
                  putative nuclear DNA-binding protein G2p [Arabidopsis
                  thaliana]
Seq. No.
                  231952
Seq. ID
                  LIB3197-043-Q1-M1-A6
Method
                  BLASTX
NCBI GI
                  g1418990
BLAST score
                  283
E value
                  3.0e-25
Match length
                  71
                  75
% identity
NCBI Description (Z75524) unknown [Lycopersicon esculentum]
Seq. No.
                  231953
Seq. ID
                  LIB3197-043-Q1-M1-B10
Method
                  BLASTX
NCBI GI
                  q3402279
BLAST score
                  622
E value
                  5.0e-65
Match length
                  127
% identity
                  91
NCBI Description
                  (AJ000999) putative beta-subunit of K+ channels [Solanum
                  tuberosum]
                  231954
Seq. No.
Seq. ID
                  LIB3197-043-Q1-M1-B11
Method
                  BLASTX
NCBI GI
                  g3236248
                  476
BLAST scòre
E value
                  6.0e-48
Match length
                  131
                  72
% identity
NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]
```

Seq. No. 231955

Seq. ID LIB3197-043-Q1-M1-B5

Method BLASTX NCBI GI g2832658



```
BLAST score
E value
                   1.0e-12
Match length
                   114
% identity
                   34
NCBI Description (AL021710) putative protein [Arabidopsis thaliana]
Seq. No.
                   231956
Seq. ID
                   LIB3197-043-Q1-M1-F2
Method
                   BLASTX
NCBI GI
                   g4455365
BLAST score
                   153
E value
                   5.0e-10
Match length
                   31
% identity
                   87
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]
Seq. No.
                   231957
Seq. ID
                   LIB3197-043-Q1-M1-G1
Method
                   BLASTX
NCBI GI
                   g4510395
BLAST score
                   545
E value
                   5.0e-56
Match length
                   133
% identity
                   73
NCBI Description
                  (AC006587) putative beta-galactosidase precursor
                   [Arabidopsis thaliana]
Seq. No.
                   231958
Seq. ID
                   LIB3197-043-Q1-M1-G3
Method
                   BLASTX
NCBI GI
                   g4521249
BLAST score
                   523
E value
                   2.0e-53
Match length
                   133
% identity
                   77
NCBI Description (AB013912) DNA helicase [Mus musculus]
Seq. No.
                   231959
Seq. ID
                   LIB3197-043-Q1-M1-G7
Method
                   BLASTX
NCBI GI
                   g2335098
BLAST score
                   481
E value
                   2.0e-48
Match length
                   146
% identity
                   63
NCBI Description (AC002339) unknown protein [Arabidopsis thaliana]
Seq. No.
                   231960
Seq. ID
                   LIB3197-043-Q1-M1-G8
Method
                   BLASTX
NCBI GI
                   g2498329
BLAST score
                   367
E value
                   4.0e-43
Match length
                   131
% identity
                   71
```

pattern-formation protein GNOM - Arabidopsis thaliana

NCBI Description PATTERN FORMATION PROTEIN EMB30 >gi\_2129665\_pir\_\_\$65571



>gi\_1209633 (U36433) GNOM gene product [Arabidopsis thaliana] >gi\_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi 1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana]

Seq. No. 231961 Seq. ID LIB3197-043-Q1-M1-G9 Method BLASTX NCBI GI q3150402 BLAST score 99 E value 3.0e-10 Match length 48 % identity 85

NCBI Description (AC004165) putative malonyl-CoA: Acyl carrier protein

transacylase [Arabidopsis thaliana]

Seq. ID LIB3197-043-Q1-M1-H1 Method BLASTX NCBI GI g2129499 BLAST score 607 E value 3.0e-63 Match length 125

Seq. No.

% identity

fiber protein E6 (clone CKE6-4A) - upland cotton NCBI Description

>gi\_1000086 (U30506) E6 [Gossypium hirsutum]

Seq. No. 231963

Seq. ID LIB3197-043-Q1-M1-H2

231962

Method BLASTX NCBI GI g2160322 BLAST score 517 E value 1.0e-52

Match length 101 % identity 95

(D16139) cytokinin binding protein CBP57 [Nicotiana NCBI Description

sylvestris]

Seq. No. 231964

Seq. ID LIB3197-043-Q1-M1-H3

Method BLASTX NCBI GI g1345132 BLAST score 698 E value 7.0e-74Match length 155 % identity 86

(U47029) ERECTA [Arabidopsis thaliana] NCBI Description

>gi\_1389566\_dbj\_BAA11869\_ (D83257) receptor protein kinase [Arabidopsis thaliana] >gi 3075386 (AC004484) receptor

protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No. 231965

Seq. ID LIB3197-043-Q1-M1-H7

Method BLASTX NCBI GI g267069



BLAST score E value 6.0e-40 <sup>-</sup>

Match length 90 % identity 92

NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi\_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 231966

Seq. ID LIB3197-043-Q1-M1-H8

Method BLASTX NCBI GI q606942 BLAST score 293 E value 2.0e-26 Match length 111 % identity 59

NCBI Description (U13760) unknown [Gossypium hirsutum]

Seq. No. 231967

Seq. ID LIB3197-044-Q1-M1-A1

Method BLASTX NCBI GI q1703115 BLAST score 439 E value 8.0e-44 Match length 83 % identity 99

NCBI Description ACTIN 3 >gi\_2129526\_pir\_\_S68112 actin 3 - Arabidopsis

thaliana >gi\_1145695 (U39480) actin [Arabidopsis thaliana]

>gi 3236244 (AC004684) actin 3 protein [Arabidopsis

thaliana]

Seq. No. 231968

Seq. ID LIB3197-044-Q1-M1-A11

Method BLASTX NCBI GI q730125 BLAST score 147 E value 2.0e-09 54 Match length % identity 59

NCBI Description NADPH-CYTOCHROME P450 REDUCTASE >gi\_322739\_pir\_\_S31502

NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Madagascar

periwinkle >gi\_18139\_emb\_CAA49446\_ (X69791)
NADPH--ferrihemoprotein reductase [Catharanthus roseus]

Seq. No. 231969

Seq. ID LIB3197-044-Q1-M1-A12

Method BLASTX NCBI GI g2642238 BLAST score 368 E value 2.0e-35 Match length 84 % identity 89

NCBI Description (AF031241) endoplasmic reticulum HSC70-cognate binding

protein precursor [Glycine max]

Seq. No. 231970

Seq. ID

Method



```
LIB3197-044-Q1-M1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3337366
BLAST score
                  299
E value
                  2.0e-27
Match length
                  108
% identity
                  57
NCBI Description
                  (AC004481) unknown protein [Arabidopsis thaliana]
Seq. No.
                  231971
Seq. ID
                  LIB3197-044-Q1-M1-A5
Method
                  BLASTX
NCBI GI
                  q267069
BLAST score
                  453
E value
                  2.0e-45
Match length
                  88
                  95
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                  231972
Seq. ID
                  LIB3197-044-Q1-M1-A6
Method
                  BLASTX
NCBI GI
                  g1527172
BLAST score
                  191
E value
                  5.0e-19
Match length
                  76
% identity
                  55
NCBI Description
                  (U67676) alpha-2 tubulin [Hirudo medicinalis]
                  >gi_1532193_gb_AAB07891_ (U67678) alpha-2 tubulin [Hirudo
                  medicinalis]
Seq. No.
                  231973
Seq. ID
                  LIB3197-044-Q1-M1-B1
Method
                  BLASTX
NCBI GI
                  g3158376
BLAST score
                  162
E value
                  1.0e-13
                  80
Match length
% identity
                  54
NCBI Description
                 (AF035385) unknown [Arabidopsis thaliana]
Seq. No.
                  231974
Seq. ID
                  LIB3197-044-Q1-M1-B12
Method
                  BLASTX
NCBI GI
                  g2245394
BLAST score
                  247
E value
                  4.0e-21
                  75
Match length
% identity
NCBI Description
                 (U89771) ARF1-binding protein [Arabidopsis thaliana]
Seq. No.
                  231975
```

LIB3197-044-Q1-M1-B3

BLASTX

BLAST score

E value

384

4.0e-37



```
q4512712
NCBI GI
BLAST score
                  144
E value
                  4.0e-09
                  97
Match length
% identity
                  30
NCBI Description (AC006569) unknown protein [Arabidopsis thaliana]
                  231976
Seq. No.
Seq. ID
                  LIB3197-044-Q1-M1-B5
Method
                  BLASTX
NCBI GI
                  q3540178
BLAST score
                  320
                  1.0e-29
E value
Match length
                  116
% identity
                  58
                  (AC004122) calcium-transporting ATPase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  231977
Seq. ID
                  LIB3197-044-Q1-M1-B7
Method
                  BLASTX
NCBI GI
                  g1174613
BLAST score
                  509
E value
                  5.0e-52
Match length
                  100
% identity
                  98
                  26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
NCBI Description
                  PROTEIN HOMOLOG 1) (TBP-1) >gi_556560_dbj_BAA04614_
                   (D17788) rice homologue of Tat binding protein [Oryza
                  sativa]
                  231978
Seq. No.
                  LIB3197-044-Q1-M1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2580440
BLAST score
                  236
E value
                  6.0e-20
                  115
Match length
% identity
                  48
NCBI Description (D87261) PCF2 [Oryza sativa]
                  231979
Seq. No.
Seq. ID
                  LIB3197-044-Q1-M1-C12
Method
                  BLASTX
NCBI GI
                  g1762142
BLAST score
                  396
                  2.0e-38
E value
                  142
Match length
% identity
                  55
NCBI Description (U48434) putative cytochrome P450 [Solanum chacoense]
                  231980
Seq. No.
Seq. ID
                  LIB3197-044-Q1-M1-C6
Method
                  BLASTX
NCBI GI
                  g2191128
```

Match length

% identity

98



```
Match length
                  64
% identity
                  (AF007269) belongs to the L5P family of ribosomal proteins
NCBI Description
                  [Arabidopsis thaliana]
                  231981
Seq. No.
Seq. ID
                  LIB3197-044-Q1-M1-C7
Method
                  BLASTX
NCBI GI
                  g2801536
BLAST score
                  435
E value
                  4.0e-43
Match length
                  141
% identity
                  60
NCBI Description
                 (AF039531) lysophospholipase homolog [Oryza sativa]
Seq. No.
                  231982
                  LIB3197-044-Q1-M1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3021506
BLAST score
                  499
                  7.0e-51
E value
Match length
                  119
% identity
                  86
                  (X96727) isocitrate dehydrogenase (NAD+) [Nicotiana
NCBI Description
                  tabacum]
                  231983
Seq. No.
Seq. ID
                  LIB3197-044-Q1-M1-D12
                  BLASTX
Method
NCBI GI
                  g731097
BLAST score
                  300
E value
                  3.0e-27
Match length
                  124
                  52
% identity
NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT)
                   (V-ATPASE 28 KD ACCESSORY PROTEIN) >gi 1083086 pir A55910
                  subunit D vacuolar H(+)-ATPase - bovine >gi 517446 (U11927)
                  vacuolar H-ATPase subunit D [Bos gaurus]
Seq. No.
                  231984
                  LIB3197-044-Q1-M1-D2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2982303
BLAST score
                  419
E value
                  3.0e-41
                  94
Match length
                  82
% identity
NCBI Description (AF051236) hypothetical protein [Picea mariana]
Seq. No.
                  231985
                  LIB3197-044-Q1-M1-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1174592
BLAST score
                  527
E value
                  5.0e-54
```

NCBI Description



```
NCBI Description TUBULIN ALPHA-1 CHAIN >gi,2119270 pir $60233 alpha-tubulin
                  - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                  sativum]
Seq. No.
                  231986
                  LIB3197-044-Q1-M1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g541951
BLAST score
                  404
E value
                  2.0e-39
Match length
                  128
% identity
                  63
                  SPCP2 protein - soybean >gi 310578 (L12258) nodulin-26
NCBI Description
                  [Glycine max]
                  231987
Seq. No.
                  LIB3197-044-Q1-M1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2398807
BLAST score
                  354
E value
                  1.0e-33
Match length
                  107
% identity
                   64
                  (Z99091) succinate dehydrogenase [Schizosaccharomyces
NCBI Description
                  pombe]
Seq. No.
                  231988
Seq. ID
                  LIB3197-044-Q1-M1-E1
Method
                  BLASTX
NCBI GI
                  g2738949
BLAST score
                  491
E value
                  1.0e-49
Match length
                  102
% identity
                  90
NCBI Description
                 (AF022213) cytosolic ascorbate peroxidase [Fragaria x
                  ananassa]
                  231989
Seq. No.
                  LIB3197-044-Q1-M1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3953470
                  251
BLAST score
E value
                  2.0e-21
                  90
Match length
                   60
% identity
NCBI Description (AC002328) F20N2.15 [Arabidopsis thaliana]
                  231990
Seq. No.
Seq. ID
                  LIB3197-044-Q1-M1-E11
Method
                  BLASTX
NCBI GI
                  q1928981
BLAST score
                  503
E value
                   4.0e-51
                  107
Match length
                   93
% identity
```

oleracea var. botrytis]

(U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica



```
231991
Seq. No.
                  LIB3197-044-Q1-M1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g464846
BLAST score
                  340
E value
                  4.0e-32
Match length
                  73
% identity
                  84
                  TUBULIN ALPHA-6 CHAIN >gi 322880 pir S28983 tubulin
NCBI Description
                  alpha-6 chain - maize >gi 22158 emb CAA44863 (X63178)
                  alpha-tubulin #6 [Zea mays]
                  231992
Seq. No.
Seq. ID
                  LIB3197-044-Q1-M1-E8
                  BLASTX
Method
NCBI GI
                  g3063396
BLAST score
                  553
                  5.0e-57
E value
Match length
                  109
% identity
                  94
NCBI Description (AB012947) vcCyP [Vicia faba]
                  231993
Seq. No.
                  LIB3197-044-Q1-M1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1174718
BLAST score
                  191
E value
                  2.0e-14
                  130
Match length
                  16
% identity
NCBI Description
                  PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR
                  >gi 322579 pir JQ1674 receptor protein kinase TMK1 (EC
                  2.7.1.-) precursor - Arabidopsis thaliana >gi_166888
                  (L00670) protein kinase [Arabidopsis thaliana]
Seq. No.
                  231994
Seq. ID
                  LIB3197-044-Q1-M1-F10
Method
                  BLASTX
                  g3024017
NCBI GI
BLAST score
                  414
E value
                  8.0e-41
Match length
                  81
% identity
                  95
NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)
                   (EIF-4C) >qi 2565421 (AF026804) eukaryotic translation
                  initiation factor eTF-1A [Onobrychis viciifolia]
Seq. No.
                  231995
Seq. ID
                  LIB3197-044-Q1-M1-F11
Method
                  BLASTX
NCBI GI
                  g4165861
BLAST score
                  284
E value
                  2.0e-25
                  136
Match length
% identity
                  24
```

NCBI Description (AF006603) histone deacetylase mHDA2 [Mus musculus]

Seq. No.

232001



```
231996
Seq. No.
Seq. ID
                  LIB3197-044-Q1-M1-F12
Method
                  BLASTX
NCBI GI
                  g2583123
BLAST score
                  340
E value
                   4.0e-32
Match length
                  94
                  70
% identity
NCBI Description
                  (AC002387) putative nucleotide sugar epimerase [Arabidopsis
                  thaliana]
Seq. No.
                  231997
Seq. ID
                  LIB3197-044-Q1-M1-F4
Method
                  BLASTX
NCBI GI
                  q3618343
BLAST score
                  195
E value
                   6.0e-15
Match length
                  104
% identity
                   41
NCBI Description
                  (AB009398) 26S proteasome subunit p40.5 [Homo sapiens]
                  >gi_4506223_ref_NP_002808.1_pPSMD13_ proteasome (prosome,
                  macropain) 26S subunit, non-ATPase,
Seq. No.
                  231998
Seq. ID
                  LIB3197-044-Q1-M1-F7
Method
                  BLASTX
NCBI GI
                  g2935298
BLAST score
                  323
E value
                  4.0e-30
Match length
                  83
                  75
% identity
NCBI Description (AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase
                  1 [Gossypium hirsutum]
Seq. No.
                  231999
Seq. ID
                  LIB3197-044-Q1-M1-F9
Method
                  BLASTX
NCBI GI
                  g2062167
BLAST score
                  329
E value
                  7.0e-31
Match length
                  93
% identity
                  67
NCBI Description
                  (AC001645) Proline-rich protein APG isolog [Arabidopsis
                  thaliana]
Seq. No.
                  232000
Seq. ID
                  LIB3197-044-Q1-M1-G10
Method
                  BLASTX
NCBI GI
                  g4204260
BLAST score
                  197
E value
                  4.0e-15
Match length
                  61
% identity
NCBI Description
                  (AC005223) 25568 [Arabidopsis thaliana]
```

33399

Method

NCBI GI

BLAST score

BLASTX

192

g1361974



```
Seq. ID
                  LIB3197-044-Q1-M1-G11
                  BLASTX
Method
NCBI GI
                  g3551960
BLAST score
                  426
                  4.0e-44
E value
Match length
                  139
% identity
                  65
                  (AF082033) senescence-associated protein 15 [Hemerocallis
NCBI Description
                  hybrid cultivar]
                  232002
Seq. No.
Seq. ID
                  LIB3197-044-Q1-M1-G2
                  BLASTX
Method
NCBI GI
                  g3176098
BLAST score
                  411
E value
                  2.0e-44
Match length
                  141
                  42
% identity
NCBI Description (Y15036) annexin [Medicago truncatula]
Seq. No.
                  232003
Seq. ID
                  LIB3197-044-Q1-M1-G4
                  BLASTX
Method
NCBI GI
                  g1724102
BLAST score
                  560
                  1.0e-57
E value
Match length
                  122
                  85
% identity
NCBI Description (U79766) S-adenosyl-L-homocystein hydrolase; SAH
                   [Mesembryanthemum crystallinum]
                  232004
Seq. No.
Seq. ID
                  LIB3197-044-Q1-M1-G5
Method
                  BLASTX
NCBI GI
                  q3600054
BLAST score
                  192
                  1.0e-14
E value
Match length
                  106
% identity
                   40
NCBI Description (AF080120) No definition line found [Arabidopsis thaliana]
Seq. No.
                  232005
Seq. ID
                  LIB3197-044-Q1-M1-G6
Method
                  BLASTX
NCBI GI
                  g1724102
BLAST score
                  509
                  9.0e-52
E value
Match length
                  117
% identity
NCBI Description (U79766) S-adenosyl-L-homocystein hydrolase; SAH
                   [Mesembryanthemum crystallinum]
Seq. No.
                   232006
Seq. ID
                  LIB3197-044-Q1-M1-H2
```

33400



```
9.0e-23
E value
Match length
                  133
                  47
% identity
                  cysteine proteinase - clove pink (fragment) >gi_595986
NCBI Description
                  (U17135) cysteine proteinase [Dianthus caryophyllus]
                  232007
Seq. No.
Seq. ID
                  LIB3197-044-Q1-M1-H4
Method
                  BLASTX
NCBI GI
                  g2252860
BLAST score
                  113
                  9.0e-13
E value
                  109
Match length
                  50
% identity
                  (AF013294) No definition line found [Arabidopsis thaliana]
NCBI Description
                  232008
Seq. No.
                  LIB3197-044-Q1-M1-H5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3163946
BLAST score
                  509
                   7.0e-52
E value
Match length
                  117
% identity
                  (AJ005599) alpha-tubulin 1 [Eleusine indica]
NCBI Description
Seq. No.
                   232009
Seq. ID
                  LIB3197-044-Q1-M1-H6
                   BLASTX
Method
NCBI GI
                   g2832672
BLAST score
                   194
                   4.0e-15
E value
Match length
                   64
                   64
% identity
                  (AL021712) nifU-like protein [Arabidopsis thaliana]
NCBI Description
                   232010
Seq. No.
                   LIB3197-044-Q1-M1-H9
Seq. ID
Method
                   BLASTX
                   g4490332
NCBI GI
BLAST score
                   160
                   7.0e-11
E value
                   65
Match length
                   55
% identity
                  (AL035656) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   232011
                   LIB3197-045-Q1-M1-A10
Seq. ID
                   BLASTX
Method
                   g3182981
NCBI GI
                   550
BLAST score
                   1.0e-56
E value
                   130
Match length
                   80
% identity
NCBI Description CELL ELONGATION PROTEIN DIMINUTO >gi_1695692_dbj_BAA13096_
```

(D86494) diminuto [Pisum sativum]

% identity

76

NCBI Description (AF043284) expansin [Gossypium hirsutum]



```
232012
Seq. No.
Seq. ID
                  LIB3197-045-Q1-M1-A2
Method
                  BLASTX
NCBI GI
                  g129232
BLAST score
                  572
                  4.0e-59
E value
Match length
                  140
                  76
% identity
                  ORYZAIN BETA CHAIN PRECURSOR >gi_67645 pir__KHRZOB oryzain
NCBI Description
                   (EC 3.4.22.-) beta precursor - rice
                  >gi 218183 dbj BAA14403_ (D90407) oryzain beta precursor
                   [Oryza sativa]
                  232013
Seq. No.
Seq. ID
                  LIB3197-045-Q1-M1-A3
Method
                  BLASTX
NCBI GI
                  g312179
BLAST score
                  566
                   2.0e-58
E value
Match length
                  113
% identity
                   94
                  (X73151) glyceraldehyde 3-phosphate dehydrogenase
NCBI Description
                   (phosphorylating) [Zea mays] >gi 1184772 (U45855) cytosolic
                  glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]
                   >gi 1185554 (U45858) glyceraldehyde-3-phosphate
                   dehydrogenase [Zea mays]
                   232014
Seq. No.
                  LIB3197-045-Q1-M1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g224159
BLAST score
                   464
E value
                   4.0e-50
Match length
                   110
% identity
                   95
NCBI Description cytochrome b559 [Spinacia oleracea]
Seq. No.
                   232015
                   LIB3197-045-Q1-M1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1350984
                   200
BLAST score
                   8.0e-24
E value
Match length
                   68
                   91
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S3A >gi 469248 (L31645) ribosomal
                   protein S3a [Helianthus annuus]
                   232016
Seq. No.
Seq. ID
                   LIB3197-045-Q1-M1-A9
Method
                   BLASTX
NCBI GI
                   g2811278
BLAST score
                   542
E value
                   1.0e-55
Match length
                   131
```

Seq. ID

Method



```
232017
Seq. No.
                  LIB3197-045-Q1-M1-B1
Seq. ID
Method
                  BLASTX
                  g4512667
NCBI GI
                  383
BLAST score
                  4.0e-37
E value
Match length
                  109
% identity
                  69
                 (AC006931) putative MAP kinase [Arabidopsis thaliana]
NCBI Description
                  232018
Seq. No.
                  LIB3197-045-Q1-M1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4508079
BLAST score
                  348
E value
                  7.0e-33
Match length
                  110
                  62
% identity
NCBI Description (AC005882) 66284 [Arabidopsis thaliana]
                  232019
Seq. No.
                  LIB3197-045-Q1-M1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g266944
BLAST score
                  597
E value
                  3.0e-62
Match length
                  117
                  95
% identity
                  60S RIBOSOMAL PROTEIN L2 (L8) (RIBOSOMAL PROTEIN TL2)
NCBI Description
                  >gi 71078 pir R5TOL8 ribosomal protein L8, cytosolic -
                  tomato >gi 19343 emb_CAA45863_ (X64562) ribosomal protein
                  L2 [Lycopersicon esculentum]
Seq. No.
                  232020
                  LIB3197-045-Q1-M1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2791834
BLAST score
                  756
E value
                  1.0e-80
                  143
Match length
                  99
% identity
NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta]
Seq. No.
                  232021
                  LIB3197-045-Q1-M1-B2
Seq. ID
                BLASTX
Method
NCBI GI
                  q2829870
BLAST score
                  453
E value
                   3.0e-45
                  135
Match length
% identity
                   65
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   232022
```

33403

LIB3197-045-Q1-M1-B3

BLASTX



```
NCBI GI
                    g1076678
BLAST score
                    392
                    3.0e - 38
E value
Match length
                    79
                    100
% identity
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)
                    232023
Seq. No.
Seq. ID
                    LIB3197-045-Q1-M1-B5
Method
                    BLASTX
NCBI GI
                    q4490317
                    235
BLAST score
                    9.0e-20
E value
Match length
                    109
                    45
% identity
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
                    232024
Seq. No.
                    LIB3197-045-Q1-M1-B6
Seq. ID
Method
                    BLASTX
NCBI GI
                    g123650
                    567
BLAST score
E value
                    1.0e-58
Match length
                    110
% identity
                    97
NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN >gi 82245 pir S03250 heat
                    shock protein 70 (clone pMON9743) - garden petunia
                    >gi_20557_emb_CAA30018_ (X06932) heat shock protein 70
                    [Petunia x hybrida]
Seq. No.
                    232025
                    LIB3197-045-Q1-M1-B9
Seq. ID
Method
                    BLASTX
NCBI GI
                    g464806
BLAST score
                    149
E value
                    1.0e-09
Match length
                    129
% identity
                    SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72)
NCBI Description
                    >gi_423182_pir__ A40692 signal recognition particle 72K
chain - dog >gi_297768_emb_CAA48014_ (X67813) signal
recognition particle,72 kDa_subunit [Canis familiaris]
Seq. No.
                    232026
                    LIB3197-045-Q1-M1-C1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3367534
BLAST score
                    157
E value
                    1.0e-10
                    92
Match length
% identity
                    41
                    (AC004392) Strong similarity to coatamer alpha subunit
NCBI Description
                     (HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis
                    thaliana]
```

Seq. No. 232027

Seq. ID LIB3197-045-Q1-M1-C10



```
BLASTX
Method
                    q464707
NCBI GI
                    530
BLAST score
E value
                    3.0e-54
                    109
Match length
                    94
% identity
                    40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal
NCBI Description
                    protein S18.A - Arabidopsis thaliana
                    >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)
                    S18 ribosomal protein [Arabidopsis thaliana]
                    >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
                    [Arabidopsis thaliana] >gi 434906 emb CAA82275 (Z28962)
                    S18 ribosomal protein [Arabidopsis thaliana]
                    >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A
[Arabidopsis thaliana] >gi_3287678 (AC003979) Match to
                    ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
                    gb R30430 come from this gene. [Arabidopsis thaliana]
                    >q\bar{i} 4538910 emb CAB39647.1 (AL049482) S18.A ribosomal
                    protein [Arabidopsis thaliana]
                    232028
Seq. No.
                    LIB3197-045-Q1-M1-C12
Seq. ID
Method
                    BLASTX
NCBI GI
                    q2811278
BLAST score
                    638
                    7.0e-67
E value
                    130
Match length
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
                     232029
Seq. No.
                    LIB3197-045-Q1-M1-C5
Seq. ID
                    BLASTX
Method
NCBI GI
                     q3913414
BLAST score
                     287
                     7.0e-51
E value
Match length
                     142
                     75
% identity
NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME 2 (ADOMETDC 2)
                     (SAMDC 2) (SAMDC16) >gi 1155242 (U38527)
                     S-adenosylmethionine decarboxylase 2 [Dianthus
                     caryophyllus]
                     232030
Seq. No.
Seq. ID
                     LIB3197-045-Q1-M1-C7
Method
                     BLASTX
NCBI GI
                     g2967452
BLAST score
                     157
E value
                     5.0e-11
Match length
                     84
% identity
                     42
                    (AB010882) hSNF2H [Homo sapiens]
NCBI Description
                     >gi_4507075_ref_NP_003592.1_pSMARCA5_ SWI/SNF related,
```

subfamily a, member

matrix associated, actin dependent regulator of chromatin,



thaliana]

% identity

NCBI Description

```
232031
Seq. No.
Seq. ID
                  LIB3197-045-Q1-M1-C9
Method
                  BLASTX
NCBI GI
                  g464707
BLAST score
                  373
                  6.0e-36
E value
Match length
                  81
% identity
                  91
                 40S RIBOSOMAL PROTEIN S18 >qi 480908 pir S37496 ribosomal
NCBI Description
                  protein S18.A - Arabidopsis thaliana
                  >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
                  [Arabidopsis thaliana] >gi 434906 emb CAA82275 (Z28962)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to
                  ribosomal S18 gene mRNA gb Z28701, DNA gb Z23165 from A.
                  thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
                  gb_R30430 come from this gene. [Arabidopsis thaliana]
                  >gi 4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal
                  protein [Arabidopsis thaliana]
Seq. No.
                  232032
                  LIB3197-045-Q1-M1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2351374
BLAST score
                  438
E value
                  2.0e-43
Match length
                  97
                  86
% identity
NCBI Description
                  (U54560) putative 26S proteasome subunit athMOV34
                  [Arabidopsis thaliana]
Seq. No.
                  232033
                  LIB3197-045-Q1-M1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4426565
BLAST score
                  158
E value
                  1.0e-10
Match length
                  144
% identity
                  26
NCBI Description (AF031483) unknown [Rattus norvegicus]
Seq. No.
                  232034
Seq. ID
                  LIB3197-045-Q1-M1-D6
Method
                  BLASTX
NCBI GI
                  g2088653
BLAST score
                  348
                  7.0e-33
E value
Match length
                  108
```

(AF002109) Hs1pro-1 related protein isolog [Arabidopsis



83

Match length % identity

```
232035
Seq. No.
                  LIB3197-045-Q1-M1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2738248
BLAST score
                  410
E value
                  2.0e-40
Match length
                  99
                  79
% identity
                  (U97200) cobalamin-independent methionine synthase
NCBI Description
                  [Arabidopsis thaliana]
                  232036
Seq. No.
                  LIB3197-045-Q1-M1-D9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1931655
BLAST score
                  538
E value
                  3.0e-55
Match length
                  141
                  74
% identity
NCBI Description (U95973) receptor-kinase isolog [Arabidopsis thaliana]
                  232037
Seq. No.
Seq. ID
                  LIB3197-045-Q1-M1-E1
Method
                  BLASTX
NCBI GI
                  q465820
BLAST score
                  438
E value
                  2.0e-43
Match length
                  105
% identity
                  69
                  HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III
NCBI Description
                  >gi_280536_pir__S28301 hypothetical protein C40H1.6 -
                  Caenorhabditis elegans >gi 3874819 emb CAA79557 (Z19154)
                  C40H1.6 [Caenorhabditis elegans]
Seq. No.
                  232038
                  LIB3197-045-Q1-M1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1174470
BLAST score
                  141
E value
                  4.0e-17
                  97
Match length
                  56
% identity
NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)
                   (INTEGRAL MEMBRANE PROTEIN 1) >gi 508543 (L34260) integral
                  membrane protein 1 [Mus musculus] >gi 1588285 prf 2208301A
                  integral membrane protein [Mus musculus]
                  232039
Seq. No.
                  LIB3197-045-Q1-M1-E11
Seq. ID
                  BLASTX
Method
                  g4098129
NCBI GI
BLAST score
                  394
                  3.0e-38
E value
```

NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]

% identity

87



```
Seq. No.
                  232040
                  LIB3197-045-Q1-M1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3335355
BLAST score
                  500
                  7.0e-51
E value
Match length
                  101
                  27
% identity
NCBI Description
                  (AC004512) Match to polyubiquitin DNA gb L05401 from A.
                  thaliana. Contains insertion of mitochondrial NADH
                  dehydrogenase gb X82618 and gb X98301. May be a pseudogene
                  with an expressed insert. EST gb AA586248 comes from this
                  region. [Arabi
Seq. No.
                  232041
                  LIB3197-045-Q1-M1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4097579
BLAST score
                  438
E value
                  2.0e-43
Match length
                  90
                  89
% identity
NCBI Description (U64922) NTGP1 [Nicotiana tabacum]
                  232042
Seq. No.
Seq. ID
                  LIB3197-045-Q1-M1-E5
Method
                  BLASTX
NCBI GI
                  q4262149
BLAST score
                  259
E value
                  2.0e-22
                  72
Match length
                  71
% identity
NCBI Description (AC005275) putative xyloglucan endotransglycosylase
                   [Arabidopsis thaliana]
Seq. No.
                  232043
                  LIB3197-045-Q1-M1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2501578
BLAST score
                  281
E value
                  1.0e-49
                  115
Match length
                   96
% identity
NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047
                  ethylene-responsive protein 1 - Para rubber tree
                   >gi 1209317 (M88254) ethylene-inducible protein [Hevea
                  brasiliensis]
                   232044
Seq. No.
Seq. ID
                  LIB3197-045-Q1-M1-E8
Method
                  BLASTX
NCBI GI
                  g950299
BLAST score
                  588
                   5.0e-61
E value
Match length
                  124
```

NCBI Description (L46792) xyloglucan endotransglycosylase precursor



Seq. No.

232045

## [Actinidia deliciosa]

```
Seq. ID
                   LIB3197-045-Q1-M1-E9
 Method
                   BLASTX
 NCBI GI
                   q2499612
                   432
 BLAST score
                    5.0e-51
 E value
 Match length
                   138
 % identity
                    76
 NCBI Description
                   MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 1 (PMEK1)
                   >gi_1076650_pir__S52989 mitogen-activated,
                    extracelluar-regulated protein kinase 1 (EC 2.7.1.-) -
                    garden petunia >gi_603871_emb_CAA58466_ (X83440) MAP/ERK
                    kinase 1 [Petunia x hybrida]
                    232046
 Seq. No.
                   LIB3197-045-Q1-M1-F1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2286153
 BLAST score
                   402
                    2.0e-39
 E value
                   83
 Match length
                    96
 % identity
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
 Seq. No.
                    232047
                   LIB3197-045-Q1-M1-F10
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g4138137
 BLAST score
                    566
                    2.0e-58
 E value
 Match length
                    134
                    71
 % identity
 NCBI Description
                   (AJ012796) ss-galactosidase [Lycopersicon esculentum]
 . . .
 Seq. No.
                   -232048
                   LIB3197-045-Q1-M1-F11
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    q126896
 BLAST score
                    611
 E value
                    9.0e-64
 Match length
                    132
 % identity
                    90
 NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
                    >gi 319831 pir DEPUMW malate dehydrogenase (EC 1.1.1.37)
                   precursor, mitochondrial - watermelon
>gi_18297_emb_CAA35239_ (X17362) precursor protein (AA -27
                    to 320) [Citrullus lanatus]
 Seq. No.
                    232049
                   LIB3197-045-Q1-M1-F12
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g2499607
 BLAST score
                    719
 E value
                    2.0e-76
                    139
 Match length
```

33409



```
% identity
NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 3 (MAP KINASE 3)
                   (ATMPK3) >gi_629544_pir__S40469 mitogen-activated protein kinase 3 (EC 2.7.1.-) - Arabidopsis thaliana
                   >gi_457398_dbj_BAA04866 (D21839) MAP kinase [Arabidopsis
                   thaliana]
Seq. No.
                   232050
Seq. ID
                   LIB3197-045-Q1-M1-F2
Method
                   BLASTX
NCBI GI
                   q3650378
BLAST score
                   156
E value
                   2.0e-10
Match length
                   56
                   52
% identity
                  (AL031740) putative rRNA biogenesis protein; rrp5 homolog;
NCBI Description
                   multiple S1 rna binding domain protein [Schizosaccharomyces
                   pombe]
                   232051
Seq. No.
Seq. ID
                   LIB3197-045-Q1-M1-F4
Method
                   BLASTX
NCBI GI
                   q3493172
BLAST score
                   623
E value
                   4.0e-65
Match length
                   133
                   92
% identity
NCBI Description (U89609) fiber annexin [Gossypium hirsutum]
Seq. No.
                   232052
Seq. ID
                   LIB3197-045-Q1-M1-F5
Method
                   BLASTX
NCBI GI
                   g2245378
BLAST score
                   679
E value
                   1.0e-71
                   139
Match length
                   88
% identity
NCBI Description (U83245) auxin response factor 1 [Arabidopsis thaliana]
                   232053
Seq. No.
Seq. ID
                   LIB3197-045-Q1-M1-F6
Method
                   BLASTX
NCBI GI
                   g125887
BLAST score
                   223
                   3.0e-18
E value
Match length
                   115
% identity
                   44
NCBI Description ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
                   >gi 82092 pir S04765 LAT52 protein precursor - tomato
                   >gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon
                   esculentum]
                   232054
Seq. No.
```

Seq. ID LIB3197-045-Q1-M1-F7

Method BLASTX NCBI GI g3334115 BLAST score 457



```
E value
                  9.0e-46
Match length
                  97
                  93
% identity
                  ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                  (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664
                  (AF006489) adenine nucleotide translocator 1 [Gossypium
                  hirsutum]
                  232055
Seq. No.
Seq. ID
                  LIB3197-045-Q1-M1-F8
                  BLASTX
Method
NCBI GI
                  g3080420
BLAST score
                  497
E value
                  2.0e-50
Match length
                  121
                  75
% identity
NCBI Description
                 (AL022604) putative sugar transporter protein [Arabidopsis
                  thaliana]
Seq. No.
                  232056
Seq. ID
                  LIB3197-045-Q1-M1-F9
Method
                  BLASTX
NCBI GI
                  q870726
BLAST score
                  427
E value
                  4.0e-42
Match length
                  116
                  76
% identity
NCBI Description
                  (L38260) biotin carboxylase subunit [Nicotiana tabacum]
                  >gi 1582354 prf 2118337A Ac-CoA carboxylase:SUBUNIT=biotin
                  carboxylase [Nicotiana tabacum]
                  232057
Seq. No.
Seq. ID
                  LIB3197-045-Q1-M1-G3
Method
                  BLASTX
NCBI GI
                  g1946355
BLAST score
                  358
E value
                  4.0e-34
Match length
                  124
% identity
                  56
NCBI Description
                  (U93215) maize transposon MuDR mudrA protein isolog
                  [Arabidopsis thaliana] >gi 2880040 (AC002340) maize
                  transposon MuDR mudrA-like protein [Arabidopsis thaliana]
Seq. No.
                  232058
Seq. ID
                  LIB3197-045-Q1-M1-G4
Method
                  BLASTX
                  q4544409
NCBI GI
BLAST score
                  404
E value
                  2.0e-39
Match length
                  123
% identity
```

NCBI Description (AC006955) putative transcription factor [Arabidopsis

thaliana]

Seq. No. 232059

Seq. ID LIB3197-045-Q1-M1-G6

Method BLASTX



```
q2129578
 NCBI GI
 BLAST score
                     224
                     1.0e-33
 E value
 Match length
                     139
 % identity
                     62
                     dTDP-glucose 4-6-dehydratases homolog - Arabidopsis
 NCBI Description
                     thaliana >gi 928932 emb CAA89205 (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana]
                     >qi 1585435 prf 2124427B diamide resistance gene
                     [Arabidopsis thaliana]
                     232060
 Seq. No.
 Seq. ID
                     LIB3197-045-Q1-M1-G8
 Method
                     BLASTX
 NCBI GI
                     q3242705
 BLAST score
                     354
                     1.0e-33
 E value
 Match length
                     82
                     77
 % identity
 NCBI Description (AC003040) putative nicotinate phosphoribosyltransferase
                     [Arabidopsis thaliana]
 Seq. No.
                     232061
 Seq. ID
                     LIB3197-045-Q1-M1-H11
 Method
                     BLASTX
- NCBI GI
                     q1220196
 BLAST score
                     586
                     8.0e-61
 E value
 Match length
                     131
  % identity
 NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
  Seq. No.
                     232062
  Seq. ID
                     LIB3197-045-Q1-M1-H4
 Method
                     BLASTX
 NCBI GI
                     q4098128
 BLAST score
                     589
 E value
                     4.0e-61
 Match length
                     130
  % identity
                     88
  NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
                     232063
  Seq. No.
                     LIB3197-045-Q1-M1-H7
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g1707017
  BLAST score
                     685
  E value
                     2.0e-72
                     143
  Match length
                     92
  % identity
  NCBI Description (U78721) RNA helicase isolog [Arabidopsis thaliana]
  Seq. No.
                     232064
                     LIB3197-045-Q1-M1-H9
  Seq. ID
```

BLASTX

578

g3925703

Method NCBI GI

BLAST score

E value

Match length

7.0e-09

55



```
7.0e-60
E value
Match length
                  126
% identity
                  88
NCBI Description (X95905) 14-3-3 protein [Lycopersicon esculentum]
Seq. No.
                  232065
                  LIB3197-046-Q1-M1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2119278
BLAST score
                  607
E value
                  3.0e-63
Match length
                  121
                  91
% identity
NCBI Description tubulin beta-1 chain - rice
                  232066
Seq. No.
                  LIB3197-046-Q1-M1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2499498
BLAST score
                  561
E value
                  6.0e-58
Match length
                  120
% identity
                  92
NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC
                  >gi_1161602_emb_CAA88840_ (Z48976) phosphoglycerate kinase
                  (PGK) [Nicotiana tabacum]
Seq. No.
                  232067
                  LIB3197-046-Q1-M1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4186184
                  248
BLAST score
E value
                  3.0e-21
Match length
                  120
% identity
                  43
NCBI Description (AF111168) unknown [Homo sapiens]
                  232068
Seq. No.
Seq. ID
                  LIB3197-046-Q1-M1-A6
Method
                  BLASTX
NCBI GI
                  g3914430
BLAST score
                  394
E value
                  2.0e-41
Match length
                  126
                  72
% identity
NCBI Description PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON
                  CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)
                  >gi 2285800_dbj_BAA21650_ (D78172) 26S proteasome beta
                  subunit [Spinacia oleracea]
Seq. No.
                   232069
Seq. ID
                  LIB3197-046-Q1-M1-A9
Method
                  BLASTX
                  g2995384
NCBI GI
BLAST score
                  138
```



```
% identity
NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]
Seq. No.
                   232070
Seq. ID
                  LIB3197-046-Q1-M1-B1
Method
                  BLASTX
NCBI GI
                   g3128234
BLAST score
                  338
E value
                   1.0e-31
Match length
                  110
% identity
                   66
                  (AC004077) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  232071
Seq. No.
Seq. ID
                  LIB3197-046-Q1-M1-B11
Method
                  BLASTX
NCBI GI
                  g4056494
BLAST score
                   368
E value
                   3.0e - 35
Match length
                  88
                   76
% identity
NCBI Description
                  (AC005896) putative protein translocase [Arabidopsis
                  thaliana]
                   232072
Seq. No.
Seq. ID
                  LIB3197-046-Q1-M1-B12
Method
                  BLASTX
NCBI GI
                  q4193388
BLAST score
                   489
E value
                   3.0e-56
Match length
                   137
% identity
                  (AF091455) translationally controlled tumor protein [Hevea
NCBI Description
                  brasiliensis]
Seq. No.
                   232073
                  LIB3197-046-Q1-M1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2497753
BLAST score
                   185
E value
                   4.0e-14
Match length
                   48
% identity
                   62
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
NCBI Description
                   >gi 1321915 emb CAA65477 (X96716) lipid transfer protein
                   [Prunus dulcis]
                   232074
Seq. No.
Seq. ID
                   LIB3197-046-Q1-M1-B6
Method
                   BLASTX
NCBI GI
                   g728880
BLAST score
                   443
E value
                   4.0e-46
Match length
                   139
% identity
                   69
NCBI Description N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG
```

>gi 517485 emb CAA54691\_ (X77588) ARD1 N-acetyl transferase

% identity

76



homologue [Homo sapiens]  $>gi_1302661$  (U52112) ARD1 N-acetyl transferase related protein [Homo sapiens]

232075 Seq. No. Seq. ID LIB3197-046-Q1-M1-B7 Method BLASTX NCBI GI g2895559 BLAST score 151 7.0e-10 E value 55 Match length 47 % identity (AF038554) drp1 [Homo sapiens] NCBI Description >gi 4503395 ref NP 003668.1 pDRP density-regulated protein 232076 Seq. No. Seq. ID LIB3197-046-Q1-M1-B9 Method BLASTX NCBI GI g2662343 BLAST score 554 E value 4.0e-57 Match length 106 99 % identity NCBI Description (D63581) EF-1 alpha [Oryza sativa] Seq. No. 232077 Seq. ID LIB3197-046-Q1-M1-C1 BLASTX Method NCBI GI g4262236 BLAST score 397 E value 1.0e-38 Match length 108 75 % identity NCBI Description (AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana] 232078 Seq. No. Seq. ID LIB3197-046-Q1-M1-C10 BLASTX Method NCBI GI g267082 BLAST score 500 E value 8.0e-51 Match length 97 94 % identity NCBI Description TUBULIN BETA-8 CHAIN >gi\_320189\_pir\_\_JQ1592 tubulin beta-8 chain - Arabidopsis thalīana >gī 166908 (M84705) beta-8 tubulin [Arabidopsis thaliana] 232079 Seq. No. Seq. ID LIB3197-046-Q1-M1-C12 BLASTX Method NCBI GI q2129540 BLAST score 561 E value 7.0e-58 Match length 139

33415

NCBI Description ATP sulfurylase (clone APS2) precursor - Arabidopsis

thaliana (fragment)



```
232080
Seq. No.
Seq. ID
                   LIB3197-046-Q1-M1-C7
Method
                   BLASTX
NCBI GI
                   q3668089
BLAST score
                   151
E value
                   7.0e-10
Match length
                   50
% identity
                    48
NCBI Description
                  (AC004667) unknown protein [Arabidopsis thaliana]
                   232081
Seq. No.
Seq. ID
                   LIB3197-046-Q1-M1-C8
Method
                   BLASTX
NCBI GI
                   q1771162
BLAST score
                   527
E value
                    6.0e-54
Match length
                   129
                    69
% identity
NCBI Description
                   (X98930) SBT2 [Lycopersicon esculentum]
                   >gi 3687307 emb CAA07000 (AJ006379) subtilisin-like
                   protease [Lycopersicon esculentum]
Seq. No.
                   232082
Seq. ID
                   LIB3197-046-Q1-M1-D10
Method
                   BLASTX
NCBI GI
                    q1703108
BLAST score
                    574
E value
                    1.0e-78
Match length
                    150
                    97
% identity
                   ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis
NCBI Description
                    thaliana >gi 1049307 (U37281) actin-2 [Arabidopsis
                    thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis
                    thaliana]
                    232083
Seq. No.
Seq. ID
                   LIB3197-046-Q1-M1-D3
Method
                   BLASTX
NCBI GI
                    g3868758
BLAST score
                    419
E value
                    3.0e-41
Match length
                    101
% identity
                    76
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
                    232084
Seq. No.
Seq. ID
                    LIB3197-046-Q1-M1-D6
Method
                   BLASTX
NCBI GI
                    g1542941
BLAST score
                    331
```

NCBI Description (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

6.0e-31

106

E value Match length

% identity



```
232085
Seq. No.
Seq. ID
                  LIB3197-046-Q1-M1-D7
Method
                  BLASTX
NCBI GI
                  g4406780
BLAST score
                  237
E value
                  6.0e-20
Match length
                  53
% identity
                  83
NCBI Description
                 (AC006532) putative multispanning membrane protein
                  [Arabidopsis thaliana]
Seq. No.
                  232086
                  LIB3197-046-Q1-M1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4056478
BLAST score
                  291
E value
                  3.0e-26
Match length
                  96
% identity
                  65
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]
                  232087
Seq. No.
                  LIB3197-046-Q1-M1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2673868
BLAST score
                  383
E value
                  5.0e-37
Match length
                  104
                  77
% identity
NCBI Description (Y14856) fimbriata-associated protein [Antirrhinum majus]
Seq. No.
                  232088
Seq. ID
                  LIB3197-046-Q1-M1-E5
Method
                  BLASTX
NCBI GI
                  g2341034
BLAST score
                  535
                  7.0e-55
E value
                  110
Match length
                  96
% identity
NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]
                  232089
Seq. No.
Seq. ID
                  LIB3197-046-Q1-M1-E6
Method
                  BLASTX
NCBI GI
                  g3608137
BLAST score
                  329
E value
                  1.0e-30
                  119
Match length
                  54
% identity
NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]
                  232090
Seq. No.
Seq. ID
                  LIB3197-046-Q1-M1-F10
```

Method BLASTX NCBI GI g4580389 BLAST score 604 E value 6.0e-63

NCBI GI

BLAST score

g475598 301



```
Match length
 % identity
                   (AC007171) unknown protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   232091
 Seq. ID
                   LIB3197-046-Q1-M1-F12
 Method
                   BLASTX
 NCBI GI
                   g1362152
 BLAST score
                    238
                    5.0e-20
 E value
 Match length
                    85
                    49
 % identity
                   ribosomal protein S6 kinase homolog (clone Aspk11) - oat
 NCBI Description
                    >gi_871986_emb_CAA56313_ (X79992) putative pp70 ribosomal
                    protein S6 kinase [Avena sativa]
                    232092
 Seq. No.
                    LIB3197-046-Q1-M1-F6
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g2500354
 BLAST score
                    625
                    2.0e-65
 E value
                    119
 Match length
                    97
% identity
                  60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462
 NCBI Description
                    (AB001891) QM family protein [Solanum melongena]
                    232093
 Seq. No.
                    LIB3197-046-Q1-M1-F7
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    q125051
 BLAST score
                    340
                    3.0e-32
 E value
 Match length
                    83
                    81
 % identity
                    ISOVALERYL-COA DEHYDROGENASE PRECURSOR (IVD)
 NCBI Description
                    >gi 88038 pir A37033 isovaleryl-CoA dehydrogenase (EC
                    1.3.99.10) precursor - human >gi 306897 (M34192)
                    isovaleryl-coA dehydrogenase (IVD) [Homo sapiens]
                    >qi 4504799 ref NP 002216.1 pIVD isovaleryl Coenzyme A
                    dehydrogenase
 Seq. No.
                    232094
                    LIB3197-046-Q1-M1-F8
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3668089
 BLAST score
                    298
                    3.0e-27
 E value
                    104
 Match length
 % identity
                    51
 NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
                    232095
 Seq. No.
                    LIB3197-046-Q1-M1-F9
 Seq. ID
                    BLASTX
 Method
```

E value

Match length

% identity

2.0e-50

91

99



```
E value
                   5.0e-28
Match length
                  62
                   95
% identity
NCBI Description (U08382) BiP isoform C [Glycine max]
                  232096
Seq. No.
Seq. ID
                  LIB3197-046-Q1-M1-G1
Method
                  BLASTX
NCBI GI
                  q475598
BLAST score
                  322
E value
                   6.0e-30
Match length
                  115
% identity
                   64
NCBI Description (U08382) BiP isoform C [Glycine max]
                  232097
Seq. No.
Seq. ID
                  LIB3197-046-Q1-M1-G10
Method
                  BLASTX
                  g2244973
NCBI GI
BLAST score
                  162
E value
                   5.0e-11
Match length
                  139
                   37
% identity
NCBI Description (Z97340) similarity to extensin class 1 protein
                   [Arabidopsis thaliana]
Seq. No.
                  232098
Seq. ID
                  LIB3197-046-Q1-M1-G11
Method
                  BLASTX
NCBI GI
                  g3170525
BLAST score
                  187
E value
                   4.0e-14
Match length
                  56
                   68
% identity
NCBI Description (AF054615) cellulase [Fragaria x ananassa]
Seq. No.
                   232099
Seq. ID
                  LIB3197-046-Q1-M1-G2
Method
                  BLASTX
NCBI GI
                  g416758
BLAST score
                  259
E value
                   2.0e-22
Match length
                  97
% identity
                   54
NCBI Description SERINE CARBOXYPEPTIDASE PRECURSOR >gi 166674 (M81130)
                  carboxypeptidase Y-like protein [Arabidopsis thaliana]
                   >gi_445120 prf 1908426A carboxypeptidase Y [Arabidopsis
                  thaliana]
                   232100
Seq. No.
                  LIB3197-046-Q1-M1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267069
BLAST score
                   497
```

33419



NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi\_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 232101

Seq. ID LIB3197-046-Q1-M1-G5

Method BLASTX
NCBI GI g3122673
BLAST score 412
E value 2.0e-40
Match length 109
% identity 76

NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi\_2245027\_emb\_CAB10447\_ (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No. 232102

Seq. ID LIB3197-046-Q1-M1-G7

Method BLASTX
NCBI GI g4512658
BLAST score 140
E value 1.0e-08
Match length 114
% identity 33

NCBI Description (AC006931) hypothetical protein [Arabidopsis thaliana]

Seq. No. 232103

Seq. ID LIB3197-046-Q1-M1-G8

Method BLASTX
NCBI GI g2213425
BLAST score 427
E value 4.0e-42
Match length 101
% identity 54

NCBI Description (Z97064) hypothetical protein [Citrus x paradisi]

Seq. No. 232104

Seq. ID LIB3197-046-Q1-M1-H10

Method BLASTX
NCBI GI g3450889
BLAST score 287
E value 7.0e-26
Match length 86
% identity 71

NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No. 232105

Seq. ID LIB3197-046-Q1-M1-H12

Method BLASTX
NCBI GI g1174592
BLAST score 244
E value 2.0e-43
Match length 90
% identity 91

NCBI Description TUBULIN ALPHA-1 CHAIN >gi\_2119270\_pir\_\_S60233 alpha-tubulin

- garden pea >gi 525332 (U12589) alpha-tubulin [Pisum

sativum]



BLASTX

LIB3197-046-Q1-M1-H2

Seq. No.

Seq. ID.

Method

```
NCBI GI
                  g123620
BLAST score
                  511
E value
                  2.0e-58
Match length
                  134
% identity
                  90
NCBI Description
                  HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi 100224 pir S14950
                  heat shock cognate protein 70 - tomato
                  >gi_19258_emb_CAA37971_ (X54030) heat shock protein cognate
                  70 [Lycopersicon esculentum]
Seq. No.
                  232107
                  LIB3197-046-01-M1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3334405
BLAST score
                  344
E value
                  8.0e-33
                  76
Match length
% identity
                  95
NCBI Description
                  VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
                  >gi 2267583 (AF009338) vacuolar H+-ATPase subunit E
                  [Gossypium hirsutum]
                  232108
Seq. No.
Seq. ID
                  LIB3197-046-Q1-M1-H4
Method
                  BLASTX
NCBI GI
                  g1764100
BLAST score
                  342
E value
                   3.0e - 32
Match length
                  96
% identity
                  73
NCBI Description
                  (U81805) GDP-D-mannose-4,6-dehydratase [Arabidopsis
                  thaliana]
                  232109
Seq. No.
Seq. ID
                  LIB3197-046-Q1-M1-H6
Method
                  BLASTX
NCBI GI
                  g1498386
BLAST score
                  497
E value
                  2.0e-50
                  97
Match length
                  97
% identity
NCBI Description (U60509) actin [Zea mays]
                  232110
Seq. No.
Seq. ID
                  LIB3197-046-Q1-M1-H7
Method
                  BLASTX
NCBI GI
                  g2244850
BLAST score
                  256
E value
                   4.0e-22
Match length
                  140
                   49
% identity
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
```



```
Seq. No.
                  232111
Seq. ID
                  LIB3197-046-Q1-M1-H8
Method
                  BLASTX
NCBI GI
                  g3043428
BLAST score
                  326
E value
                  2.0e-30
Match length
                  96
% identity
                  74
NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
Seq. No.
                  232112
Seq. ID
                  LIB3197-047-Q1-M1-A1
Method
                  BLASTX
NCBI GI
                  q3420751
BLAST score
                  343
E value
                  2.0e-32
Match length
                  121
                  52
% identity
NCBI Description (AF079448) cytochrome c oxidase assembly protein
                  [Dictyostelium discoideum]
Seq. No.
                  232113
Seq. ID
                  LIB3197-047-Q1-M1-A10
Method
                  BLASTX
NCBI GI
                  q1168972
BLAST score
                  369
E value
                  2.0e-35
Match length
                  115
% identity
                  42
NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA
                  PRECURSOR >gi_480969_pir__S37557 clpA protein - rape
                  (fragment) >gi_406311_emb_CAA53077_ (X75328) clpA [Brassica
                  napus]
                  232114
Seq. No.
Seq. ID
                  LIB3197-047-Q1-M1-A11
Method
                  BLASTX
NCBI GI
                  g2160151
BLAST score
                  362
E value
                  1.0e-34
Match length
                  122
% identity
                  61
NCBI Description (AC000375) Strong similarity to Brassica aspartic protease
                  (gb X77260). [Arabidopsis thaliana]
Seq. No.
                  232115
                  LIB3197-047-Q1-M1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1107526
BLAST score
                  142
E value
                  1.0e-08
Match length
                  59
% identity
NCBI Description (X87931) SIEP1L protein [Beta vulgaris]
```

Seq. No. 232116

Seq. ID LIB3197-047-Q1-M1-A4



```
Method
                  BLASTX
NCBI GI
                  q1871577
BLAST score
                  149
E value
                   4.0e-12
Match length
                  95
                  43
% identity
NCBI Description (Y11553) putative 21kD protein precursor [Medicago sativa]
Seq. No.
                  232117
Seq. ID
                  LIB3197-047-Q1-M1-A6
Method
                  BLASTX
NCBI GI
                  q3881189
BLAST score
                  402
E value
                  4.0e-39
Match length
                  103
% identity
NCBI Description
                  (Z99281) similar to ADP-ribosylation factor; cDNA EST
                  EMBL: C08179 comes from this gene; cDNA EST EMBL: C08337
                  comes from this gene; cDNA EST EMBL: C09829 comes from this
                  gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4
                  232118
Seq. No.
Seq. ID
                  LIB3197-047-Q1-M1-A9
Method
                  BLASTX
NCBI GI
                  q1617270
                  375
BLAST score
                  3.0e-36
E value
Match length
                  104
                  69
% identity
NCBI Description (X94624) acyl-CoA synthetase [Brassica napus]
Seq. No.
                  232119
Seq. ID
                  LIB3197-047-Q1-M1-B1
Method
                  BLASTX
NCBI GI
                  g3023816
BLAST score
                  487
E value
                  3.0e-49
Match length
                  109
% identity
                  82
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
                  232120
Seq. No.
Seq. ID
                  LIB3197-047-Q1-M1-B10
Method
                  BLASTX
NCBI GI
                  g4098129
BLAST score
                  460
E value
                  6.0e-46
                  88
Match length
```

% identity 98

NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]

232121 Seq. No.

Seq. ID LIB3197-047-Q1-M1-B12

Method BLASTX NCBI GI q870726

Seq. ID

Method

NCBI GI



```
BLAST score
                   480
E value
                   3.0e-48
Match length
                   113
% identity
                   84
NCBI Description
                   (L38260) biotin carboxylase subunit [Nicotiana tabacum]
                   >gi_1582354_prf__2118337A Ac-CoA carboxylase:SUBUNIT=biotin
                   carboxylase [Nicotiana tabacum]
Seq. No.
                   232122
Seq. ID
                   LIB3197-047-Q1-M1-B3
Method
                   BLASTX
NCBI GI
                   g3213227
BLAST score
                   150
E value
                   1.0e-09
Match length
                   89
% identity
                   31
NCBI Description
                   (AF035209) putative v-SNARE Vtila [Mus musculus]
                   >gi 3421062 (AF035823) 29-kDa Golgi SNARE [Mus musculus]
Seq. No.
                   232123
Seq. ID
                   LIB3197-047-Q1-M1-B6
Method
                   BLASTX
NCBI GI
                   q870726
BLAST score
                   379
E value
                   2.0e-36
Match length
                   99
                   77
% identity
NCBI Description
                   (L38260) biotin carboxylase subunit [Nicotiana tabacum]
                   >gi_1582354_prf__2118337A Ac-CoA carboxylase:SUBUNIT=biotin
                   carboxylase [Nicotiana tabacum]
Seq. No.
                   232124
Seq. ID
                   LIB3197-047-Q1-M1-B7
Method
                   BLASTX
NCBI GI
                   q2493131
BLAST score
                   414
E value
                   1.0e-40
                   90
Match length
                   92
% identity
NCBI Description
                   VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B
                   SUBUNIT) > gi 167108 (L11862) vacuolar ATPase B subunit
                   [Hordeum vulgare]
Seq. No.
                   232125
Seq. ID
                   LIB3197-047-Q1-M1-B8
Method
                   BLASTX
NCBI GI
                   g4538913
BLAST score
                   352
E value
                   2.0e-33
Match length
                   84
% identity
                   80
NCBI Description
                 (AL049482) putative protein [Arabidopsis thaliana]
                   232126
Seq. No.
```

LIB3197-047-Q1-M1-B9

BLASTX

q4249382



```
BLAST score
                   3.0e-52
E value
Match length
                   119
                   82
 % identity
                   (AC005966) Strong similarity to gi 3337350 F13P17.3
NCBI Description
                   putative permease from Arabidopsis thaliana BAC
                   gb AC004481. [Arabidopsis thaliana]
 Seq. No.
                   232127
 Seq. ID
                   LIB3197-047-Q1-M1-C2
Method
                   BLASTX
NCBI GI
                   g3142294
BLAST score
                   378
                   2.0e-36
E value
Match length
                   83
 % identity
                   87
                   (AC002411) Strong similarity to initiation factor eIF-2,
NCBI Description
                   gb_U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and
                   gb_N37529 come from this gene. [Arabidopsis thaliana]
 Seq. No.
                   232128
 Seq. ID
                   LIB3197-047-Q1-M1-C3
Method
                   BLASTX
· NCBI GI
                   g627469
BLAST score
                   244
E value
                   1.0e-20
Match length
                   140
 % identity
NCBI Description hypothetical protein 2 - human (fragment)
 Seq. No.
                   232129
Seq. ID
                   LIB3197-047-Q1-M1-C5
Method
                   BLASTX
NCBI GI
                   g832876
BLAST score
                   639
E value
                   6.0e-67
Match length
                   140
                   89
 % identity
NCBI Description
                   (L41345) ascorbate free radical reductase [Solanum
                   lycopersicum] >gi 1097368 prf 2113407A ascorbate free
                   radical reductase [Lycopersicon esculentum]
                   232130
 Seq. No.
 Seq. ID
                   LIB3197-047-Q1-M1-C6
Method
                   BLASTX
NCBI GI
                   g2213590
BLAST score
                   215
E value
                   2.0e-21
Match length
                   102
 % identity
                   51
NCBI Description (AC000348) T7N9.10 [Arabidopsis thaliana]
```

Seq. No. 232131

Seq. ID LIB3197-047-Q1-M1-C7

Method BLASTX NCBI GI q267069 BLAST score 648



E value 5.0e-68 Match length 120 % identity 98

NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi\_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 232132

Seq. ID LIB3197-047-Q1-M1-C8

Method BLASTX
NCBI GI g1350944
BLAST score 386
E value 2.0e-37
Match length 80
% identity 95

NCBI Description 40S RIBOSOMAL PROTEIN S17

Seq. No. 232133

Seq. ID LIB3197-047-Q1-M1-C9

Method BLASTX
NCBI GI g485126
BLAST score 175
E value 1.0e-12
Match length 73
% identity 51

NCBI Description (U00052) similar to RNA binding proteins [Caenorhabditis

elegans]

Seq. No. 232134

Seq. ID LIB3197-047-Q1-M1-D10

Method BLASTX
NCBI GI g586038
BLAST score 718
E value 3.0e-76
Match length 152
% identity 94

NCBI Description SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN CHLOROPLAST

PRECURSOR (SRP54) (54 CHLOROPLAST PROTEIN) (54CP) (FFC) >gi 480296 pir S36637 signal recognition particle 54CP

protein precursor - Arabidopsis thaliana

>gi 396701 emb CAA79981 (Z21970) 54CP [Arabidopsis

thaliana]

Seq. No. 232135

Seq. ID LIB3197-047-Q1-M1-D11

Method BLASTX
NCBI GI g120669
BLAST score 523
E value 2.0e-53
Match length 122
% identity 82

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]



```
Seq. No.
                    232136
Seq. ID
                   LIB3197-047-Q1-M1-D12
Method
                    BLASTX
NCBI GI
                    g119351
BLAST score
                    203
E value
                    8.0e-16
Match length
                    52
% identity
                    77
NCBI Description
                   ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                    (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_84950_pir__S07586
                   phosphopyruvate hydratase (EC 4.2.1.11) - fruit fly (Drosophila melanogaster) >gi_7946_emb_CAA34895_ (X17034)
                    enolase (AA 1-433) [Drosophila melanogaster]
                    232137
Seq. No.
                    LIB3197-047-Q1-M1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                    q135535
BLAST score
                    300
E value
                    2.0e-27
Match length
                    67
% identity
                    88
NCBI Description T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)
                    (CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide
                   Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_ (D11351) t-complex polypeptide 1 homologue [Arabidopsis
                    thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT
                    alpha/TCP-1 [Arabidopsis thaliana]
Seq. No.
                    232138
                    LIB3197-047-Q1-M1-D5
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2102696
                    259
BLAST score
E value
                    2.0e-22
Match length
                    128
                    38
% identity
                   (U72761) karyopherin beta 3 [Homo sapiens]
NCBI Description
                    >gi 4504909 ref NP 002262.1 pKPNB3 karyopherin (importin)
                    beta
                    232139
Seq. No.
Seq. ID
                    LIB3197-047-Q1-M1-D8
Method
                    BLASTX
NCBI GI
                    g1169534
BLAST score
                    645
                    9.0e-68
E value
                    134
Match length
                    93
% identity
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                    (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi 542019 pir S39203
                    phosphopyruvate hydratase (EC 4.2.1.11) - castor bean
```

Seq. No. 232140

communis]

>gi\_433609\_emb\_CAA82232\_ (Z28386) enolase [Ricinus

Method

NCBI GI

BLASTX

g3318611



```
LIB3197-047-Q1-M1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q541951
BLAST score
                  449
E value
                  1.0e-44
Match length
                  143
% identity
                  64
NCBI Description SPCP2 protein - soybean >gi 310578 (L12258) nodulin-26
                  [Glycine max]
Seq. No.
                  232141
Seq. ID
                  LIB3197-047-Q1-M1-E12
Method
                  BLASTX
NCBI GI
                  q4539351
BLAST score
                  573
E value
                  3.0e-59
Match length
                  145
                  74
% identity
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
Seq. No.
                  232142
Seq. ID
                  LIB3197-047-Q1-M1-E2
Method
                  BLASTX
NCBI GI
                  g2289961
BLAST score
                  319
E value
                  2.0e-29
Match length
                  89
% identity
                  75
NCBI Description (U82434) AtRAB8 [Arabidopsis thaliana]
Seq. No.
                  232143
Seq. ID
                  LIB3197-047-Q1-M1-F3
Method
                  BLASTX
NCBI GI
                  g2702281
BLAST score
                  235
E value
                  4.0e-39
Match length
                  159
% identity
                  46
NCBI Description (AC003033) putative protein disulfide isomerase precursor
                  [Arabidopsis thaliana]
Seq. No.
                  232144
                  LIB3197-047-Q1-M1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2500521
BLAST score
                  186
E value
                  5.0e-14
                  46
Match length
                  76
% identity
NCBI Description EUKARYOTIC INITIATION FACTOR 4A-15 (EIF-4A-15)
                  >gi 485945 emb CAA55739 (X79138) NeIF-4A15 [Nicotiana
                  tabacum]
                  232145
Seq. No.
Seq. ID
                  LIB3197-047-Q1-M1-F7
```

Match length

% identity

112

37



```
BLAST score
E value
                   1.0e-27
Match length
                   118
% identity
                   57
                  (AB016063) mitochondrial phosphate transporter [Glycine
NCBI Description
Seq. No.
                   232146
Seq. ID
                   LIB3197-047-Q1-M1-F8
Method
                   BLASTX
NCBI GI
                   g586076
BLAST score
                   615
E value
                   2.0e-64
Match length
                   115
                   97
% identity
                   TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta
NCBI Description
                   tubulin 1 [Lupinus albus]
Seq. No.
                   232147
Seq. ID
                   LIB3197-047-Q1-M1-F9
Method
                   BLASTX
NCBI GI
                   g2431769
BLAST score
                   233
E value
                   1.0e-23
Match length
                   78
% identity
                   78
NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]
Seq. No.
                   232148
Seq. ID
                   LIB3197-047-Q1-M1-G1
Method
                   BLASTX
NCBI GI
                   g2811278
BLAST score
                   651
E value
                   2.0e-68
Match length
                   133
% identity
                   88
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                   232149
Seq. ID
                   LIB3197-047-Q1-M1-G10
Method
                   BLASTX
NCBI GI
                   g3176387
BLAST score
                   473
E value
                   1.0e-47
Match length
                   99
% identity
NCBI Description (AB009849) neuropsin [Homo sapiens]
                   232150
Seq. No.
Seq. ID
                   LIB3197-047-Q1-M1-G11
                   BLASTX
Method
NCBI GI
                   g399082
BLAST score
                   148
E value
                   2.0e-09
```



NCBI Description ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi\_322713\_pir\_\_S28171 H+-transporting ATP synthase (EC 3.6.1.34) delta chain, chloroplast - garden pea >gi\_169045 (M94558) ATP synthase delta subunit [Pisum sativum]

Seq. No. 232151

Seq. ID LIB3197-047-Q1-M1-G2

Method BLASTX NCBI GI g2736147 BLAST score 446 2.0e-44 E value Match length 104 75 % identity

NCBI Description (AF021804) fatty acid hydroxylase Fahlp [Arabidopsis thaliana] >gi 3132481 (AC003096) fatty acid hydroxylase,

FAH1 [Arabidopsis thaliana]

Seq. No. 232152

Seq. ID LIB3197-047-Q1-M1-G3

Method BLASTX NCBI GI g3355486 BLAST score 315 E value 4.0e-29 Match length 102 % identity 62

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

232153 Seq. No.

Seq. ID LIB3197-047-Q1-M1-G5

Method BLASTX NCBI GI g3775987 BLAST score 497 E value 2.0e-50 Match length 118 % identity 86

NCBI Description (AJ010457) RNA helicase [Arabidopsis thaliana]

Seq. No. 232154

Seq. ID LIB3197-047-Q1-M1-G6

BLASTX Method NCBI GI g2213884 BLAST score 416 E value 5.0e-45 Match length 137 % identity 70

NCBI Description (AF004166) 2-isopropylmalate synthase [Lycopersicon

pennellii]

Seq. No. 232155

Seq. ID LIB3197-047-Q1-M1-G8

Method BLASTX NCBI GI q3024127 BLAST score 481 E value 1.0e-48 Match length 95

% identity 96

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

Seq. ID

Method



## ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi\_1655578\_emb\_CAA95857\_ (Z71272) S-adenosyl-L-methionine synthetase 2 [Catharanthus roseus]

```
Seq. No.
                  232156
Seq. ID
                  LIB3197-047-Q1-M1-G9
Method
                  BLASTX
NCBI GI
                  g4490332
BLAST score
                  170
E value
                  6.0e-12
Match length
                  74
% identity
                  51
NCBI Description (AL035656) putative protein [Arabidopsis thaliana]
                  232157
Seq. No.
Seq. ID
                  LIB3197-047-Q1-M1-H1
Method
                  BLASTX
NCBI GI
                  g445613
BLAST score
                  418
E value
                  2.0e-41
Match length
                  95
% identity
                  84
NCBI Description ribosomal protein L7 [Solanum tuberosum]
Seq. No.
                  232158
Seq. ID
                  LIB3197-047-Q1-M1-H12
Method
                  BLASTX
NCBI GI
                  g2935416
BLAST score
                  465
E value
                  1.0e-46
Match length
                  116
                  78
% identity
NCBI Description (AF047896) isoflavone reductase homolog [Betula pendula]
Seq. No.
                  232159
Seq. ID
                  LIB3197-047-Q1-M1-H2
Method
                  BLASTX
NCBI GI
                  g1707018
BLAST score
                  137
E value
                  1.0e-18
Match length
                  126
% identity
                  53
NCBI Description (U78721) CutA isolog [Arabidopsis thaliana]
Seq. No.
                  232160
Seq. ID
                  LIB3197-047-Q1-M1-H3
                  {\tt BLASTX}
Method
NCBI GI
                  g2811278
BLAST score
                  309
                  2.0e-28
E value
Match length
                  108
% identity
                  60
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                  232161
```

33431

LIB3197-047-Q1-M1-H4

BLASTX

E value

1.0e-31



```
NCBI GI
                  g2384671
BLAST score
                  580
E value
                  4.0e-60
Match length
                  144
                  78
% identity
NCBI Description
                  (AF012657) putative potassium transporter AtKT2p
                  [Arabidopsis thaliana]
Seq. No.
                  232162
Seq. ID
                  LIB3197-047-Q1-M1-H5
Method
                  BLASTX
NCBI GI
                  q3413700
BLAST score
                  419
E value
                  2.0e-41
Match length
                  117
                  71
% identity
NCBI Description (AC004747) putative YME1 protein [Arabidopsis thaliana]
Seq. No.
                  232163
Seq. ID
                  LIB3197-047-Q1-M1-H6
Method
                  BLASTX
NCBI GI
                  g2811278
BLAST score
                  247
E value
                  2.0e-35
Match length
                  110
% identity
                  69
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                  232164
                  LIB3197-047-Q1-M1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267069
BLAST score
                  596
E value
                  6.0e-62
Match length
                  110
% identity
                  99
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                  232165
                  LIB3197-047-Q1-M1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2119278
BLAST score
                  669
E value
                  1.0e-70
Match length
                  127
                  99
% identity
NCBI Description tubulin beta-1 chain - rice
Seq. No.
                  232166
Seq. ID
                  LIB3197-048-Q1-M1-A10
Method
                  BLASTX
NCBI GI
                  g1172872
BLAST score
                  338
```



Match length 102 % identity 67 CYSTEINE PROTEINASE RD19A PRECURSOR >gi 541856 pir JN0718 NCBI Description drought-inducible cysteine proteinase ( $\overline{\text{EC}}$  3.4. $\overline{22}$ .-) RD19A precursor - Arabidopsis thaliana >gi 435618 dbj BAA02373\_ (D13042) thiol protease [Arabidopsis thaliana] >gi\_4539328\_emb\_CAB38829.1\_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana] Seq. No. 232167 Seq. ID LIB3197-048-Q1-M1-B10 Method BLASTX NCBI GI q4539324 BLAST score 205 E value 4.0e-19 Match length 134 % identity 46 NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana] Seq. No. 232168 Seq. ID LIB3197-048-Q1-M1-B11 Method BLASTX NCBI GI g1155261 BLAST score 347 E value 8.0e-33 Match length 95 % identity 74 (U40217) eukaryotic release factor 1 homolog [Arabidopsis NCBI Description thaliana] Seq. No. 232169 Seq. ID LIB3197-048-Q1-M1-B4 Method BLASTX NCBI GI g2961300 BLAST score 517 E value 1.0e-52 107 Match length 93 % identity NCBI Description (AJ225027) ribosomal protein L24 [Cicer arietinum] Seq. No. 232170 Seq. ID LIB3197-048-Q1-M1-B5 Method BLASTX NCBI GI g3914097 BLAST score 191 E value 1.0e-14 68 Match length % identity 60 MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE (IMP) (INOSITOL NCBI Description MONOPHOSPHATASE) >gi 2708322 (AF037220) inositol monophosphatase [Mesembryanthemum crystallinum] 232171 Seq. No.

Seq. ID LIB3197-048-Q1-M1-B6

Method BLASTX NCBI GI g3522929 BLAST score 708



E value 4.0e-75 Match length 142 % identity 92

NCBI Description (AC002535) putative dTDP-glucose 4-6-dehydratase

[Arabidopsis thaliana] >gi\_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No. 232172

Seq. ID LIB3197-048-Q1-M1-C10

Method BLASTX
NCBI GI g120649
BLAST score 444
E value 8.0e-54
Match length 140
% identity 79

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER

>gi\_625203\_pir\_\_DEHUG3 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - human >gi\_182861 (M17851)
glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]

>gi\_182863 (J02642) glyceraldehyde 3-phosphate

dehydrogenase (EC 1.2.1.12) [Homo sapiens] >gi\_182977 (M33197) glyceraldehyde-3-phosphate dehydrogenase (EC

1.2.1.12) [Homo sapiens] >gi\_182981 (J04038)

glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]

>gi\_224880\_prf\_\_1203217A

dehydrogenase, glyceraldehydephosphate [Homo sapiens]

Seq. No. 232173

Seq. ID LIB3197-048-Q1-M1-C11

Method BLASTX
NCBI GI g2651303
BLAST score 230
E value 5.0e-19
Match length 101
% identity 59

NCBI Description (AC002336) putative potassium transporter [Arabidopsis

thaliana]

Seq. No. 232174

Seq. ID LIB3197-048-Q1-M1-C4

Method BLASTX
NCBI GI g3868758
BLAST score 460
E value 4.0e-46
Match length 113
% identity 74

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 232175

Seq. ID LIB3197-048-Q1-M1-D10

Method BLASTX
NCBI GI g3236237
BLAST score 403
E value 2.0e-39
Match length 124
% identity 61

NCBI Description (AC004684) putative ribotol dehydrogenase [Arabidopsis

Seq. No.

232181



## thaliana]

```
Seq. No.
                  232176
Seq. ID
                  LIB3197-048-Q1-M1-D11
Method
                  BLASTX
NCBI GI
                  g3894193
BLAST score
                  158
                  1.0e-10
E value
Match length
                  54
                  57
% identity
NCBI Description
                  (AC005662) putative strictosidine synthase [Arabidopsis
                  thaliana]
                  232177
Seq. No.
Seq. ID
                  LIB3197-048-Q1-M1-D6
Method
                  BLASTX
NCBI GI
                  q2894612
                  571
BLAST score
E value
                  4.0e-59
Match length
                  128
% identity
                  77
NCBI Description
                  (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                  232178
Seq. ID
                  LIB3197-048-Q1-M1-H1
Method
                  BLASTX
NCBI GI
                  g1658197
BLAST score
                   707
                  6.0e-75
E value
Match length
                  150
% identity
                  85
NCBI Description
                  (U74630) calreticulin [Ricinus communis] >gi_1763297
                   (U74631) calreticulin [Ricinus communis]
Seq. No.
                  232179
Seq. ID
                  LIB3197-048-Q1-M1-H2
Method
                  BLASTX
NCBI GI
                  g1296805
BLAST score
                  208
E value
                  1.0e-16
Match length
                  55
% identity
                  64
                  (X90929) C-terminal peptidase of the D1 protein [Hordeum
NCBI Description
                  vulgare]
Seq. No.
                  232180
Seq. ID
                  LIB3197-048-Q1-M1-H3
Method
                  BLASTX
NCBI GI
                  g2689030
BLAST score
                  196
E value
                  5.0e-15
Match length
                  121
% identity
                  40
                  (AF034568) RNA guanylyltransferase [Mus musculus]
NCBI Description
                  >gi_2697127 (AF025653) mRNA capping enzyme [Mus musculus]
```



```
Seq. ID
                  LIB3197-048-Q1-M1-H7
Method
                  BLASTX
NCBI GI
                   q3282505
BLAST score
                   202
                   8.0e-16
E value
Match length
                  134
% identity
                   45
NCBI Description
                  (AF020786) polyphenol oxidase precursor [Prunus armeniaca]
                  232182
Seq. No.
Seq. ID
                  LIB3197-048-Q1-M1-H9
Method
                  BLASTX
NCBI GI
                  g2129887
BLAST score
                  269
E value
                  1.0e-23
Match length
                  132
% identity
                   45
                  major inner envelope protein precursor, 96K, chloroplast -
NCBI Description
                  garden pea
Seq. No.
                  232183
Seq. ID
                  LIB3197-049-Q1-M1-A1
Method
                  BLASTX
NCBI GI
                  g3513738
BLAST score
                   327
E value
                   2.0e-30
Match length
                  91
                   69
% identity
NCBI Description
                   (AF080118) similar to the GDSL family of lipolytic enzymes
                   [Arabidopsis thaliana]
Seq. No.
                  232184
                  LIB3197-049-Q1-M1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2618689
BLAST score
                  364
E value
                   3.0e-35
                  78
Match length
                   90
% identity
NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]
                  232185
Seq. No.
Seq. ID
                  LIB3197-049-Q1-M1-A12
Method
                  BLASTX
NCBI GI
                  g4239845
BLAST score
                  478
E value
                  2.0e-48
Match length
                  101
                  92
% identity
NCBI Description (AB015855) transcription factor TEIL [Nicotiana tabacum]
                  232186
Seq. No.
Seq. ID
                  LIB3197-049-Q1-M1-A5
```

Method BLASTX
NCBI GI g4455323
BLAST score 280
E value 3.0e-25

NCBI Description

norvegicus]



```
Match length
                  72
% identity
NCBI Description
                  (AL035525) aminopeptidase-like protein [Arabidopsis
                  thaliana]
                  232187
Seq. No.
Seq. ID
                  LIB3197-049-Q1-M1-A7
Method
                  BLASTX
NCBI GI
                  g1213629
BLAST score
                  342
E value
                  4.0e-32
Match length
                  93
                  70
% identity
NCBI Description
                 (X95991) pectinesterase [Prunus persica]
                  232188
Seq. No.
                  LIB3197-049-Q1-M1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4567235
BLAST score
                  365
E value
                  8.0e-35
Match length
                  114
% identity
                  61
                  (AC007119) putative phosphatidylinositol/phophatidylcholine
NCBI Description
                  transfer protein [Arabidopsis thaliana]
Seq. No.
                  232189
                  LIB3197-049-Q1-M1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3668089
BLAST score
                  212
                  6.0e-17
E value
                  78
Match length
% identity
                  47
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
                  232190
Seq. No.
Seq. ID
                  LIB3197-049-Q1-M1-B2
Method
                  BLASTX
NCBI GI
                  g3738320
BLAST score
                  257
E value
                  4.0e-22
                  123
Match length
                  43
% identity
NCBI Description
                 (AC005170) putative cinnamoyl CoA reductase [Arabidopsis
                  thaliana]
                  232191
Seq. No.
                  LIB3197-049-Q1-M1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1477468
BLAST score
                  114
E value
                  7.0e-12
                  85
Match length
% identity
```

33437

(U35244) vacuolar protein sorting homolog r-vps33a [Rattus



```
232192
Seq. No.
Seq. ID
                  LIB3197-049-01-M1-B5
Method
                  BLASTX
NCBI GI
                  q1619297
                  483
BLAST score
                  7.0e-49
E value
Match length
                  92
                  97
% identity
                  (Y08490) alpha-tubulin 2 [Hordeum vulgare]
NCBI Description
                  232193
Seq. No.
                  LIB3197-049-Q1-M1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  a130696
                  452
BLAST score
                  2.0e-45
E value
                  89
Match length
                  97
% identity
NCBI Description
                  PLACENTAL PROTEIN 11 PRECURSOR (PP11)
                  >gi_107308_pir__A34614 placental protein 11 precursor -
                  human >gi_190211 (M32402) placental protein 11 (PP11)
                  precursor [Homo sapiens] >gi_190213 (M36109) placental
                  protein 11 [Homo sapiens]
                  232194
Seq. No.
                  LIB3197-049-Q1-M1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1619297
BLAST score
                   585
E value
                   1.0e-60
Match length
                   109
                   98
% identity
NCBI Description
                  (Y08490) alpha-tubulin 2 [Hordeum vulgare]
Seq. No.
                  232195
Seq. ID
                  LIB3197-049-Q1-M1-B9
Method
                  BLASTX
NCBI GI
                   q2791834
BLAST score
                   636
E value
                   1.0e-66
                   123
Match length
                   98
% identity
                  (AF041463) elongation factor 1-alpha [Manihot esculenta]
NCBI Description
                   232196
Seq. No.
Seq. ID
                  LIB3197-049-Q1-M1-C1
Method
                  BLASTX
                  g267069
NCBI GI
BLAST score
                   772
E value
                   1.0e-82
Match length
                   148
% identity
                   97
NCBI Description
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
                   tubulin alpha chain - Arabidopsis thaliana >gi 166914
```

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

(M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916

NCBI GI

BLAST score

g870726



```
Seq. No.
                  232197
Seq. ID
                  LIB3197-049-Q1-M1-C10
Method
                  BLASTX
NCBI GI
                  g529516
BLAST score
                  537
E value
                  3.0e-55
Match length
                  99
% identity
                  89
NCBI Description (L29099) beta-fructosidase [Solanum tuberosum]
Seq. No.
                  232198
Seq. ID
                  LIB3197-049-Q1-M1-C11
Method
                  BLASTX
NCBI GI
                  q541951
BLAST score
                  223
E value
                  1.0e-18
Match length
                  70
                  66
% identity
NCBI Description SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26
                  [Glycine max]
Seq. No.
                  232199
Seq. ID
                  LIB3197-049-Q1-M1-C7
Method
                  BLASTX
NCBI GI
                  q4490332
BLAST score
                  293
E value
                  2.0e-26
Match length
                  103
                  58
% identity
NCBI Description (AL035656) putative protein [Arabidopsis thaliana]
Seq. No.
                  232200
Seq. ID
                  LIB3197-049-Q1-M1-C8
Method
                  BLASTX
NCBI GI
                  g4101564
BLAST score
                  223
E value
                  3.0e-18
Match length
                  130
% identity
                  43
NCBI Description (AF004556) IFA-binding protein [Arabidopsis thaliana]
Seq. No.
                  232201
Seq. ID
                  LIB3197-049-Q1-M1-C9
Method
                  BLASTX
NCBI GI
                  g2244732
BLAST score
                  483
E value
                  9.0e-49
                  93
Match length
                  100
% identity
NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
Seq. No.
                  232202
                  LIB3197-049-Q1-M1-D12
Seq. ID
                  BLASTX
Method
```



```
E value
                   1.0e-29
                   84
Match length
                   76
% identity
NCBI Description
                   (L38260) biotin carboxylase subunit [Nicotiana tabacum]
                  >gi 1582354 prf 2118337A Ac-CoA carboxylase:SUBUNIT=biotin
                  carboxylase [Nicotiana tabacum]
Seq. No.
                   232203
Seq. ID
                  LIB3197-049-Q1-M1-D2
Method
                  BLASTX
NCBI GI
                  q3097321
BLAST score
                  196
E value
                   3.0e-15
                  88
Match length
% identity
                   44
NCBI Description (AB013289) Bd 30K [Glycine max]
Seq. No.
                  232204
Seq. ID
                  LIB3197-049-Q1-M1-D4
Method
                  BLASTX
NCBI GI
                  g3132696
BLAST score
                   436
E value
                  2.0e-43
Match length
                  98
% identity
                  85
NCBI Description (AF061962) SAR DNA-binding protein-1 [Pisum sativum]
Seq. No.
                  232205
Seq. ID
                  LIB3197-049-Q1-M1-D6
Method
                  BLASTX
NCBI GI
                  g133940
BLAST score
                  557
E value
                  2.0e-57
Match length
                  124
                  92
% identity
                  40S RIBOSOMAL PROTEIN S3A (S1A) >gi_70851_pir__R3XL3A
NCBI Description
                  ribosomal protein S3a - African clawed frog
                  >gi_65091_emb_CAA40592_ (X57322) ribosomal protein S1a
                  [Xenopus laevis]
Seq. No.
                  232206
Seq. ID
                  LIB3197-049-Q1-M1-D9
Method
                  BLASTX
NCBI GI
                  g4204300
BLAST score
                  188
                  3.0e-14
E value
Match length
                  72
% identity
```

NCBI Description

(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No. 232207

Seq. ID LIB3197-049-Q1-M1-E1

Method BLASTX NCBI GI g4220512 BLAST score 188 E value 4.0e-14 Match length 57

Match length

% identity

70



```
% identity
NCBI Description (AL035356) putative pectate lyase [Arabidopsis thaliana]
Seq. No.
                  232208
Seq. ID
                  LIB3197-049-Q1-M1-E11
Method
                  BLASTX
NCBI GI
                  g4508073
BLAST score
                  303
E value
                   9.0e-28
Match length
                  82
% identity
                   67
NCBI Description (AC005882) 43220 [Arabidopsis thaliana]
Seq. No.
                  232209
Seq. ID
                  LIB3197-049-Q1-M1-E4
Method
                  BLASTX
NCBI GI
                  g3080420
BLAST score
                  256
E value
                  3.0e-22
Match length
                  122
% identity
                  50
NCBI Description
                  (AL022604) putative sugar transporter protein [Arabidopsis
                  thaliana]
                  232210
Seq. No.
Seq. ID
                  LIB3197-049-01-M1-E5
Method
                  BLASTX
NCBI GI
                  q131770
BLAST score
                  284
E value
                  1.0e-25
Match length
                  80
% identity
                   65
NCBI Description
                 40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
                   (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3D024
                  ribosomal protein S9.e - slime mold (Dictyostelium
                  discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein
                   [Dictyostelium discoideum]
Seq. No.
                  232211
Seq. ID
                  LIB3197-049-Q1-M1-E6
Method
                  BLASTX
NCBI GI
                  g3319882
BLAST score
                  550
E value
                  1.0e-56
Match length
                  113
% identity
                  95
NCBI Description (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
                  arietinum]
Seq. No.
                  232212
Seq. ID
                  LIB3197-049-Q1-M1-E7
Method
                  BLASTX
NCBI GI
                  g3319882
BLAST score
                  337
E value
                  3.0e-32
```

Seq. ID Method



```
NCBI Description (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
                  arietinum]
                  232213
Seq. No.
Seq. ID
                  LIB3197-049-Q1-M1-F1
Method
                  BLASTX
NCBI GI
                  g3702339
BLAST score
                  149
E value
                  9.0e-10
Match length
                  55
% identity
                  62
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.
                  232214
                  LIB3197-049-Q1-M1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2842490
BLAST score
                  431
E value
                  1.0e-42
Match length
                  120
                  70
% identity
NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]
Seq. No.
                  232215
Seq. ID
                  LIB3197-049-Q1-M1-F4
Method
                  BLASTX
NCBI GI
                  g4510406
BLAST score
                  543
E value
                  9.0e-56
Match length
                  130
                  76
% identity
NCBI Description (AC006587) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  232216
Seq. ID
                  LIB3197-049-Q1-M1-F5
Method
                  BLASTX
NCBI GI
                  g2129499
BLAST score
                  289
E value
                  6.0e-26
                  52
Match length
                  100
% identity
NCBI Description fiber protein E6 (clone CKE6-4A) - upland cotton
                  >gi_1000086 (U30506) E6 [Gossypium hirsutum]
Seq. No.
                  232217
Seq. ID
                  LIB3197-049-Q1-M1-G5
Method
                  BLASTX
NCBI GI
                  g2558654
BLAST score
                  365
E value
                  7.0e-35
Match length
                  114
% identity
                  54
NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]
Seq. No.
                  232218
```

33442

LIB3197-049-Q1-M1-G6

BLASTX



```
NCBI GI
                   q4539292
BLAST score
                   406
E value
                   7.0e-40
Match length
                   85
% identity
                  (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   232219
Seq. ID
                   LIB3197-049-Q1-M1-G8
Method
                   BLASTX
NCBI GI
                   q3182981
BLAST score
                   298
E value
                   2.0e-27
Match length
                   80
                   72
% identity
NCBI Description CELL ELONGATION PROTEIN DIMINUTO >qi 1695692 dbj BAA13096
                   (D86494) diminuto [Pisum sativum]
Seq. No.
                   232220
Seq. ID
                   LIB3197-049-Q1-M1-G9
Method
                   BLASTX
NCBI GI
                   q267069
BLAST score
                   308
E value
                   2.0e-28
Match length
                   59
                   93
% identity
NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir__JQ1594
                   tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                   232221
Seq. ID
                   LIB3197-049-Q1-M1-H10
Method
                   BLASTX
NCBI GI
                   g3402279
BLAST score
                   462
E value
                   2.0e-46
Match length
                   94
                   91
% identity
NCBI Description (AJ000999) putative beta-subunit of K+ channels [Solanum
                   tuberosum]
                   232222
Seq. No.
Seq. ID
                   LIB3197-049-Q1-M1-H12
Method
                   BLASTX
NCBI GI
                   g4544443
BLAST score
                   459
E value
                   7.0e-46
                   145
Match length
% identity
                   29
NCBI Description (AC006592) putative mitochondrial uncoupling protein
                   [Arabidopsis thaliana]
Seq. No.
                   232223
Seq. ID
                   LIB3197-049-Q1-M1-H4
```

BLASTX

Method

E value

Match length

2.0e-20

90\_



```
q2130051
NCBI GI
BLAST score
                  344
E value
                  1.0e-32
Match length
                  92
                  67
% identity
NCBI Description
                  xylose isomerase (EC 5.3.1.5) - barley
                  >gi_1296807_emb_CAA64544_ (X95256) xylose isomerase
                  [Hordeum vulgare] >gi_1588664_prf__2209268A xylose
                  isomerase [Hordeum vulgare]
Seq. No.
                  232224
Seq. ID
                  LIB3197-050-Q1-M1-A11
Method
                  BLASTX
NCBI GI
                  q4102634
BLAST score
                  206
E value
                  3.0e-16
Match length
                  37
% identity
                  86
NCBI Description (AF014396) Snakin-1 [Solanum tuberosum]
Seq. No.
                  232225
                  LIB3197-050-Q1-M1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1684857
BLAST score
                  445
E value
                  1.0e-44
Match length
                  90
                  37
% identity
NCBI Description (U77940) polyubiquitin [Phaseolus vulgaris]
Seq. No.
                  232226
Seq. ID
                  LIB3197-050-Q1-M1-A2
Method
                  BLASTX
NCBI GI
                  g2586127
BLAST score
                  229
E value
                  5.0e-19
                  98
Match length
% identity
                  47
NCBI Description (U89510) b-keto acyl reductase [Hordeum vulgare]
Seq. No.
                  232227
Seq. ID
                  LIB3197-050-Q1-M1-A6
Method
                  BLASTX
NCBI GI
                  g3901272
BLAST score
                  472
E value
                  2.0e-47
Match length
                  122
                  77
% identity
NCBI Description (AF067656) ZW10 interactor Zwint [Homo sapiens]
Seq. No.
                  232228
Seq. ID
                  LIB3197-050-Q1-M1-A8
Method
                  BLASTX
NCBI GI
                  g2501490
BLAST score
                  241
```

BLAST score

E value

277

1.0e-24



```
% identity
                  FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVONOID
NCBI Description
                   3-O-GLUCOSYLTRANSFERASE) >gi 1620013 dbj BAA12737 (D85186)
                  UDP-glucose:flavonoid-3-glucosyltransferase [Gentiana
                  triflora]
Seq. No.
                  232229
Seq. ID
                  LIB3197-050-Q1-M1-B10
Method
                  BLASTX
NCBI GI
                  q475048
BLAST score
                  609
E value
                  2.0e-63
Match length
                  132
% identity
NCBI Description
                  (X72581) tonoplast intrinsic protein gamma (gamma-TIP)
                   [Arabidopsis thaliana]
                  232230
Seq. No.
Seq. ID
                  LIB3197-050-Q1-M1-B11
Method
                  BLASTX
NCBI GI
                  q870726
BLAST score
                  379
E value
                  2.0e-36
Match length
                  93
                  82
% identity
NCBI Description
                  (L38260) biotin carboxylase subunit [Nicotiana tabacum]
                  >gi_1582354_prf__2118337A Ac-CoA carboxylase:SUBUNIT=biotin
                  carboxylase [Nicotiana tabacum]
Seq. No.
                  232231
Seq. ID
                  LIB3197-050-Q1-M1-B12
Method
                  BLASTX
NCBI GI
                  g1351867
BLAST score
                  635
E value
                  2.0e-66
Match length
                  118
% identity
                  100
NCBI Description ACTIN, CYTOPLASMIC 1 (BETA-ACTIN) >gi 761724 (U20114)
                  beta-actin [Cricetulus griseus]
Seq. No.
                  232232
Seq. ID
                  LIB3197-050-Q1-M1-B3
Method
                  BLASTX
NCBI GI
                  g4538939
BLAST score
                  697
E value
                  8.0e-74
Match length
                  140
                  94
% identity
                  (AL049483) Col-0 casein kinase I-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  232233
Seq. ID
                  LIB3197-050-Q1-M1-B6
Method
                  BLASTX
NCBI GI
                  g3319921
```



```
Match length
% identity
NCBI Description
                   (AJ223388) Hev b 3 [Hevea brasiliensis]
                   >gi_3319923_emb_CAA11304_ (AJ223389) Hev b 3 [Hevea
brasiliensis] >gi_3319925_emb_CAA11305_ (AJ223390) Hev b 3
[Hevea brasiliensis] >gi_3818475 (AF051317) small rubber
                    particle protein [Hevea brasiliensis]
Seq. No.
                    232234
                   LIB3197-050-Q1-M1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g484656
                   476
BLAST score
                    7.0e-48
E value
Match length
                   145
                    63
% identity
NCBI Description monodehydroascorbate reductase (NADH) (EC 1.6.5.4) -
                    cucumber >gi_452165_dbj_BAA05408_ (D26392)
                   monodehydroascorbate reductase [Cucumis sativus]
Seq. No.
                    232235
Seq. ID
                   LIB3197-050-Q1-M1-B9
Method
                   BLASTX
NCBI GI
                   g1762945
BLAST score
                   237
E value
                    7.0e-20
                   79
Match length
                    59
% identity
NCBI Description (U66269) ORF; able to induce HR-like lesions [Nicotiana
                    tabacum]
Seq. No.
                    232236
Seq. ID
                   LIB3197-050-Q1-M1-C1
Method
                   BLASTX
                   q3970973
NCBI GI
BLAST score
                   379
E value
                    2.0e-36
Match length
                   140
% identity
                    51
NCBI Description
                   (AC004812) similar to human HsGCN1 U77700 (PID:g2282576);
                    similar to yeast translation activator GCN1 (PID:g462168)
                    [Homo sapiens]
Seq. No.
                    232237
Seq. ID
                   LIB3197-050-Q1-M1-C10
Method
                   BLASTX
NCBI GI
                    g584867
BLAST score
                    288
E value
                    7.0e-26
Match length
                   95
% identity
                   56
NCBI Description CYTOCHROME P450 77A2 (CYPLXXVIIA2) (P-450EG5)
                   >gi 481959 pir S40266 gene CYP77A2 protein - eggplant
                    >gi_542071_pir__S41598 cytochrome P450 77A2 - eggplant
```

melongena]

>gi 438241 emb CAA50646 (X71655) CYP77A2 [Solanum



98

% identity

NCBI Description

```
232238
Seq. No.
Seq. ID
                  LIB3197-050-Q1-M1-C11
Method
                  BLASTX
NCBI GI
                  g4210948
BLAST score
                  454
                  3.0e-45
E value
Match length
                  96
% identity
                  91
NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]
Seq. No.
                  232239
                  LIB3197-050-Q1-M1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3881649
BLAST score
                  478
E value
                  4.0e-48
Match length
                  89
                  90
% identity
NCBI Description
                  (Z70757) Similarity to yeast hypothetical protein PIR
                  accession number S52511; cDNA EST EMBL:D73067 comes from
                  this gene; cDNA EST EMBL: D74461 comes from this gene; cDNA
                  EST EMBL:D76044 comes from this gene; cDNA EST yk504c7.3
Seq. No.
                  232240
                  LIB3197-050-Q1-M1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4049341
BLAST score
                  331
E value
                  7.0e-31
Match length
                  142
% identity
                  46
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
Seq. No.
                  232241
Seq. ID
                  LIB3197-050-Q1-M1-C5
Method
                  BLASTX
NCBI GI
                  q267069
BLAST score
                  611
E value
                  1.0e-63
Match length
                  113
% identity
                  98
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                  232242
                  LIB3197-050-Q1-M1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267069
BLAST score
                  606
E value
                   4.0e-63
                  112
Match length
```

TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594

tubulin alpha chain - Arabidopsis thaliana > gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] > gi 166916

NCBI Description



(M84697) alpha-4 tubulin [Arabidopsis thaliana]

```
Seq. No.
                  232243
                  LIB3197-050-Q1-M1-C7
Seq. ID
                  BLASTX
Method
                  g135452
NCBI GI
                  599
BLAST score
E value
                  3.0e-62
Match length
                  118
% identity
                  92
                  TUBULIN BETA-1 CHAIN >gi 170060 (M21296) S-beta-1 tubulin
NCBI Description
                  [Glycine max]
                  232244
Seq. No.
                  LIB3197-050-Q1-M1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462760
BLAST score
                  141
E value
                  1.0e-08
Match length
                  41
% identity
NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  232245
                  LIB3197-050-Q1-M1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132944
BLAST score
                  616
E value
                  3.0e-64
Match length
                  122
                  91
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi 81658 pir JQ0772 ribosomal
NCBI Description
                  protein L3 (ARP2) - Arabidopsis thaliana >gi_806279
                   (M32655) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                  232246
                  LIB3197-050-Q1-M1-D1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2811278
BLAST score
                  555
E value
                  4.0e-57
Match length
                  133
                  77
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                  232247
Seq. ID
                  LIB3197-050-Q1-M1-D10
                  BLASTX
Method
NCBI GI
                  g3176709
BLAST score
                  159
E value
                  1.0e-10
                  133
Match length
                   32
% identity
```

33448

N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis

(AC002392) putative anthranilate

thaliana]



```
232248
Seq. No.
Seq. ID
                  LIB3197-050-Q1-M1-D12
Method
                  BLASTX
NCBI GI
                  g4210330
BLAST score
                  580
                  3.0e-60
E value
Match length
                  114
% identity
                  93
                 (AJ223802) 2-oxoglutarate dehydrogenase, El subunit
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  232249
                  LIB3197-050-Q1-M1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4467158
BLAST score
                  182
E value
                  2.0e-13
Match length
                  136
% identity
                  39
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
                  232250
Seq. No.
                  LIB3197-050-Q1-M1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2119935
BLAST score
                  726
                  3.0e-77
E value
Match length
                  143
                  99
% identity
NCBI Description translation initiation factor eIF-4A.15 - common tobacco
Seq. No.
                  232251
                  LIB3197-050-Q1-M1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115492
BLAST score
                  630
E value
                  6.0e-66
Match length
                  123
                  55
% identity
NCBI Description CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)
                  calmodulin-related protein [Petunia hybrida]
                  232252
Seq. No.
                  LIB3197-050-Q1-M1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2464905
BLAST score
                  310
                  2.0e-28
E value
                  120
Match length
                   54
% identity
NCBI Description (Z99708) minor allergen [Arabidopsis thaliana]
                  232253
Seq. No.
```

Seq. ID LIB3197-050-Q1-M1-E6

BLASTX Method NCBI GI g4063751 198 BLAST score



```
E value
                   3.0e-15
Match length
                  139
% identity
                   32
NCBI Description
                  (AC005851) putative white protein [Arabidopsis thaliana]
                  >gi_4510409_gb_AAD21495.1_ (AC006929) putative white
                  protein [Arabidopsis thaliana]
Seq. No.
                  232254
Seq. ID
                  LIB3197-050-Q1-M1-F1
Method
                  BLASTX
NCBI GI
                  q2738949
BLAST score
                  602
E value
                  1.0e-62
Match length
                  123
% identity
                  89
NCBI Description
                  (AF022213) cytosolic ascorbate peroxidase [Fragaria x
                  ananassa]
Seq. No.
                  232255
Seq. ID
                  LIB3197-050-Q1-M1-F10
Method
                  BLASTX
NCBI GI
                  q1771162
BLAST score
                  441
E value
                  7.0e-44
Match length
                  123
% identity ~
                  71
NCBI Description
                  (X98930) SBT2 [Lycopersicon esculentum]
                  >gi_3687307_emb_CAA07000 (AJ006379) subtilisin-like
                  protease [Lycopersicon esculentum]
Seq. No.
                  232256
Seq. ID
                  LIB3197-050-Q1-M1-F12
Method
                  BLASTX
NCBI GI
                  g3193288
BLAST score
                  531
E value
                  2.0e-54
Match length
                  135
                  70
% identity
NCBI Description
                  (AF069298) similar to bacterial and fungi pectinesterases
                  [Arabidopsis thaliana]
Seq. No.
                  232257
Seq. ID
                  LIB3197-050-Q1-M1-F2
Method
                  BLASTX
NCBI GI
                  g135406
BLAST score
                  597
E value
                  4.0e-62
Match length
                  116
                  96
% identity
NCBI Description
                  TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir_ A32712 tubulin
                  alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189)
                  alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)
                  alpha-5 tubulin [Arabidopsis thaliana]
```

Seq. No. 232258

Seq. ID LIB3197-050-Q1-M1-F3

Method BLASTX



```
NCBI GI
                   g135406
BLAST score
                   508
E value
                   1.0e-51
Match length
                   106
                   91
% identity
NCBI Description
                   TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi 99768 pir A32712 tubulin
                   alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)
                   alpha-5 tubulin [Arabidopsis thaliana]
Seq. No.
                   232259
Seq. ID
                   LIB3197-050-Q1-M1-F4
Method
                   BLASTX
NCBI GI
                   g2286153
BLAST score
                   587
E value
                   6.0e-61
Match length
                   120
% identity
                   98
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
Seq. No.
                   232260
Seq. ID
                   LIB3197-050-Q1-M1-F6
Method
                   BLASTX
NCBI GI
                   q1171642
BLAST score
                   387
E value
                   2.0e-37
Match length
                   131
% identity
                   60
NCBI Description
                  PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK
                   >gi 481206 pir S38326 protein kinase - Arabidopsis
                   thaliana >gi 166809 (L07248) protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   232261
Seq. ID
                   LIB3197-050-Q1-M1-F9
Method
                   BLASTX
NCBI GI
                   g1771162
BLAST score
                   201
E value
                   3.0e-16
Match length
                   69
% identity
                   58
NCBI Description
                   (X98930) SBT2 [Lycopersicon esculentum]
                   >gi_3687307_emb_CAA07000_ (AJ006379) subtilisin-like
                   protease [Lycopersicon esculentum]
Seq. No.
                   232262
Seq. ID
                   LIB3197-050-Q1-M1-G11
Method
                   BLASTX
NCBI GI
                   g1321627
BLAST score
                   317
E value
                   3.0e-29
Match length
                   85
% identity
NCBI Description
                   (D83656) thylakoid-bound ascorbate peroxidase [Cucurbita
```

Seq. No. 232263

sp.]



```
Seq. ID
                   LIB3197-050-Q1-M1-G5
Method
                  BLASTX
NCBI GI
                  q3024126
BLAST score
                   461
E value
                   7.0e-58
Match length
                  130
% identity
                   95
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine
                   synthetase 1 [Catharanthus roseus]
Seq. No.
                  232264
Seq. ID
                  LIB3197-050-01-M1-G9
Method
                  BLASTX
NCBI GI
                  g267082
BLAST score
                  435
E value
                   4.0e-43
Match length
                  109
% identity
                   77
NCBI Description TUBULIN BETA-8 CHAIN >gi_320189_pir__JQ1592 tubulin beta-8
                  chain - Arabidopsis thal\overline{i}ana >g\overline{i}_16\overline{69}08 (M84705) beta-8
                  tubulin [Arabidopsis thaliana]
Seq. No.
                  232265
Seq. ID
                  LIB3197-050-01-M1-H1
Method
                  BLASTX
NCBI GI
                  q3023751
BLAST score
                  156
E value
                  2.0e-10
Match length
                  72
                  51
% identity
NCBI Description
                  70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS
                   ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__$55383
                  peptidylprolyl isomerase (EC 5.2.1.8) - wheat
                   >gi_854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase
                   [Triticum aestivum]
Seq. No.
                  232266
Seq. ID
                  LIB3197-050-Q1-M1-H10
Method
                  BLASTX
NCBI GI
                  g4539333
BLAST score
                  216
E value
                  1.0e-17
Match length
                  107
% identity
                  44
NCBI Description (AL035539) putative amino acid transport protein
                   [Arabidopsis thaliana]
Seq. No.
                  232267
Seq. ID
                  LIB3197-050-Q1-M1-H11
Method
                  BLASTX
NCBI GI
                  g2498076
```

NCBI GI g2498076
BLAST score 425
E value 6.0e-42
Match length 90
% identity 91

NCBI Description NUCLEOSIDE DIPHOSPHATE KINASE (NDK) (NDP KINASE) >qi 1619958 (U72142) nucleoside diphosphate kinase [Helianthus annuus] Seq. No. 232268 Seq. ID LIB3197-050-Q1-M1-H12 Method BLASTX NCBI GI g1174621 BLAST score 340 E value 6.0e-32 Match length 104 64 % identity T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA) NCBI Description (CCT-THETA) >gi 1083259 pir JC4073 TCP-1 containing cytosolic chaperonin ( $\overline{\text{CCT}}$ )  $\overline{\text{theta}}$  chain - mouse >gi 695625 emb CAA85521 (Z37164) CCTtheta, theta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus] Seq. No. 232269 Seq. ID LIB3197-050-Q1-M1-H3 Method BLASTX NCBI GI q267069 BLAST score 596 6.0e-62 E value Match length 110 % identity 99 TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594 NCBI Description tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana] 232270 Seq. No. LIB3197-050-Q1-M1-H4 Seq. ID Method BLASTX NCBI GI g4185141 BLAST score 161 E value 4.0e-11 Match length 67 72 % identity NCBI Description (AC005724) putative calmodulin-binding protein [Arabidopsis thaliana] 232271 Seq. No.

Seq. ID LIB3197-050-Q1-M1-H8

Method BLASTX NCBI GI q1168750 BLAST score 152 E value 5.0e-10 Match length 63

% identity 49

CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY NCBI Description

SUBUNIT) >qi 458230 (U04380) calcineurin B [Naegleria

gruberi]

Seq. No. 232272

LIB3197-051-Q1-M1-A12 Seq. ID

Method BLASTX



```
NCBI GI
                  q4539435
BLAST score
                  336
                  2.0e-31
E value
Match length
                  137
                  57
% identity
                 (AL049523) putative protein [Arabidopsis thaliana]
NCBI Description
                  232273
Seq. No.
Seq. ID
                  LIB3197-051-Q1-M1-A3
Method
                  BLASTX
NCBI GI
                  g2384758
BLAST score
                  426
                  4.0e-42
E value
Match length
                  85
% identity
                  93
                  (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza
NCBI Description
                  sativa]
                  232274
Seq. No.
Seq. ID
                  LIB3197-051-Q1-M1-A5
Method
                  BLASTX
NCBI GI
                  q267069
BLAST score
                  401
E value
                  3.0e-39
Match length
                  73
% identity
                  99
NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
                  tubulin alpha chain - Arabidopsis thaliana > gi_1 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  232275
Seq. No.
Seq. ID
                  LIB3197-051-Q1-M1-B1
Method
                  BLASTX
NCBI GI
                  q135406
BLAST score
                  276
E value
                  3.0e-25
Match length
                  70
% identity
                  76
                  TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi 99768 pir A32712 tubulin
NCBI Description
                  alpha-5 chain - Arabidopsis thaliana >qi 166912 (M17189)
                  alpha-tubulin [Arabidopsis thaliana] >gi 166918 (M84698)
                  alpha-5 tubulin [Arabidopsis thaliana]
Seq. No.
                  232276
Seq. ID
                  LIB3197-051-Q1-M1-C1
Method
                  BLASTX
NCBI GI
                  q2384673
BLAST score
                  245
E value
                  8.0e-21
Match length
                  72
                  61
% identity
                  (AF012658) putative potassium transporter AtKT3p
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 232277

Seq. ID LIB3197-051-Q1-M1-C11

Method

NCBI GI

BLASTX

g2706450



```
Method
                  BLASTX
NCBI GI
                  q3236238
BLAST score
                  184
E value
                  9.0e-14
Match length
                  58
                  60
% identity
                 (AC004684) putative ARF1 GTPase activating protein
NCBI Description
                  [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_
                  (AB017876) Aspl [Arabidopsis thaliana]
Seq. No.
                  232278
Seq. ID
                  LIB3197-051-Q1-M1-C2
Method
                  BLASTX
NCBI GI
                  g115492
BLAST score
                  288
E value
                  1.0e-26
Match length
                  66
                  52
% identity
NCBI Description CALMODULIN-RELATED PROTEIN >gi_169205 (M80831)
                  calmodulin-related protein [Petunia hybrida]
                  232279
Seq. No.
Seq. ID
                  LIB3197-051-Q1-M1-C4
Method
                  BLASTX
NCBI GI
                  g82426
BLAST score
                  581
E value
                  3.0e-60
Match length
                  121
                  45
% identity
NCBI Description ubiquitin precursor - barley (fragment)
                  >gi_755763_emb_CAA27751_ (X04133) ubiquitin polyprecursor
                  (171 aa) [Hordeum vulgare]
Seq. No.
                  232280
Seq. ID
                  LIB3197-051-Q1-M1-C7
Method
                  BLASTX
NCBI GI
                  q2662343
BLAST score
                  594
E value
                  8.0e-62
Match length
                  113
% identity
                  100
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  232281
Seq. No.
Seq. ID
                  LIB3197-051-Q1-M1-D1
Method
                  BLASTX
NCBI GI
                  q4098128
BLAST score
                  359
                  2.0e-34
E value
Match length
                  98
                  75
% identity
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
                  232282
Seq. No.
                  LIB3197-051-Q1-M1-D10
Seq. ID
```



```
BLAST score 481
E value 2.0e-48
Match length 112
% identity 85
```

NCBI Description (AJ225172) magnesium dependent soluble inorganic

pyrophosphatase [Solanum tuberosum]

Seq. No. 232283

Seq. ID LIB3197-051-Q1-M1-D2

Method BLASTX
NCBI GI g2244749
BLAST score 433
E value 5.0e-43
Match length 88
% identity 93

NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 232284

Seq. ID LIB3197-051-Q1-M1-D4

Method BLASTX
NCBI GI g3687237
BLAST score 341
E value 3.0e-32
Match length 111
% identity 59

NCBI Description (AC005169) putative Cys3His zinc-finger protein

[Arabidopsis thaliana]

Seq. No. 232285

Seq. ID LIB3197-051-Q1-M1-D5

Method BLASTX
NCBI GI g1362086
BLAST score 372
E value 2.0e-38
Match length 124
% identity 73

NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi\_2129919\_pir\_\_\$65957

5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi 886471 emb CAA58474 (X83499) methionine synthase

[Catharanthus roseus]

Seq. No. 232286

Seq. ID LIB3197-051-Q1-M1-D6

Method BLASTX 93334115
BLAST score 194
E value 2.0e-27
Match length 83
% identity 78

NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)

(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi\_2463664 (AF006489) adénine nucleotide translocator 1 [Gossypium

hirsutum]



```
Seq. No.
                   232287
Seq. ID
                   LIB3197-051-Q1-M1-D9
Method
                   BLASTX
NCBI GI
                   q1531674
BLAST score
                   503
                   5.0e-54
E value
Match length
                   105
                   100
% identity
NCBI Description
                  (U68462) actin [Striga asiatica]
Seq. No.
                   232288
Seq. ID
                   LIB3197-051-Q1-M1-E12
Method
                   BLASTX
NCBI GI
                   q2980775
BLAST score
                   487
E value
                   4.0e-49
Match length
                   149
% identity
                   68
                   (AL022198) leucyl aminopeptidase - like protein (partial)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   23228 3
                   LIB3197-051-Q1-M1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2062167
BLAST score
                   345
E value
                   9.0e-33
Match length
                   103
% identity
                   64
NCBI Description
                   (AC001645) Proline-rich protein APG isolog [Arabidopsis
                   thaliana]
Seq. No.
                   232290
Seq. ID
                   LIB3197-051-Q1-M1-E4
Method
                   BLASTX
NCBI GI
                   g2129559
BLAST score
                   338
                   5.0e-32
E value
Match length
                   86
                   78
% identity
NCBI Description
                   cellulase homolog OR16pep - Arabidopsis thaliana
                   >gi_1022807 (U37702) cellulase [Arabidopsis thaliana]
>gi_3493633 (AF074092) cellulase [Arabidopsis thaliana]
                   >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana]
                   >gi 3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN
                   [Arabidopsis thaliana]
Seq. No.
                   232291
Seq. ID
                   LIB3197-051-Q1-M1-E6
Method
                   BLASTX
NCBI GI
                   q4510356
BLAST score
                   426
E value
                   5.0e-42
Match length
                   96
% identity
                   84
NCBI Description
                   (AC006921) putative kinesin-related protein TKRP125
```

33457

[Arabidopsis thaliana]

NCBI Description



```
Seq. No.
                    232292
 Seq. ID
                   LIB3197-051-Q1-M1-E8
 Method
                   {\tt BLASTX}
 NCBI GI
                   g2497753
 BLAST score
                    376
 E value
                    3.0e-36
 Match length
                   123
 % identity
                    55
 NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
                    >gi 1321915 emb CAA65477_{-} (X96716) lipid transfer protein
                    [Prunus dulcis]
                    232293
 Seq. No.
 Seq. ID
                   LIB3197-051-Q1-M1-F1
 Method
                   BLASTX
 NCBI GI
                   g3913366
 BLAST score
                   294
                    9.0e-27
 E value
                   94
 Match length
 % identity
                    61
 NCBI Description PUTATIVE RECEPTOR PROTEIN KINASE CRINKLY4 PRECURSOR
                   >gi_1597723 (U67422) CRINKLY4 precursor [Zea mays]
 Seq. No.
                   232294
 Seq. ID
                   LIB3197-051-Q1-M1-F10
 Method
                   BLASTX
 NCBI GI
                   g267069
 BLAST score
                   688
 E value
                   1.0e-72
 Match length
                   130
 % identity
                    98
 NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
                    tubulin alpha chain - Arabidopsis thaliana >gi 166914
                    (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                    (M84697) alpha-4 tubulin [Arabidopsis thaliana]
 Seq. No.
                    232295
 Seq. ID
                   LIB3197-051-Q1-M1-F11
 Method
                   BLASTX
 NCBI GI
                   q485742
 BLAST score
                    731
 E value
                    9.0e-78
 Match length
                   149
 % identity
 NCBI Description (L32791) pyrophosphatase [Beta vulgaris]
 Seq. No.
                   232296
 Seq. ID
                   LIB3197-051-Q1-M1-F12
 Method
                   BLASTX
 NCBI GI
                   g4580389
BLAST score
                   509
 E value
                   8.0e-52
 Match length
                   130
 % identity
                   73
```

(AC007171) unknown protein [Arabidopsis thaliana]

BLAST score



```
Seq. No.
                     232297
   Seq. ID
                     LIB3197-051-Q1-M1-F5
   Method
                     BLASTX
   NCBI GI
                     g3869088
BLAST score
                     611
  E value
                     1.0e-63
  Match length
                     117
   % identity
                     100
   NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
   Seq. No.
                     232298
   Seq. ID
                     LIB3197-051-Q1-M1-F6
   Method
                     BLASTX
  NCBI GI
                     g2738949
   BLAST score
                     278
  E value
                     3.0e-25
  Match length
                     68
                     78
   % identity
   NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x
                     ananassa]
  Seq. No.
                     232299
  Seq. ID
                     LIB3197-051-Q1-M1-F8
  Method
                     BLASTX
  NCBI GI
                     q3024501
  BLAST score
                     494
  E value
                     5.0e-50
  Match length
                     103
   % identity
                     93
  NCBI Description RAS-RELATED PROTEIN RAB11C >gi 1370146 emb CAA98179
                     (Z73951) RAB11C [Lotus japonicus]
  Seq. No.
                     232300
  Seq. ID
                     LIB3197-051-Q1-M1-G10
  Method
                     BLASTX
  NCBI GI
                     g1495273
  BLAST score
                     333
                     4.0e-31
  E value
  Match length
                     80
   % identity
                     81
  NCBI Description (Z50752) sugar transporter [Arabidopsis thaliana]
   Seq. No.
                     232301
   Seq. ID
                     LIB3197-051-Q1-M1-G11
  Method
                     BLASTX
  NCBI GI
                     g3341694
  BLAST score
                     516
  E value
                     1.0e-52
  Match length
                     130
   % identity
                     77
  NCBI Description (AC003672) PREG-like protein [Arabidopsis thaliana]
  Seq. No.
                     232302
  Seq. ID
                     LIB3197-051-Q1-M1-G12
  Method
                     BLASTX
  NCBI GI
                     q4337195
```



```
E value
                    1.0e-71
 Match length
                    143
 % identity
                    87
 NCBI Description (AC006403) putative protein kinase [Arabidopsis thaliana]
 Seq. No.
                    232303
                   LIB3197-051-Q1-M1-G4
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g4490310
 BLAST score
                    255
 E value
                    6.0e-37
 Match length
                    98
 % identity
                    83
 NCBI Description (AL035678) somatic embryogenesis receptor-like kinase-like
                   protein [Arabidopsis thaliana]
 Seq. No. Seq. ID
                    232304
                   LIB3197-051-Q1-M1-G6
 Method
                   BLASTX
 NCBI GI
                    g2613143
 BLAST score
                    227
 E value
                    7.0e-19
Match length
                   81
 % identity
                    62
 NCBI Description (AF030548) tubulin [Oryza sativa]
 Seq. No.
                    232305
 Seq. ID
                   LIB3197-051-Q1-M1-G7
 Method
                   BLASTX
 NCBI GI
                    g2613143
 BLAST score
                   208
 E value
                    1.0e-16
 Match length
                   60
 % identity
                   70
 NCBI Description (AF030548) tubulin [Oryza sativa]
 Seq. No.
                    232306
 Seq. ID
                   LIB3197-051-Q1-M1-H2
 Method
                   BLASTX
 NCBI GI
                   g2506139
 BLAST score
                   223
 E value
                    2.0e-18
 Match length
                   80
                    57
 % identity
 NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
                    (ARCHAIN) >gi_1314049_emb_CAA91901 (Z67962)
                   archain/delta-COP [Oryza sativa]
 Seq. No.
                   232307
 Seq. ID
                   LIB3197-051-Q1-M1-H3
 Method
                   BLASTX
 NCBI GI
                   g2662341
 BLAST score
                   570
 E value
                   5.0e-59
 Match length
                   110
 % identity
```

NCBI Description (D63580) EF-1 alpha [Oryza sativa]



>gi\_2662345\_dbj\_BAA23659\_ (D63582) EF-1 alpha [Oryza sativa] >gi\_2662347\_dbj\_BAA23660\_ (D63583) EF-1 alpha [Oryza sativa]

Seq. No. 232308

Seq. ID LIB3197-051-Q1-M1-H4

Method BLASTX
NCBI GI 94519262
BLAST score 354
E value 5.0e-34
Match length 98

% identity 55

NCBI Description (AB024276) vacuolar H+-ATPase c subunit [Citrus unshiu]

Seq. No. 232309

Seq. ID LIB3197-051-Q1-M1-H6

Method BLASTX
NCBI GI g1076668
BLAST score 354
E value 9.0e-34
Match length 98
% identity 68

NCBI Description NADH dehydrogenase (EC 1.6.99.3) - potato

>gi 639834 emb CAA58823 (X83999) NADH dehydrogenase

[Solanum tuberosum]

Seq. No. 232310

Seq. ID LIB3197-051-Q1-M1-H8

Method BLASTX
NCBI GI g2506139
BLAST score 323
E value 4.0e-30
Match length 82
% identity 77

NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)

(ARCHAIN) >gi 1314049 emb CAA91901 (Z67962)

archain/delta-COP [Oryza sativa]

Seq. No. 232311

Seq. ID LIB3197-051-Q1-M1-H9

Method BLASTX
NCBI GI g123620
BLAST score 423
E value 2.0e-48
Match length 111
% identity 89

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi 100224 pir S14950

heat shock cognate protein 70 - tomato

>gi\_19258\_emb\_CAA37971\_ (X54030) heat shock protein cognate

70 [Lycopersicon esculentum]

Seq. No. 232312

Seq. ID LIB3197-052-Q1-M1-A1

Method BLASTX
NCBI GI g1155261
BLAST score 401
E value 3.0e-39



```
Match length
% identity
NCBI Description
                  (U40217) eukaryotic release factor 1 homolog [Arabidopsis
                  thaliana]
                  232313
Seq. No.
                  LIB3197-052-Q1-M1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1174592
BLAST score
                  724
E value
                  5.0e-77
Match length
                  137
                  99
% identity
                  TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
NCBI Description
                   - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                  sativum]
                  232314
Seq. No.
                  LIB3197-052-Q1-M1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2662341
BLAST score
                  693
E válue
                  2.0e-73
Match length
                  133
                   98
% identity
NCBI Description
                  (D63580) EF-1 alpha [Oryza sativa]
                  >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza
                  sativa] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha
                   [Oryza sativa]
Seq. No.
                  232315
                  LIB3197-052-Q1-M1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1843527
BLAST score
                  491
E value
                  1.0e-49
                  129
Match length
                   44
% identity
NCBI Description (U73747) annexin [Gossypium hirsutum]
Seq. No.
                   232316
Seq. ID
                  LIB3197-052-Q1-M1-A5
                  BLASTX
Method
NCBI GI
                  g464849
BLAST score
                  628
E value
                  1.0e-65
                  142
Match length
                  88
% identity
NCBI Description TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha
                   chain - almond >gi 20413 emb CAA47635 (X67162)
                  alpha-tubulin [Prunus dulcis]
```

Seq. No. 232317

Seq. ID LIB3197-052-Q1-M1-A6

Method BLASTX NCBI GI g3757514 BLAST score 352



E value 2.0e-33 Match length 71 % identity 93

NCBI Description (AC005167) putative plasma membrane intrinsic protein

[Arabidopsis thaliana]

Seq. No. 232318

Seq. ID LIB3197-052-Q1-M1-A7

Method BLASTX
NCBI GI g1155261
BLAST score 379
E value 1.0e-36
Match length 85
% identity 88

NCBI Description (U40217) eukaryotic release factor 1 homolog [Arabidopsis

thaliana]

Seq. No. 232319

Seq. ID LIB3197-052-Q1-M1-A8

Method BLASTX
NCBI GI g1703129
BLAST score 544
E value 6.0e-56
Match length 103
% identity 98

NCBI Description ACTIN 11 >gi 2129522 pir \$68109 actin 11 - Arabidopsis

thaliana >gi 1002533 (U27981) actin-11 [Arabidopsis

thaliana]

Seq. No. 232320

Seq. ID LIB3197-052-Q1-M1-B1

Method BLASTX
NCBI GI g3874433
BLAST score 220
E value 7.0e-18
Match length 106
% identity 42

NCBI Description (Z81038) predicted using Genefinder; Similarity to Yeast

ABD1 protein (SW:P32783); cDNA EST EMBL:T01105 comes from

this gene [Caenorhabditis elegans]

Seq. No. 232321

Seq. ID LIB3197-052-Q1-M1-B12

Method BLASTX
NCBI GI g2104681
BLAST score 359
E value 3.0e-34
Match length 132
% identity 60

NCBI Description (X97907) transcription factor [Vicia faba]

Seq. No. 232322

Seq. ID LIB3197-052-Q1-M1-B3

Method BLASTX
NCBI GI g2832643
BLAST score 167
E value 1.0e-11

NCBI Description



```
Match length
                  64
% identity
                  58
NCBI Description (AL021710) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  232323
                  LIB3197-052-Q1-M1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3152613
BLAST score
                  286
E value
                  1.0e-25
Match length
                  144
                  36
% identity
NCBI Description (AC004482) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  232324
                  LIB3197-052-Q1-M1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2739168
BLAST score
                  360
E value
                  3.0e-34
Match length
                  129
% identity
                  57
                  (AF032386) aldose-1-epimerase-like protein [Nicotiana
NCBI Description
                  tabacum]
                  232325
Seq. No.
                  LIB3197-052-Q1-M1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3046731
BLAST score
                  219
E value
                  9.0e-18
                  53
Match length
                  87
% identity
NCBI Description (AJ005373) protein kinase [Craterostigma plantagineum]
                  232326
Seq. No.
Seq. ID
                  LIB3197-052-Q1-M1-B8
                  BLASTX
Method
NCBI GI
                  q1351014
BLAST score
                  356
E value
                  7.0e-34
                  72
Match length
                   93
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj BAA07207 (D38010)
                  ribosomal protein S8 [Oryza sativa]
                  232327
Seq. No.
Seq. ID
                  LIB3197-052-Q1-M1-C1
                  BLASTX
Method
NCBI GI
                  q1724102
BLAST score
                  469
E value
                   5.0e-47
Match length
                  121
                   78
% identity
```

[Mesembryanthemum crystallinum]

(U79766) S-adenosyl-L-homocystein hydrolase; SAH



```
Seq. No.
                  232328
Seq. ID
                  LIB3197-052-Q1-M1-C10
Method
                  BLASTX
NCBI GI
                  g267069
BLAST score
                  475
                  7.0e-48
E value
Match length
                  93
% identity
                  95
NCBI Description
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                  232329
                  LIB3197-052-Q1-M1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1632831
BLAST score
                  633
E value
                  2.0e-66
Match length
                  135
% identity
                  93
NCBI Description (Z49698) orf [Ricinus communis]
Seq. No.
                  232330
Seq. ID
                  LIB3197-052-Q1-M1-C4
Method
                  BLASTX
NCBI GI
                  q3334113
BLAST score
                  466
E value
                  1.0e-46
Match length
                  89
% identity
                  100
NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >gi 1006831 (U35015)
                  acyl-CoA-binding protein [Gossypium hirsutum]
Seq. No.
                  232331
Seq. ID
                  LIB3197-052-Q1-M1-C8
Method
                  BLASTX
NCBI GI
                  q2102696
BLAST score
                  254
E value
                  8.0e-22
Match length
                  146
% identity
                  40
                  (U72761) karyopherin beta 3 [Homo sapiens]
NCBI Description
                  >gi_4504909_ref_NP_002262.1_pKPNB3_ karyopherin (importin)
                  beta
                  232332
Seq. No.
Seq. ID
                  LIB3197-052-Q1-M1-C9
Method
                  BLASTX
NCBI GI
                  g730463
BLAST score
                  322
E value
                  8.0e-30
Match length
                  105
                  59
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
```

>gi\_630323\_pir\_\_S44069 ribosomal protein L35a.e.c15 - yeast
(Saccharomyces cerevisiae) >gi 484241 (L23923) ribosomal



protein L37 [Saccharomyces cerevisiae]
>gi\_1420537\_emb\_CAA99454\_ (Z75142) ORF YOR234c
[Saccharomyces cerevisiae]

Seq. No. 232333

Seq. ID LIB3197-052-Q1-M1-D1

Method BLASTX
NCBI GI g2995953
BLAST score 282
E value 3.0e-25
Match length 85
% identity 64

NCBI Description (AF053565) glutaredoxin I [Mesembryanthemum crystallinum]

Seq. No. 232334

Seq. ID LIB3197-052-Q1-M1-D11

Method BLASTX
NCBI GI g2062167
BLAST score 489
E value 2.0e-49
Match length 105
% identity 86

NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis

thaliana]

Seq. No. 232335

Seq. ID LIB3197-052-Q1-M1-D2

Method BLASTX
NCBI GI g3176690
BLAST score 580
E value 4.0e-60
Match length 133
% identity 80

NCBI Description (AC003671) Similar to ubiquitin ligase gb D63905 from S.

cerevisiae. EST gb R65295 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 232336

Seq. ID LIB3197-052-Q1-M1-D3

Method BLASTX
NCBI GI g1361155
BLAST score 150
E value 1.0e-09
Match length 66
% identity 53

NCBI Description hypothetical protein o215b - Escherichia coli >gi\_537235

(U14003) Kenn Rudd identifies as gpmB [Escherichia coli] >gi 1790856 (AE000509) phosphoglyceromutase 2 [Escherichia

coli]

Seq. No. 232337

Seq. ID LIB3197-052-Q1-M1-E1

Method BLASTX
NCBI GI g2190419
BLAST score 187
E value 5.0e-14
Match length 54

% identity NCBI Description (Y13632) dem [Lycopersicon esculentum] Seq. No. 232338 Seq. ID LIB3197-052-Q1-M1-E10 Method BLASTX NCBI GI g113944 532 BLAST score E value 2.0e-54 Match length 108 % identity 58 NCBI Description ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9) (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN) >gi\_71756\_pir\_\_LUHU annexin I - human
>gi\_34388\_emb\_CAA29338\_ (X05908) lipocortin (AA 1-346) [Homo sapiens] >gi 224956 prf 1204261A lipocortin [Homo sapiens] >gi 4502101 ref  $\overline{\text{NP}}$  000691.1 pANX1 annexin I (lipocortin  $\overline{I}$ )

Seq. No. 232339

Seq. ID LIB3197-052-Q1-M1-E11 Method BLASTX NCBI GI g4455202

NCBI GI g4455202
BLAST score 259
E value 2.0e-22
Match length 101
% identity 52
NCBI Description (AL03544

NCBI Description (AL035440) putative APG protein [Arabidopsis thaliana]

Seq. No. 232340

Seq. ID LIB3197-052-Q1-M1-E12

Method BLASTX
NCBI GI g2342682
BLAST score 436
E value 3.0e-43
Match length 112
% identity 79

NCBI Description (AC000106) Contains similarity to Rattus AMP-activated protein kinase (gb X95577). [Arabidopsis thaliana]

Seq. No. 232341

Seq. ID LIB3197-052-Q1-M1-E2

Method BLASTX
NCBI GI g267069
BLAST score 596
E value 6.0e-62
Match length 110
% identity 99

NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi\_166914

(M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 232342

Seq. ID LIB3197-052-Q1-M1-E4

Method BLASTX NCBI GI g1732511



```
BLAST score
                   420
E value
                   3.0e-41
                   96
Match length
                   81
% identity
NCBI Description (U62742) Ran binding protein 1 homolog [Arabidopsis
                   thaliana]
Seq. No.
                   232343
Seq. ID
                   LIB3197-052-Q1-M1-E6
Method
                   BLASTX
NCBI GI
                   g3075398
BLAST score
                   460
E value
                   5.0e-46
Match length
                   146
                   58
% identity
NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]
Seq. No.
                   232344
Seq. ID
                   LIB3197-052-Q1-M1-E8
Method
                   BLASTX
NCBI GI
                   g3925703
BLAST score
                   556
E value
                   3.0e-57
Match length
                   122
% identity
                   89
NCBI Description (X95905) 14-3-3 protein [Lycopersicon esculentum]
Seq. No.
                   232345
Seq. ID
                   LIB3197-052-Q1-M1-E9
Method
                   BLASTX
NCBI GI
                   g113944
BLAST score
                   607
E value
                   3.0e-63
Match length
                   125
% identity
                   60
NCBI Description ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9)
                   (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN)
                   >gi_71756_pir LUHU annexin I - human
                   >gi_34388_emb_CAA29338_ (X05908) lipocortin (AA 1-346)
                   [Homo sapiens] >gi 224956 prf 1204261A lipocortin [Homo
                   sapiens] >gi_4502101_ref_NP_000691.1_pANX1_ annexin I
                   (lipocortin \overline{I})
Seq. No.
                   232346
Seq. ID
                   LIB3197-052-Q1-M1-F10
Method
                   BLASTX
NCBI GI
                   g1362086
BLAST score
                   616
E value
                   3.0e-64
Match length
                   125
```

% identity

NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi\_2129919 pir S65957

5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi\_886471\_emb\_CAA58474\_ (X83499) methionine synthase



## [Catharanthus roseus]

```
Seq. No.
                  232347
Seq. ID
                  LIB3197-052-Q1-M1-F11
Method
                  BLASTX
NCBI GI
                  g3128175
BLAST score
                  142
E value
                  7.0e-09
                  88
Match length
% identity
                  36
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                  232348
Seq. ID
                  LIB3197-052-Q1-M1-F2
Method
                  BLASTX
NCBI GI
                  q2130073
BLAST score
                  524
E value
                  2.0e-53
Match length
                  122
% identity
                  85
NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
                  cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
                  C-1 [Oryza sativa] >gi_790970_dbj_BAA08830 (D50301)
                  aldolase C-1 [Oryza sativa]
Seq. No.
                  232349
Seq. ID
                  LIB3197-052-Q1-M1-F3
Method
                  BLASTX
NCBI GI
                  g2130073
BLAST score
                  330
E value
                  7.0e-31
Match length
                  85
% identity
                  80
                  fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
NCBI Description
                  cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
                  C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301)
                  aldolase C-1 [Oryza sativa]
Seq. No.
                  232350
Seq. ID
                  LIB3197-052-Q1-M1-F5
Method
                  BLASTX
NCBI GI
                  g4455192
BLAST score
                  380
E value
                  1.0e-36
Match length
                  140
% identity
                  38
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  232351
Seq. ID
                  LIB3197-052-Q1-M1-F6
Method
                  BLASTX
NCBI GI
                  g425194
BLAST score
                  573
E value
                  3.0e-59
Match length
                  121
% identity
```

NCBI Description (L26243) heat shock protein [Spinacia oleracea] >gi 2660772



(AF034618) cytosolic heat shock 70 protein [Spinacia oleracea]

Seq. No. 232352 Seq. ID LIB3197-052-Q1-M1-F7 Method BLASTX NCBI GI q1890281 BLAST score 336 E value 2.0e-31 Match length 103 % identity 22

NCBI Description (U89984) transformation-sensitive protein homolog

[Acanthamoeba castellanii]

Seq. No. 232353

Seq. ID LIB3197-052-Q1-M1-F8

Method BLASTX
NCBI GI g1771780
BLAST score 492
E value 7.0e-50
Match length 125
% identity 82

NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]

Seq. No. 232354

Seq. ID LIB3197-052-Q1-M1-F9

Method BLASTX
NCBI GI g2827621
BLAST score 411
E value 3.0e-40
Match length 98
% identity 79

NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 232355

Seq. ID LIB3197-052-Q1-M1-G10

Method BLASTX
NCBI GI 94006893
BLAST score 288
E value 5.0e-26
Match length 60
% identity 92

NCBI Description (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No. 232356

Seq. ID LIB3197-052-Q1-M1-G12

Method BLASTX
NCBI GI g559713
BLAST score 216
E value 2.0e-17
Match length 108
% identity 40

NCBI Description (D38552) The ha1539 protein is related to cyclophilin.

[Homo sapiens]

Seq. No. 232357

Seq. ID LIB3197-052-Q1-M1-G4



```
BLASTX
Method
NCBI GI
                  q4455158
                  709
BLAST score
E value
                  3.0e-75
                  145
Match length
                  87
% identity
                  (AL021687) kinase-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  232358
                  LIB3197-052-Q1-M1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2811278
                  555
BLAST score
                  4.0e-57
E value
Match length
                  133
                   77
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
                  232359
Seq. No.
Seq. ID
                  LIB3197-052-Q1-M1-H1
Method
                  BLASTX
NCBI GI
                  g3212877
BLAST score
                  261
E value
                   4.0e-39
                  100
Match length
                   80
% identity
NCBI Description (AC004005) Lea-like protein [Arabidopsis thaliana]
                   232360
Seq. No.
                   LIB3197-052-Q1-M1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2369714
BLAST score
                   636
E value
                   1.0e-66
Match length
                   133
% identity
                   94
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]
                   232361
Seq. No.
                   LIB3197-052-Q1-M1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2584721
BLAST score
                   540
                   1.0e-55
E value
                  110
Match length
% identity
                   88
NCBI Description (Y10157) sulfite reductase [Arabidopsis thaliana]
                   232362
Seq. No.
Seq. ID
                   LIB3197-053-Q1-M1-A11
Method
                   BLASTX
NCBI GI
                   g4544399
BLAST score
                   380
                   1.0e-36
E value
Match length
                  145
% identity
```

NCBI GI

E value

BLAST score

Match length

q2244806

1.0e-43

439

94



## thaliana]

```
232363
Seq. No.
                   LIB3197-053-Q1-M1-A2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q464734
BLAST score
                   357
                   3.0e-59
E value
Match length
                   132
                   82
% identity
                   ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                   HYDROLASE) (ADOHCYASE) >gi_481237_pir__S38379
adenosylhomocysteinase (EC 3.3.1.1) - Madagascar periwinkle
                   >gi_407412_emb_CAA81527_ (Z26881) S-adenosyl-L-homocysteine
                   hydrolase [Catharanthus roseus]
                   232364
Seq. No.
Seq. ID
                   LIB3197-053-Q1-M1-A3
Method
                   BLASTX
NCBI GI
                   q1749546
                   223
BLAST score
                   4.0e-18
E value
Match length
                   98
% identity
                   52
                  (D89169) similar to Saccharomyces cerevisiae SCD6 protein,
NCBI Description
                   SWISS-PROT Accession Number P45978 [Schizosaccharomýces
                   pombe]
                   232365
Seq. No.
Seq. ID
                   LIB3197-053-Q1-M1-A4
Method
                   BLASTX
NCBI GI
                   g3023847
                   600
BLAST score
E value
                   2.0e-62
Match length
                   132
% identity
                   46
                   GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                   PROTEIN >qi 2385376 emb CAA69934 (Y08678) G protein beta
                   subunit-like [Medicago sativa]
                   232366
Seq. No.
Seq. ID
                   LIB3197-053-Q1-M1-A6
                   BLASTX
Method
NCBI GI
                   g2792364
BLAST score
                   148
                   2.0e-09
E value
                   150
Match length
                   26
% identity
NCBI Description (AF040964) unknown protein IT1 [Homo sapiens]
                   232367
Seq. No.
                   LIB3197-053-Q1-M1-A8
Seq. ID
Method
                   BLASTX
```

E value

Match length

2.0e-26



```
% identity
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   232368
                   LIB3197-053-Q1-M1-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2494905
BLAST score
                   220
E value
                   8.0e-18
                   126
Match length
% identity
                   41
                  MICROTUBULE-ASSOCIATED PROTEIN YTM1 >qi 2132107 pir S67174
NCBI Description
                   hypothetical protein YOR272w - yeast (Saccharomyces
                   cerevisiae) >gi_1279699_emb_CAA61778_ (X89633) hypothetical
                   protein [Saccharomyces cerevisiae]
                   >gi_1420610_emb_CAA99497_ (Z75180) ORF YOR272w [Saccharomyces cerevisiae] >gi_1928989 (U92821)
                   microtubule-associated protein [Saccharomyces cerevisiae]
Seq. No.
                   232369
                   LIB3197-053-Q1-M1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4204695
BLAST score
                   276
                   1.0e-24
E value
Match length
                   118
% identity
                   53
                  (AF117062) putative inositol polyphosphate 5-phosphatase
NCBI Description
                   At5P1 [Arabidopsis thaliana]
Seq. No.
                   232370
                   LIB3197-053-Q1-M1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3355486
BLAST score
                   384
E value
                   4.0e-37
                   124
Match length
% identity
                   63
NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]
Seq. No.
                   232371
                   LIB3197-053-Q1-M1-B6
Seq. ID
Method
                   BLASTX
                   g2983325
NCBI GI
BLAST score
                   142
                   1.0e-08
E value
Match length
                   81
% identity
NCBI Description (AE000705) hypothetical protein [Aquifex aeolicus]
Seq. No.
                   232372
                   LIB3197-053-Q1-M1-C2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1705678
BLAST score
                   291
```

Match length

% identity

134



```
% identity
                   CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
NCBI Description
                   PROTEIN HOMOLOG) (VCP) >gi 862480 (U20213)
                   valosin-containing protein [Glycine max]
                   232373
Seq. No.
                   LIB3197-053-Q1-M1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2244734
                   258
BLAST score
E value
                   1.0e-22
                   57
Match length
                   89
% identity
NCBI Description (D88414) actin [Gossypium hirsutum]
Seq. No.
                   232374
                   LIB3197-053-Q1-M1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3914468
BLAST score
                   437
                   2.0e-43
E value
                   112
Match length
% identity
                   79
NCBI Description 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
                   >gi_478411_pir__JQ2257 nuclear antigen 21D7 - carrot >gi_217911_dbj_BAA02696_ (D13434) 21D7 antigen [Daucus
                   carota]
                   232375
Seq. No.
                   LIB3197-053-Q1-M1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2789660
BLAST score
                   224
E value
                   1.0e-18
Match length
                   74
% identity
                   64
NCBI Description (AF040102) p105 [Arabidopsis thaliana]
                   232376
Seq. No.
Seq. ID
                   LIB3197-053-Q1-M1-C7
Method
                   BLASTX
NCBI GI
                   g4220535
                   152
BLAST score
                   6.0e-18
E value
Match length
                   121
% identity
                   54
NCBI Description (AL035356) clathrin coat assembly like protein [Arabidopsis
                   thaliana]
                   232377
Seq. No.
                   LIB3197-053-Q1-M1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3834321
BLAST score
                   439
E value
                   1.0e-43
```

% identity

74

NCBI Description porin, plastid - garden pea



```
(AC005679) Strong similarity to F13P17.9 gi 3337356
NCBI Description
                  transport protein SEC61 alpha subunit homolog from
                  Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis
                  thaliana]
                  232378
Seq. No.
                  LIB3197-053-Q1-M1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3608171
                  394
BLAST score
E value
                  2.0e-38
Match length
                  112
% identity
                  73
                  (D86306) proton-translocating inorganic pyrophosphatase
NCBI Description
                  [Cucurbita moschata]
                  232379
Seq. No.
                  LIB3197-053-Q1-M1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914007
                  280
BLAST score
                  2.0e-25
E value
Match length
                  62
                  87
% identity
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi 1848291
                  (U88087) LON protease homolog [Arabidopsis thaliana]
                  232380
Seq. No.
                  LIB3197-053-Q1-M1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                  558
                  1.0e-57
E value
Match length
                  109
% identity
                  99
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  232381
Seq. No.
                  LIB3197-053-Q1-M1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244826
BLAST score
                  654
E value
                  1.0e-68
Match length
                  148
% identity
                  81
NCBI Description (Z97336) replication control protein homolog [Arabidopsis
                 "thaliana]
Seq. No.
                   232382
                  LIB3197-053-Q1-M1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g625990
BLAST score
                  141
E value
                   7.0e-09
Match length
                  35
```

% identity

94



```
232383
Seq. No.
Seq. ID
                  LIB3197-053-Q1-M1-E7
Method
                  BLASTX
NCBI GI
                  g129916
BLAST score
                  714
E value
                  9.0e-76
Match length
                  152
                  93
% identity
                 PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi 66911 pir TVWTGY
NCBI Description
                  phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                  >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                  (AA 1 - 401) [Triticum aestivum]
Seq. No.
                  232384
Seq. ID
                  LIB3197-053-Q1-M1-F11
Method
                  BLASTX
NCBI GI
                  g2281094
BLAST score
                  463
E value
                  2.0e-46
Match length
                  124
                  70
% identity
                  (AC002333) molybdenum cofactor biosynthesis protein E
NCBI Description
                  isolog [Arabidopsis thaliana] >gi 4469121 emb CAB38428
                  (AJ133519) molybdopterin synthase large subunit
                  [Arabidopsis thaliana]
Seq. No.
                  232385
Seq. ID
                  LIB3197-053-Q1-M1-F12
Method
                  BLASTX
NCBI GI
                  g2583108
BLAST score
                  567
E value
                  2.0e-58
Match length
                  152
                  76
% identity
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]
                  232386
Seq. No.
Seq. ID
                  LIB3197-053-Q1-M1-F2
Method
                  BLASTX
NCBI GI
                  g1332411
BLAST score
                  270
E value
                  2.0e-24
Match length
                  56
% identity
                  91
NCBI Description (D85102) dihydroflavonol 4-reductase [Rosa hybrida]
                  232387
Seq. No.
Seq. ID
                  LIB3197-053-Q1-M1-F4
Method
                  BLASTX
NCBI GI
                  q417060
BLAST score
                  626
E value
                  2.0e-65
Match length
                  121
```

LIGASE) (GS) >gi 170637 (M94765) glutamine synthetase

NCBI Description GLUTAMINE SYNTHETASE NODULE ISOZYME (GLUTAMATE--AMMONIA

Match length

% identity

143

93



[Vigna aconitifolia] >gi\_1094850\_prf\_\_2106409A Gln synthetase [Vigna aconitifolia]

```
Seq. No.
                   232388
                   LIB3197-053-Q1-M1-F5
Seq. ID
Method
                   BLASTX
                   q462013
NCBI GI
                   391
BLAST score
E value
                   6.0e-38
                   121
Match length
% identity
NCBI Description
                   ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
                   >gi_542022_pir__S39558 HSP90 homolog - Madagascar periwinkle >gi_348696 (L14594) heat shock protein 90
                   [Catharanthus roseus]
                   232389
Seq. No.
                   LIB3197-053-Q1-M1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2661422
                   143
BLAST score
                   6.0e-09
E value
Match length
                   39
                   77
% identity
                   (AJ001342) Putative S-phase-specific ribosomal protein
NCBI Description
                    [Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_
                    (AL023094) Putative S-phase-specific ribosomal protein
                    [Arabidopsis thaliana]
                   232390
Seq. No.
Seq. ID
                   LIB3197-053-Q1-M1-F7
                   BLASTX
Method
NCBI GI
                   g2791834
BLAST score
                   487
E value
                   3.0e-49
Match length
                   95
                   99
% identity
NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta]
Seq. No.
                   232391
                   LIB3197-053-Q1-M1-G2
Seq. ID
Method
                   BLASTX
                   g1657948
NCBI GI
                   472
BLAST score
E value
                    2.0e-47
Match length
                   117
% identity
                    80
                   (U73466) MipC [Mesembryanthemum crystallinum]
NCBI Description
                    232392
Seq. No.
Seq. ID
                   LIB3197-053-Q1-M1-G4
                   BLASTX
Method
NCBI GI
                   g3493172
BLAST score
                   683
E value
                    4.0e-72
```

% identity

NCBI Description

65



```
NCBI Description (U89609) fiber annexin [Gossypium hirsutum]
                   232393
Seq. No.
Seq. ID
                   LIB3197-053-Q1-M1-G6
Method
                   BLASTX
NCBI GI
                   g2118231
BLAST score
                   578
                   8.0e-60
E value
Match length
                   149
                   79
% identity
NCBI Description
                   H+-transporting ATPase (EC 3.6.1.35) AHA10 - Arabidopsis
                   thaliana >gi_765354_bbs_157347 (S74033) plasma membrane
                   H(+)-ATPase isoform AHA10=P-type ATPase [Arabidopsis
                   thaliana, cv. Columbia, Peptide, 946 aa] [Arabidopsis
                   thaliana]
                   232394
Seq. No.
                   LIB3197-053-Q1-M1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3264759
BLAST score
                   562
E value
                   6.0e-58
Match length
                   127
                   87
% identity
NCBI Description (AF071889) 40S ribosomal protein S8 [Prunus armeniaca]
Seq. No.
                   232395
                   LIB3197-053-Q1-M1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g464846
BLAST score
                   645
E value
                   1.0e-67
Match length
                   145
% identity
                   TUBULIN ALPHA-6 CHAIN >gi_322880_pir__S28983 tubulin alpha-6 chain - maize >gi_22158_emb_CAA44863_ (X63178)
NCBI Description
                   alpha-tubulin #6 [Zea mays]
                   232396
Seq. No.
Seq. ID
                   LIB3197-053-Q1-M1-H12
Method
                   BLASTX
NCBI GI
                   g4262140
BLAST score
                   336
E value
                   2.0e-31
Match length
                   95
% identity
                   72
NCBI Description (AC005275) putative C-type U1 snRNP [Arabidopsis thaliana]
                   232397
Seq. No.
Seq. ID
                   LIB3197-053-Q1-M1-H5
Method
                   BLASTX
NCBI GI
                   g2462741
BLAST score
                   281
E value
                   2.0e-42
Match length
                   136
```

(AC002292) Highly similar to auxin-induced protein



```
(aldo/keto reductase family) [Arabidopsis thaliana]
```

```
Seq. No.
                    232398
  Seq. ID
                    LIB3197-053-Q1-M1-H7
 Method
                    BLASTX
 NCBI GI
                    g1498053
 BLAST score
                    122
                    4.0e-13
 E value
 Match length
                    87
  % identity
                    56
 NCBI Description (U64436) ribosomal protein S8 [Zea mays]
  Seq. No.
                    232399
                    LIB3197-054-Q1-M1-A10
  Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4103342
  BLAST score
                    626
                    2.0e-65
 E value
 Match length
                    143
  % identity
                    87
                   (AF022377) agamous-like putative transcription factor
  NCBI Description
                    [Cucumis sativus]
  Seq. No.
                    232400
                    LIB3197-054-Q1-M1-A4
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q477226
  BLAST score
                    287
  E value
                    5.0e-26
 Match length
                    69
  % identity
                    90
  NCBI Description heat shock protein HSP82 - maize >gi 300083 bbs 130886
                    (S59780) HSP82=82 kda heat shock protein [Zea mays,
                    seedling, leaves, Peptide, 715 aa] [Zea mays]
  Seq. No.
                    232401
                    LIB3197-054-Q1-M1-A6
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q3875246
* BLAST score
                    374
                    7.0e-36
  E value
  Match length
                    140
  % identity
                    54
  NCBI Description
                    (Z81490) similar to WD domain, G-beta repeats (2 domains);
                    cDNA EST EMBL:T00482 comes from this gene; cDNA EST
                    EMBL: T00923 comes from this gene; cDNA EST yk449d4.3 comes
                    from this gene; cDNA EST yk449d4.5 comes from this gene;
  Seq. No.
                    232402
  Seq. ID
                    LIB3197-054-Q1-M1-A8
  Method
                    BLASTX
  NCBI GI
                    g3281868
  BLAST score
                    540
  E value
                    2.0e-55
  Match length
                    121
  % identity
  NCBI Description (AL031004) putative protein [Arabidopsis thaliana]
```

Seq. No.

Seq. ID Method

232408

BLASTX

LIB3197-054-Q1-M1-B4



```
232403
Seq. No.
Seq. ID
                  LIB3197-054-Q1-M1-A9
Method
                  BLASTX
NCBI GI
                  g2129473
BLAST score
                  145
                  4.0e-09
E value
Match length
                  50
% identity
                  52
NCBI Description arabinogalactan-like protein - loblolly pine >gi_607774
                  (U09556) arabinogalactan-like protein [Pinus taeda]
                  232404
Seq. No.
                  LIB3197-054-Q1-M1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3702328
BLAST score
                  493
                  6.0e-50
E value
Match length
                  113
                  77
% identity
NCBI Description (AC005397) putative cytochrome b5 [Arabidopsis thaliana]
Seq. No.
                  232405
                  LIB3197-054-Q1-M1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3776005
                  155
BLAST score
                  3.0e-10
E value
                  33
Match length
% identity
                  91
NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]
                  232406
Seq. No.
Seq. ID
                  LIB3197-054-Q1-M1-B12
Method
                  BLASTX
NCBI GI
                  g3860277
BLAST score
                  475
E value
                  9.0e-48
Match length
                  127
                  75
% identity
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                  thaliana] >gi 4314394 gb AAD15604 (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.
                  232407
Seq. ID
                  LIB3197-054-Q1-M1-B3
                  BLASTX
Method
NCBI GI
                  q71634
BLAST score
                  560
E value
                  1.0e-57
                  104
Match length
                  99
% identity
NCBI Description actin 1 - rice
```

BLAST score

E value

750

5.0e-80



```
q586076
NCBI GI
BLAST score
                  668
E value
                  2.0e-70
Match length
                  125
% identity
                  98
                  TUBULIN BETA-1 CHAIN >gi 486734 pir S35142 tubulin beta
NCBI Description
                  chain - white lupine >gi 402636 emb CAA49736 (X70184) Beta
                  tubulin 1 [Lupinus albus]
                  232409
Seq. No.
                  LIB3197-054-Q1-M1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1914683
BLAST score
                  318
E value
                  2.0e-29
Match length
                  147
% identity
                  51
NCBI Description (Y12013) RAD23, isoform I [Daucus carota]
Seq. No.
                  232410
                  LIB3197-054-Q1-M1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914467
BLAST score
                  142
E value
                  1.0e-08
Match length
                  90
% identity
                  40
                  26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
NCBI Description
                  >gi 1864003 dbj BAA19252_ (AB001422) 21D7 [Nicotiana
                  tabacum]
                  232411
Seq. No.
Seq. ID
                  LIB3197-054-Q1-M1-B7
                  BLASTX
Method
NCBI GI
                  g1771780
BLAST score
                  526
                  9.0e-54
E value
Match length
                  132
                  81
% identity
NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]
                  232412
Seq. No.
Seq. ID
                  LIB3197-054-Q1-M1-C10
                  BLASTX
Method
NCBI GI
                  q4455192
BLAST score
                  225
                  2.0e-18
E value
                  125
Match length
                  42
% identity
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
                  232413
Seq. No.
                  LIB3197-054-Q1-M1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g266463
```



```
Match length
                  99
% identity
                  3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM
NCBI Description
                  DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi 82259 pir S25670
                  3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor -
                  potato >gi_22643_emb_CAA47720_ (X67310) 3-isopropylmalate
                  dehydrogenase [Solanum tuberosum] >gi_445064_prf__1908380A
                  beta isopropylmalate dehydrogenase [Solanum tuberosum]
Seq. No.
                  232414
                  LIB3197-054-Q1-M1-C3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2160322
                  296
BLAST score
                  7.0e-27
E value
                  58
Match length
                  93
% identity
                  (D16139) cytokinin binding protein CBP57 [Nicotiana
NCBI Description
                  sylvestris]
                  232415
Seq. No.
                  LIB3197-054-Q1-M1-C4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2791806
BLAST score
                  216
                  2.0e-17 `
E value
Match length
                  60
                  67
% identity
NCBI Description (AF041433) bet3 [Mus musculus]
                  232416
Seq. No.
Seq. ID
                  LIB3197-054-Q1-M1-C5
Method
                  BLASTX
NCBI GI
                  g4406372
BLAST score
                  322
                  8.0e-30
E value
                  108
Match length
                  59
% identity
NCBI Description (AF109156) thiosulfate sulfurtransferase [Datisca
                  glomerata]
                   232417
Seq. No.
Seq. ID
                  LIB3197-054-Q1-M1-C9
Method
                  BLASTX
                  q3377797
NCBI GI
BLAST score
                  594
                   1.0e-61
E value
                  143
Match length
% identity
                   81
                  (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                   H36046; coded for by A. thaliana cDNA T44067; coded for by
```

Seq. No. 232418

LIB3197-054-Q1-M1-D11 Seq. ID

R90691 [Ara

A. thaliana cDNA T14056; coded for by A. thaliana cDNA



```
Method
                  BLASTX
NCBI GI
                  g2493129
BLAST score
                  735
E value
                  3.0e-78
                  147
Match length
                  98
% identity
NCBI Description
                  VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B
                  SUBUNIT) >gi 459198 (U07052) vacuolar H+-ATPase subunit B
                  [Gossypium hirsutum]
                  232419
Seq. No.
Seq. ID
                  LIB3197-054-Q1-M1-D3
                  BLASTX
Method
NCBI GI
                  q2440044
BLAST score
                  586
E value
                  9.0e-61
                  134
Match length
                  85
% identity
                 (AJ001293) major intrinsic protein PIPB [Craterostigma
NCBI Description
                  plantagineum]
Seq. No.
                  232420
Seq. ID
                  LIB3197-054-Q1-M1-D4
                  BLASTX
Method
NCBI GI
                  g1172558
BLAST score
                  262
                  9.0e-23
E value
                  82
Match length
                  63
% identity
NCBI Description OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT
                  ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                  >gi 480122 pir S36454 porin porl - garden pea
                  >gi 396819 emb CAA80988 (Z25540) Porin [Pisum sativum]
                  232421
Seq. No.
Seq. ID
                  LIB3197-054-Q1-M1-D5
Method
                  BLASTX
NCBI GI
                  q3873823
                  179
BLAST score
                  5.0e-13
E value
                  96
Match length
% identity
NCBI Description
                 (Z73422) predicted using Genefinder [Caenorhabditis
                  elegans]
                  232422
Seq. No.
                  LIB3197-054-01-M1-D6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3650032
```

BLAST score 241 E value 2.0e-20 Match length 55 67

NCBI Description (AC005396) gibberellin-regulated protein GAST1-like

[Arabidopsis thaliana]

Seq. No. 232423

% identity



```
LIB3197-054-Q1-M1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1351595
BLAST score
                  263
                  5.0e-23
E value
Match length
                  116
                  43
% identity
                  HYPOTHETICAL 88.2 KD PROTEIN C4G8.03C IN CHROMOSOME I
NCBI Description
                  >gi_2130430_pir__S62480 hypothetical protein SPAC4G8.03c -
                  fission yeast (Schizosaccharomyces pombe)
                  >gi 1022348 emb CAA91204 (Z56276) unknown
                  [Schizosaccharomyces pombe]
                  232424
Seq. No.
Seq. ID
                  LIB3197-054-Q1-M1-E1
Method
                  BLASTX
                  q136739
NCBI GI
                  329
BLAST score
                  1.0e-30
E value
Match length
                  99
                  67
% identity
NCBI Description UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
                  PYROPHOSPHORYLASE) (UDPGP) >gi 67061 pir XNPOU
                  UTP--glucose-1-phosphate uridy Tyltransferase (EC 2.7.7.9) -
                  potato >gi_218001_dbj BAA00570_ (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
                  232425
Seq. No.
                  LIB3197-054-Q1-M1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q267069
BLAST score
                  697
E value
                  8.0e-74
Match length
                  129
% identity
                  99
NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                  232426
                  LIB3197-054-Q1-M1-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3914467
BLAST score
                  316
E value
                  2.0e-36
                  127
Match length
                   59
% identity
NCBI Description 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
                  >gi 1864003 dbj BAA19252 (AB001422) 21D7 [Nicotiana
                   tabacum]
                  232427
Seq. No.
Seq. ID
                  LIB3197-054-Q1-M1-E12
```

BLASTX

434

g3912988

Method

NCBI GI BLAST score

NCBI GI

BLAST score



```
6.0e-43
E value
Match length
                   93 -
                   95
% identity
                   FLORAL HOMEOTIC PROTEIN AGL9 >gi 2345158 (AF015552) AGL9
NCBI Description
                    [Arabidopsis thaliana] >gi_28298\overline{7}8 (AC002396) AGL9
                    [Arabidopsis thaliana]
                   232428
Seq. No.
                   LIB3197-054-Q1-M1-E2
Seq. ID
Method
                   BLASTX
                   q498038
NCBI GI
BLAST score
                   612
                   8.0e-64
E value
Match length
                   146
                    80
% identity
                   (L33792) lipid transfer protein [Senecio odorus]
NCBI Description
                   232429
Seq. No.
                   LIB3197-054-Q1-M1-E4
Seq. ID
Method
                   BLASTX
                   q135535
NCBI GI
                    439
BLAST score
                    2.0e-43
E value
                    97
Match length
% identity
                    91
NCBI Description
                   T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)
                    (CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide
                    Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_(D11351) t-complex polypeptide 1 homologue [Arabidopsis
                    thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT
                    alpha/TCP-1 [Arabidopsis thaliana]
                    232430
Seq. No.
                    LIB3197-054-Q1-M1-E5
Seq. ID
                    BLASTX
Method
NCBI GI
                    g3218396
BLAST score
                    246
                    7.0e-21
E value
Match length
                    96
                    49
% identity
NCBI Description (AL023860) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                    232431
                    LIB3197-054-Q1-M1-E6
Seq. ID
Method
                    BLASTX
NCBI GI
                    g992706
                    566
BLAST score
                    2.0e-58
E value
                    110
Match length
                    92
% identity
NCBI Description (U33758) UBC13 [Arabidopsis thaliana]
                    232432
Seq. No.
                    LIB3197-054-Q1-M1-E8
Seq. ID
                    BLASTX
Method
```

g1658197 684

Seq. ID

Method



```
3.0e-72
E value
                  140
Match length
% identity
                  88
                  (U74630) calreticulin [Ricinus communis] >gi_1763297
NCBI Description
                  (U74631) calreticulin [Ricinus communis]
                  232433
Seq. No.
                  LIB3197-054-Q1-M1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1491615
                  250
BLAST score
                  2.0e-21
E value
Match length
                  91
% identity
                  54
                  (X99923) male sterility 2-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  232434
                  LIB3197-054-Q1-M1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g123650
BLAST score
                  657
E value
                  4.0e-69
Match length
                  132
                  95
% identity
                  HEAT SHOCK COGNATE 70 KD PROTEIN >gi_82245_pir__S03250 heat
NCBI Description
                  shock protein 70 (clone pMON9743) - garden petunia
                  >gi 20557 emb_CAA30018_ (X06932) heat shock protein 70
                   [Petunia x hybrida]
                   232435
Seq. No.
                  LIB3197-054-Q1-M1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g416758
BLAST score
                   320
E value
                   1.0e-29
                  115
Match length
                   56
% identity
NCBI Description SERINE CARBOXYPEPTIDASE PRECURSOR >gi 166674 (M81130)
                   carboxypeptidase Y-like protein [Arabīdopsis thaliana]
                   >gi 445120 prf 1908426A carboxypeptidase Y [Arabidopsis
                   thaliana]
                   232436
Seq. No.
                  LIB3197-054-Q1-M1-F11
Seq. ID
Method
                  BLASTX
                   g3687235
NCBI GI
BLAST score
                   269
                   1.0e-23
E value
                   104
Match length
                   57
% identity
NCBI Description (AC005169) putative copia-like transposable element
                   [Arabidopsis thaliana]
Seq. No.
                   232437
```

33486

LIB3197-054-Q1-M1-F12

BLASTX

Method

BLASTX



```
q2213619
NCBI GI
                   171
BLAST score
E value
                   4.0e-12
Match length
                   121
% identity
                   40
                  (AC000103) F21J9.14 [Arabidopsis thaliana]
NCBI Description
                   232438
Seq. No.
Seq. ID
                   LIB3197-054-Q1-M1-F2
Method
                   BLASTX
NCBI GI
                   g123650
BLAST score
                   160
E value
                   7.0e-13
Match length
                   67
% identity
                   69
                   HEAT SHOCK COGNATE 70 KD PROTEIN >gi_82245_pir S03250 heat
NCBI Description
                   shock protein 70 (clone pMON9743) - garden petunia
                   >gi_20557_emb_CAA30018_ (X06932) heat shock protein 70
                   [Petunia x hybrida]
Seq. No.
                   232439
Seq. ID
                   LIB3197-054-Q1-M1-F8
Method
                   BLASTX
NCBI GI
                   q461735
BLAST score
                   617
E value
                   2.0e-64
Match length
                   145
                   84
% identity
                   MITOCHONDRIAL CHAPERONIN HSP60-1 PRECURSOR
NCBI Description
                   >gi_478785_pir__S29315 chaperonin 60 - cucurbit
>gi_12544_emb_CAA50217_ (X70867) chaperonin 60 [Cucurbita
                   sp.]
Seq. No.
                   232440
                   LIB3197-054-Q1-M1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3912929
BLAST score
                   155
                   3.0e-14
E value
Match length
                   83
                   51
% identity
                  (AF001308) predicted protein of unknown function
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                   232441
Seq. ID
                   LIB3197-054-Q1-M1-G2
                   BLASTX
Method
NCBI GI
                   q730456
BLAST score
                   573
                   3.0e-59
E value
                   133
Match length
                   77
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S19
Seq. No.
                   232442
                   LIB3197-054-Q1-M1-G4
Seq. ID
```

E value

Match length

2.0e-70

135



```
q2894378
NCBI GI
BLAST score
                  255
                  6.0e-22
E value
Match length
                  117
% identity
                  48
                  (Y14573) putative ribophorin I homologue [Hordeum vulgare]
NCBI Description
                  232443
Seq. No.
                  LIB3197-054-Q1-M1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1326163
                  295
BLAST score
                  9.0e-27
E value
                  130
Match length
                  55
% identity
                  (U54704) stress related protein PvSRP [Phaseolus vulgaris]
NCBI Description
                  232444
Seq. No.
                  LIB3197-054-Q1-M1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2317910
BLAST score
                  249
E value
                  2.0e-31
Match length
                  129
% identity
                   56
NCBI Description (U89959) CER1 protein [Arabidopsis thaliana]
                  232445
Seq. No.
                  LIB3197-054-Q1-M1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2894598
BLAST score
                   385
                   3.0e-37
E value
Match length
                  128
% identity
                   62
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                   232446
                   LIB3197-054-Q1-M1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g728868
BLAST score
                   160
                   7.0e-11
E value
                   100
Match length
                   44
% identity
                  ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
NCBI Description
                   >qi 99824 pir S16748 proline-rich protein - rape
                   (fragment) >gi 22597 emb CAA42924 (X60376) proline-rich
                   protein [Brassica napus]
Seq. No.
                   232447
Seq. ID
                   LIB3197-054-Q1-M1-H2
                   BLASTX
Method
                   g2811278
NCBI GI
BLAST score
                   669
```



```
% identity
                  (AF043284) expansin [Gossypium hirsutum]
- NCBI Description
                   232448
Seq. No.
                   LIB3197-054-Q1-M1-H3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2921213
BLAST score
                   151
E value
                   9.0e-10
Match length
                   44
 % identity
                   64
                   (AF026150) beta-ketoacyl-ACP synthase IIIA [Perilla
NCBI Description
                   frutescens]
                   232449
 Seq. No.
                   LIB3197-054-Q1-M1-H6
 Seq. ID
                   BLASTX
Method
NCBI GI
                   g2271477
BLAST score
                   345
                   2.0e-32
E value
Match length
                   96
                   74
 % identity
NCBI Description (AF009631) AP47/50p [Arabidopsis thaliana]
 Seq. No.
                   232450
                   LIB3197-054-Q1-M1-H7
Seq. ID
Method
                   BLASTX
                   g123650
NCBI GI
BLAST score
                   346
                   8.0e-59
E value
Match length
                   134
                   90
 % identity
 NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN >gi 82245 pir S03250 heat
                   shock protein 70 (clone pMON9743) - garden petunia
                   >qi 20557 emb CAA30018 (X06932) heat shock protein 70
                   [Petunia x hybrida]
                   232451
 Seq. No.
                   LIB3197-054-Q1-M1-H8
 Seq. ID
                   BLASTX
 Method
                   q3169287
 NCBI GI
 BLAST score
                   138
 E value
                   1.0e-08
 Match length
                   78
 % identity
                   (AF050673) vacuolar H+-ATPase catalytic subunit [Gossypium
 NCBI Description
                   hirsutum]
 Seq. No.
                    232452
                   LIB3197-055-Q1-M1-A11
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                    g232024
 BLAST score
                    680
 E value
                   7.0e-72
 Match length
                   126
 % identity
                   100
```

NCBI Description PROTEIN E6 >gi\_421806\_pir\_\_A46130 fiber protein - upland



cotton >gi\_2129498\_pir\_\_S65061 fiber protein E6 (clone CKE6-1A) - upland cotton >gi\_167323 (M92051) 5' start site is putative; putative [Gossypium hirsutum] >gi\_1000084 (U30505) 'E6 [Gossypium hirsutum]

Seq. No. 232453

Seq. ID LIB3197-055-Q1-M1-A2

Method BLASTX
NCBI GI g4539543
BLAST score 471
E value 2.0e-47
Match length 115
% identity 79

NCBI Description (AJ133422) glyceraldehyde-3-phosphate dehydrogenase

[Nicotiana tabacum]

Seq. No. 232454

Seq. ID LIB3197-055-Q1-M1-A4

Method BLASTX
NCBI GI g1914683
BLAST score 329
E value 9.0e-31
Match length 94
% identity 70

NCBI Description (Y12013) RAD23, isoform I [Daucus carota]

Seq. No. 232455

Seq. ID LIB3197-055-Q1-M1-A7

Method BLASTX
NCBI GI g3334405
BLAST score 280
E value 2.0e-29
Match length 79
% identity 95

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)

>gi 2267583 (AF009338) vacuolar H+-ATPase subunit E

[Gossypium hirsutum]

Seq. No. 232456

Seq. ID LIB3197-055-Q1-M1-A9

Method BLASTX
NCBI GI g1703108
BLAST score 645
E value 9.0e-68
Match length 127
% identity 98

NCBI Description ACTIN 2/7 >gi\_2129525\_pir\_\_S71210 actin 2 - Arabidopsis

thaliana >gi\_2129528\_pir\_\_\$\overline{5}68107\ actin 7 - Arabidopsis thaliana >gi\_1049307 (U37281)\ actin-2 [Arabidopsis thaliana] >gi\_1943863 (U27811)\ actin7 [Arabidopsis

thaliana]

Seq. No. 232457

Seq. ID LIB3197-055-Q1-M1-B11

MethodBLASTXNCBI GIg1174592BLAST score320



```
E value
                  1.0e-29
Match length
                  62
                  98
% identity
                  TUBULIN ALPHA-1 CHAIN >gi_2119270_pir__S60233 alpha-tubulin
NCBI Description
                  - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                  sativum]
                  232458
Seq. No.
Seq. ID
                  LIB3197-055-Q1-M1-B12
                  BLASTX
Method
NCBI GI
                  q4455202
BLAST score
                  259
                  2.0e-22
E value
Match length
                  101
                  52
% identity
NCBI Description (AL035440) putative APG protein [Arabidopsis thaliana]
                  232459
Seq. No.
Seq. ID
                  LIB3197-055-Q1-M1-B4
Method
                  BLASTX
NCBI GI
                  q3885343
BLAST score
                  208
                  2.0e-16
E value
Match length
                  93
                  45
% identity
NCBI Description (AC005623) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  232460
                  LIB3197-055-Q1-M1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3915866
                  236
BLAST score
E value
                  9.0e-20
Match length
                  61
                  69
% identity
NCBI Description GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS)
                  >gi 2995455 emb CAA62901 (X91787) tRNA-glutamine
                  synthetase [Lupinus luteus]
Seq. No.
                  232461
Seq. ID
                  LIB3197-055-Q1-M1-B6
                  BLASTX
Method
NCBI GI
                  q3212869
BLAST score
                  546
E value
                  4.0e-56
Match length
                  115
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  232462
                  LIB3197-055-Q1-M1-C11
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g1361979
BLAST score 445
E value 2.0e-44
Match length 108
% identity 81



```
serine O-acetyltransferase (EC 2.3.1.30) - watermelon
NCBI Description
                  >gi 1350550 dbj BAA12843 (D85624) serine acetyltransferase
                  [Citrullus lanatus] >gi 1841312 dbj BAA08479 (D49535)
                  serine acetyltransferase. [Citrullus lanatus]
                  >gi 2337772_dbj_BAA21827_ (AB006530) serine
                  acetyltransferase [Citrullus lanatus]
                  232463
Seq. No.
Seq. ID
                  LIB3197-055-Q1-M1-C12
Method
                  BLASTX
NCBI GI
                  g1213460
BLAST score
                  345
                  2.0e-32
E value
                  141
Match length
                  46
% identity
NCBI Description (U03374) C subunit of V-ATPase [Amblyomma americanum]
                  232464
Seq. No.
                  LIB3197-055-Q1-M1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4220476
BLAST score
                  311
E value
                  1.0e-28
                  100
Match length
                  61
% identity
NCBI Description (AC006069) ribophorin I-like protein [Arabidopsis thaliana]
Seq. No.
                  232465
                  LIB3197-055-Q1-M1-D5
Seq. ID
Method
                  BLASTX
                  q3935173
NCBI GI
BLAST score
                  252
E value
                  1.0e-21
Match length
                  93
% identity
NCBI Description (AC004557) F17L21.16 [Arabidopsis thaliana]
Seq. No.
                  232466
                  LIB3197-055-Q1-M1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244749
BLAST score
                  673
E value
                  5.0e-71
Match length
                  131
% identity
                  95
NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
Seq. No.
                  232467
                  LIB3197-055-Q1-M1-E10
Seq. ID
                  BLASTX
Method
                  g2736147
NCBI GI
                  442
```

Method BLASTX
NCBI GI g2736147
BLAST score 442
E value 6.0e-44
Match length 103
% identity 75

NCBI Description (AF021804) fatty acid hydroxylase Fahlp [Arabidopsis thaliana] >qi 3132481 (AC003096) fatty acid hydroxylase,

Match length

137



## FAH1 [Arabidopsis thaliana]

```
Seq. No.
                  232468
Seq. ID
                  LIB3197-055-Q1-M1-F10
Method
                  BLASTX
NCBI GI
                  g870726
BLAST score
                  450
E value
                  7.0e-45
                  109
Match length
% identity
                  83
                  (L38260) biotin carboxylase subunit [Nicotiana tabacum]
NCBI Description
                  >gi 1582354 prf 2118337A Ac-CoA carboxylase:SUBUNIT=biotin
                  carboxylase [Nicotiana tabacum]
Seq. No.
                  232469
Seq. ID
                  LIB3197-055-Q1-M1-F12
Method
                  BLASTX
NCBI GI
                  g2833389
BLAST score
                  617
E value
                  2.0e-64
Match length
                  138
                  79
% identity
NCBI Description
                  SOLUBLE GLYCOGEN (STARCH) SYNTHASE PRECURSOR (SS III)
                  >gi 1200154 emb CAA65065 (X95759) glycogen (starch) ·
                  synthase [Solanum tuberosum]
Seq. No.
                  232470
Seq. ID
                  LIB3197-055-Q1-M1-F4
Method
                  BLASTX
NCBI GI
                  g4469010
BLAST score
                  167
E value
                  1.0e-11
                  43
Match length
% identity
                  72
NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  232471
Seq. ID
                  LIB3197-055-Q1-M1-F6
Method
                  BLASTX
NCBI GI
                  q729623
BLAST score
                  529
E value
                  4.0e-54
Match length
                  115
% identity
                  90
NCBI Description
                  78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 5 PRECURSOR (GRP
                  78-5) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG
                  5) (BIP 5) >gi 100340 pir S21880 heat shock protein BiP
                  homolog blp5 - common tobacco >gi 19813 emb CAA42660
                  (X60058) luminal binding protein (BiP) [Nicotiana tabacum]
                  232472
Seq. No.
Seq. ID
                  LIB3197-055-Q1-M1-G11
Method
                  BLASTX
NCBI GI
                  q1916807
BLAST score
                  505
E value
                  3.0e-51
```



% identity NCBI Description (U&1162) auxin-binding protein [Prunus persica] 232473 Seq. No. Seq. ID LIB3197-055-Q1-M1-G2 BLASTX Method NCBI GI q3873710 BLAST score 351 3.0e-33 E value Match length 105 59 % identity (Z73102) predicted using Genefinder; similar to Zinc NCBI Description finger, C2H2 type; cDNA EST EMBL:M89161 comes from this gene; cDNA EST EMBL: T01394 comes from this gene; cDNA EST EMBL:T02192 comes from this gene; cDNA EST EMBL:D71409 comes 232474 Seq. No. Seq. ID LIB3197-055-Q1-M1-G4 Method BLASTX NCBI GI g2497543 BLAST score 461 4.0e-46 E value Match length 112 % identity 83 NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >qi 542061 pir S41379 pyruvate kinase - common tobacco >gi 444023 emb CAA82628 (Z29492) pyruvate kinase [Nicotiana tabacum] 232475 Seq. No. LIB3197-055-Q1-M1-G5 Seq. ID Method BLASTX NCBI GI q4490316 BLAST score 273 E value 4.0e-24 Match length 134 % identity 45 NCBI Description (AL035678) nucellin-like protein [Arabidopsis thaliana] 232476 Seq. No. Seq. ID LIB3197-055-Q1-M1-G8 Method BLASTX NCBI GI q4204300 BLAST score 223 3.0e-18 E value 81 Match length % identity NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana] Seq. No. 232477

LIB3197-055-Q1-M1-G9 Seq. ID

Method BLASTX NCBI GI g2662343 BLAST score 595 E value 7.0e-62 Match length 116 % identity 98

Seq. No.

232483



```
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  232478
Seq. No.
Seq. ID
                  LIB3197-055-Q1-M1-H1
Method
                  {\tt BLASTX}
NCBI GI
                  g2583108
BLAST score
                  349
E value
                  5.0e-33
Match length
                  107
                  65
% identity
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]
Seq. No.
                  232479
Seq. ID
                  LIB3197-055-Q1-M1-H10
Method
                  BLASTX
NCBI GI
                  g1174592
BLAST score
                  527
E value
                  6.0e-54
Match length
                  98
% identity
                  99
NCBI Description TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
                   - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                  sativum]
Seq. No.
                  232480
Seq. ID
                  LIB3197-055-Q1-M1-H2
Method
                  BLASTX
NCBI GI
                  g4580394
BLAST score
                  332
E value
                  5.0e-31
Match length
                  95
                  65
% identity
NCBI Description (AC007171) putative fatty acid elongase [Arabidopsis
                  thaliana]
Seq. No.
                  232481
                  LIB3197-055-Q1-M1-H3
Seq. ID
Method
                  BLASTX
                  g2982259
NCBI GI
BLAST score
                  566
E value
                  2.0e-58
Match length
                  129
% identity
                  82
NCBI Description
                  (AF051212) probable 60s ribosomal protein L13a [Picea
                  mariana]
Seq. No.
                  232482
Seq. ID
                  LIB3197-055-Q1-M1-H4
Method
                  BLASTX
NCBI GI
                  g2739383
BLAST score
                  486
E value
                  4.0e-49
Match length
                  114
% identity
                  76
NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]
```

% identity

87



```
Seq. ID
                    LIB3197-055-Q1-M1-H6
Method
                    BLASTX
NCBI GI
                    g4469023
BLAST score
                    415
E value
                    7.0e-41
                    98
Match length
% identity
                    82
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                    232484
                    LIB3197-055-Q1-M1-H7
Seq. ID
Method
                    BLASTX
NCBI GI
                    q2494113
BLAST score
                    436
E value
                    3.0e-43
Match length
                    109
                    72
% identity
NCBI Description
                   (AC002376) Strong similarity to Musa pectate lyase
                    (gb_X92943). ESTs gb_AA042458, gb_ATTS4502, gb_N38552 come
                    from this gene. [Arabidopsis thaliana]
Seq. No.
                    232485
Seq. ID
                    LIB3197-055-Q1-M1-H8
Method
                    BLASTX
NCBI GI
                    g2498490
BLAST score
                    273
E value
                    4.0e-24
Match length
                    109
% identity
                    46
NCBI Description
                   VIRAL INTEGRATION SITE PROTEIN INT-6 >gi_1854579 (L35556)
                    Int-6 [Mus musculus] >gi_2114363 (U62962) similar to mouse Int-6 [Homo sapiens] >gi_2351382 (U54562) eIF3-p48 [Homo sapiens] >gi_2688818 (U85947) Int-6 [Homo sapiens]
                    >gi 2695701 (U94175) mammary tumor-associated protein INT6
                    [Homo sapiens] >gi_4503521_ref_NP_001559.1_pEIF3S6_ murine
                    mammary tumor integration site 6 (oncogene homolog)
Seq. No.
                    232486
Seq. ID
                    LIB3197-055-Q1-M1-H9
Method
                    BLASTX
NCBI GI
                    g2062167
BLAST score
                    203
E value
                    5.0e-16
Match length
                    69
% identity
                    65
NCBI Description
                   (AC001645) Proline-rich protein APG isolog [Arabidopsis
                    thaliana]
Seq. No.
                    232487
Seq. ID
                    LIB3197-056-Q1-M1-A10
Method
                    BLASTX
NCBI GI
                    g3548803
BLAST score
                    573
E value
                    2.0e-59
Match length
                    126
```

NCBI Description (AC005313) putative DNA-binding protein [Arabidopsis



thaliana] >gi\_4335770\_gb\_AAD17447\_ (AC006284) putative SMUBP-2 [mouse] DNA-binding protein [Arabidopsis thaliana]

Seq. No. 232488

Seq. ID LIB3197-056-Q1-M1-A11

Method BLASTX
NCBI GI g462187
BLAST score 338
E value 1.0e-31
Match length 108
% identity 69

NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR

(SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)

(SHMT) >gi\_282928\_pir\_\_A42906 serine

hydroxymethyltransferase - garden pea >gi 169158 (M87649)

serine hydroxymethyltransferase [Pisum sativum]

Seq. No. 232489

Seq. ID LIB3197-056-Q1-M1-A12

Method BLASTX
NCBI GI g2662341
BLAST score 694
E value 2.0e-73
Match length 134
% identity 99

NCBI Description (D63580) EF-1 alpha [Oryza sativa]

>gi\_2662345\_dbj\_BAA23659 (D63582) EF-1 alpha [Oryza sativa] >gi\_2662347\_dbj\_BAA23660 (D63583) EF-1 alpha

[Oryza sativa]

Seq. No. 232490

Seq. ID LIB3197-056-Q1-M1-A2

Method BLASTX
NCBI GI g2995405
BLAST score 337
E value 7.0e-32
Match length 97
% identity 66

NCBI Description (Y12432) polyprotein [Ananas comosus]

Seq. No. 232491

Seq. ID LIB3197-056-Q1-M1-A4

Method BLASTX
NCBI GI g1703108
BLAST score 699
E value 5.0e-74
Match length 134
% identity 99

NCBI Description ACTIN 2/7 >gi\_2129525\_pir\_\_S71210 actin 2 - Arabidopsis

thaliana >gi\_2129528\_pir\_\_S68107 actin 7 - Arabidopsis thaliana >gi\_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi\_1943863 (U27811) actin7 [Arabidopsis

thaliana]

Seq. No. 232492

Seq. ID LIB3197-056-Q1-M1-A7

Method BLASTX



```
NCBI GI
                  g1170898
BLAST score
                  322
E value
                  4.0e-30
                  92
Match length
                  78
% identity
NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
                  >gi 629659 pir S44167 malate dehydrogenase, mitochondrial
                  - cider tree >gi 473206 emb CAA55383 (X78800)
                  mitochondrial malate dehydrogenase [Eucalyptus gunnii]
Seq. No.
                  232493
Seq. ID
                  LIB3197-056-Q1-M1-A9
Method
                  BLASTX
NCBI GI
                  q2811278
BLAST score
                  434
E value
                  8.0e-43
Match length
                  122
                  74
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                  232494
Seq. ID
                  LIB3197-056-Q1-M1-B1
Method
                  BLASTX
NCBI GI
                  g2463509
BLAST score
                  442
E value
                  3.0e-44
Match length
                  89
                  89
% identity
NCBI Description (Y09541) pectate lyase [Zinnia elegans]
Seq. No.
                  232495
Seq. ID
                  LIB3197-056-Q1-M1-B10
Method
                  BLASTX
NCBI GI
                  g2811278
BLAST score
                  637
E value
                  9.0e-67
Match length
                  130
% identity
                  88
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                  232496
Seq. ID
                  LIB3197-056-Q1-M1-B11
Method
                  BLASTX
NCBI GI
                  g1890317
BLAST score
                  262
                  5.0e-23
E value
Match length
                  60
% identity
NCBI Description (Y11791) peroxidase ATP26a [Arabidopsis thaliana]
Seq. No.
                  232497
Seq. ID
                  LIB3197-056-Q1-M1-B12
```

Method BLASTX
NCBI GI g1351303
BLAST score 245
E value 6.0e-21
Match length 62



% identity NCBI Description INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE PRECURSOR (IGPS) >gi\_619732 (U18770) indole-3-glycerol phosphate synthase [Arabidopsis thaliana] Seq. No. 232498 Seq. ID LIB3197-056-Q1-M1-B3 Method BLASTX NCBI GI g1899188 BLAST score 419 3.0e-41E value Match length 141 % identity 40 NCBI Description (U90212) DNA binding protein ACBF [Nicotiana tabacum] Seq. No. 232499 Seq. ID LIB3197-056-Q1-M1-B6 Method BLASTX NCBI GI g1905876 BLAST score 720 2.0e-76 E value Match length 142 99 % identity NCBI Description (U90879) biotin carboxylase subunit [Arabidopsis thaliana] >gi\_1916300 (U91414) heteromeric acetyl-CoA carboxylase biotin carboxylase subunit [Arabidopsis thaliana] >gi 3047099 (AF058826) Arabidopsis thaliana biotin carboxylase subunit (GB:U90879) [Arabidopsis thaliana] Seq. No. 232500 Seq. ID LIB3197-056-Q1-M1-C1  ${\tt BLASTX}$ Method NCBI GI g2465160 BLAST score 199 2.0e-15 E value Match length 109 % identity NCBI Description (Z99753) hypothetical protein [Schizosaccharomyces pombe] Seq. No. 232501 Seq. ID LIB3197-056-Q1-M1-C10 Method BLASTX NCBI GI q1658197 BLAST score 626 E value 2.0e-65 Match length 120 % identity 93 NCBI Description (U74630) calreticulin [Ricinus communis] >qi 1763297 (U74631) calreticulin [Ricinus communis] Seq. No. 232502

Seq. ID LIB3197-056-Q1-M1-C11

Method BLASTX NCBI GI q1524370 BLAST score 299 E value 3.0e-27Match length 98

Seq. No.

Seq. ID

232508

LIB3197-056-Q1-M1-C9



```
% identity
NCBI Description (X92491) TOM20 [Solanum tuberosum]
Seq. No.
                  232503
Seq. ID
                  LIB3197-056-Q1-M1-C2
Method
                  BLASTX
NCBI GI
                  g643469
BLAST score
                  398
E value
                  9.0e-39
Match length
                  138
                  57
% identity
NCBI Description (U19886) unknown [Lycopersicon esculentum]
Seq. No.
                  232504
Seq. ID
                  LIB3197-056-Q1-M1-C3
Method
                  BLASTX
NCBI GI
                  g2213425
BLAST score
                  512
E value
                  3.0e-52
Match length
                  109
                  51
% identity
NCBI Description (Z97064) hypothetical protein [Citrus x paradisi]
                  232505
Seq. No.
Seq. ID
                  LIB3197-056-Q1-M1-C4
Method
                  BLASTX
NCBI GI
                  g2213425
BLAST score
                  179
E value
                  3.0e-17
Match length
                  64
% identity
                  41
NCBI Description (Z97064) hypothetical protein [Citrus x paradisi]
                  232506
Seq. No.
Seq. ID
                  LIB3197-056-Q1-M1-C5
Method
                  BLASTX
NCBI GI
                  g1181333
BLAST score
                  184
E value
                  1.0e-13
Match length
                  40
                  78
% identity
NCBI Description (X78057) calreticulin [Zea mays]
Seq. No.
                  232507
Seq. ID
                  LIB3197-056-Q1-M1-C8
Method
                  BLASTX
NCBI GI
                  q1076746
BLAST score
                  289
E value
                  9.0e-37
Match length
                  99
                  76
% identity
NCBI Description
                  heat shock protein 70 - rice (fragment)
                  >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                  [Oryza sativa]
```



Method BLASTX NCBI GI a586076 BLAST score 640 E value 3.0e-67 Match length 121 97 % identity TUBULIN BETA-1 CHAIN >gi\_486734\_pir\_\_S35142 tubulin beta chain - white lupine >gi\_402636\_emb\_CAA49736\_ (X70184) Beta NCBI Description tubulin 1 [Lupinus albus] Seq. No. 232509 Seq. ID LIB3197-056-Q1-M1-D10 Method BLASTX NCBI GI q3193234 BLAST score 180 E value 2.0e-13 Match length 55 62 % identity NCBI Description (AF068690) peroxisomal targeting signal-1 receptor [Citrullus lanatus] 232510 Seq. No. Seq. ID LIB3197-056-Q1-M1-D11 Method BLASTX NCBI GI q4204300 BLAST score 165 E value 2.0e-11 Match length 63 % identity 56 NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana] Seq. No. 232511 LIB3197-056-Q1-M1-D2 Seq. ID Method BLASTX NCBI GI q1916807 BLAST score 409 E value 5.0e-40Match length 121 69 % identity NCBI Description (U81162) auxin-binding protein [Prunus persica] Seq. No. 232512 LIB3197-056-Q1-M1-D4 Seq. ID Method BLASTX NCBI GI g3513738 BLAST score 475 E value 9.0e-48

142 Match length 63 % identity

NCBI Description (AF080118) similar to the GDSL family of lipolytic enzymes

[Arabidopsis thaliana]

Seq. No. 232513

Seq. ID LIB3197-056-Q1-M1-D6

Method BLASTX NCBI GI g1174498 384 BLAST score

Match length

% identity

90

71



```
4.0e-37
E value
Match length
                  99
% identity
                  69
NCBI Description SYNAPTOBREVIN-RELATED PROTEIN >gi 600710 (M90418) formerly
                  called HAT24; synaptobrevin-related protein [Arabidopsis
                  thaliana]
                  232514
Seq. No.
Seq. ID
                  LIB3197-056-Q1-M1-D7
Method
                  BLASTX
NCBI GI
                  g3650032
                  237
BLAST score
E value
                  7.0e-20
                  49
Match length
                  73
% identity
NCBI Description (AC005396) gibberellin-regulated protein GAST1-like
                  [Arabidopsis thaliana]
                  232515
Seq. No.
Seq. ID
                  LIB3197-056-Q1-M1-D9
Method
                  BLASTX
NCBI GI
                  g3603353
BLAST score
                  253
E value
                  9.0e-22
                  62
Match length
                  73
% identity
NCBI Description (AF074843) peroxisomal targeting signal type 1 receptor
                  [Arabidopsis thaliana]
                  232516
Seq. No.
Seq. ID
                  LIB3197-056-Q1-M1-E1
Method
                  BLASTX
NCBI GI
                  g2811278
BLAST score
                  530
                  3.0e-54
E value
                  129
Match length
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
                  232517
Seq. No.
Seq. ID
                  LIB3197-056-Q1-M1-E12
Method
                  BLASTX
NCBI GI
                  q4559292
BLAST score
                  471
E value
                  3.0e-47
Match length
                  141
% identity
NCBI Description (AF124148) trehalase 1 GMTRE1 [Glycine max]
Seq. No.
                  232518
                  LIB3197-056-Q1-M1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131772
BLAST score
                  308
E value
                  3.0e-28
```

% identity



```
40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                  >qi 82723 pir A30097 ribosomal protein S14 (clone MCH1) -
                  maize
Seq. No.
                  232519
                  LIB3197-056-Q1-M1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244734
BLAST score
                  670
E value
                  1.0e-70
                  131
Match length
                  100
% identity
NCBI Description (D88414) actin [Gossypium hirsutum]
Seq. No.
                  232520
                  LIB3197-056-Q1-M1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4567260
BLAST score
                  455
E value
                  2.0e-45
Match length
                  122
% identity
                  69
NCBI Description (AC006841) putative NADPH dependent mannose 6-phosphate
                  reductase [Arabidopsis thaliana]
Seq. No.
                  232521
                  LIB3197-056-Q1-M1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3395432
BLAST score
                  168
                  9.0e-12
E value
                  75
Match length
                  49
% identity
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                  232522
Seq. No.
Seq. ID
                  LIB3197-056-Q1-M1-F1
Method
                  BLASTX
NCBI GI
                  g1708313
BLAST score
                  562
E value
                  6.0e-58
Match length
                  120
                  94
% identity
NCBI Description HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi 999396 bbs 163637
                  (S77849) heat-shock Protein=HSP81-3 [Arabidopsis
                  thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis
                  thaliana]
                  232523
Seq. No.
Seq. ID
                  LIB3197-056-Q1-M1-F12
                  BLASTX
Method
NCBI GI
                  g3493172
                  627
BLAST score
E value
                  1.0e-65
Match length
                  133
```

33503

NCBI Description (U89609) fiber annexin [Gossypium hirsutum]

Seq. ID

Method



```
232524
Seq. No.
Seq. ID
                  LIB3197-056-Q1-M1-F2
Method
                  BLASTX
NCBI GI
                  g1565225
BLAST score
                  141
E value
                  1.0e-08
Match length
                  27
% identity
                  89
NCBI Description (X95572) salt-tolerance protein [Arabidopsis thaliana]
Seq. No.
                  232525
Seq. ID
                  LIB3197-056-Q1-M1-F3
Method
                  BLASTX
NCBI GI
                  g1103318
BLAST score
                  403
E value
                  2.0e-39
Match length
                  135
% identity
                  61
                  (X78818) casein kinase I [Arabidopsis thaliana]
NCBI Description
                  >gi_2244791_emb_CAB10213.1_ (Z97336) casein kinase I
                   [Arabidopsis thaliana]
Seq. No.
                  232526
Seq. ID
                  LIB3197-056-Q1-M1-F4
Method
                  BLASTX
NCBI GI
                  g3059131
BLAST score
                  256
E value
                  4.0e-22
Match length
                  143
                  37
% identity
NCBI Description (AJ000478) cytochrome P450 [Helianthus tuberosus]
Seq. No.
                  232527
Seq. ID
                  LIB3197-056-Q1-M1-F6
Method
                  BLASTX
NCBI GI
                  g2583133
BLAST score
                  158
E value
                  1.0e-10
Match length
                  106
% identity
                  35
NCBI Description (AC002387) unknown protein [Arabidopsis thaliana]
Seq. No.
                  232528
Seq. ID
                  LIB3197-056-Q1-M1-F7
Method
                  BLASTX
NCBI GI
                  g3851001
BLAST score
                  439
E value
                  1.0e-43
Match length
                  114
% identity
                  78
NCBI Description
                  (AF069909) pyruvate dehydrogenase E1 beta subunit isoform 2
                  [Zea mays]
Seq. No.
                  232529
```

33504

LIB3197-056-Q1-M1-F9

BLASTX



```
NCBI GI
                  g267079
                  276
BLAST score
E value
                  2.0e-24
Match length
                  52
% identity
                  100
NCBI Description TUBULIN BETA-6 CHAIN >gi_320187_pir__JQ1590 tubulin beta-6
                  chain - Arabidopsis thaliana >gi 166904 (M84703) beta-6
                  tubulin [Arabidopsis thaliana]
Seq. No.
                  232530
Seq. ID
                  LIB3197-056-Q1-M1-G1
                  BLASTX
Method
NCBI GI
                  g2507281
BLAST score
                  571
                  5.0e-59
E value
                  104
Match length
                  100
% identity
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_
                  (X97380) atran2 [Arabidopsis thaliana]
Seq. No.
                  232531
Seq. ID
                  LIB3197-056-Q1-M1-G3
Method
                  BLASTX
NCBI GI
                  g267069
BLAST score
                  515
E value
                  2.0e-52
Match length
                  95
                  99
% identity
NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  232532
Seq. No.
Seq. ID
                  LIB3197-056-Q1-M1-G7
Method
                  BLASTX
NCBI GI
                  q3914996
BLAST score
                  160
E value
                  4.0e-11
Match length
                  78
% identity
                  51
NCBI Description PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT)
                  >gi 1665831 dbj BAA13640 (D88541) phosphoserine
                  aminotransferase [Arabidopsis thaliana]
                  >gi_2804260_dbj_BAA24441_ (AB010408) phosphoserine
                  aminotransferase [Arabidopsis thaliana]
                  >gi 3367581 emb CAA20033 (AL031135) phosphoserine
                  aminotransferase [Arabidopsis thaliana]
                  232533
Seq. No.
                  LIB3197-056-Q1-M1-G8
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI g267069
BLAST score 437
E value 2.0e-43
Match length 86
% identity 94



NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana] Seq. No. 232534 Seq. ID LIB3197-056-Q1-M1-G9 Method BLASTX NCBI GI g974782 BLAST score 161 E value 5.0e-11 Match length 34 % identity 97 NCBI Description (Z49150) cobalamine-independent methionine synthase [Solenostemon scutellarioides] Seq. No. 232535 Seq. ID LIB3197-056-Q1-M1-H1 Method BLASTX NCBI GI g267069 BLAST score 525 E value 1.0e-53 99 Match length % identity 97 NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana] Seq. No. 232536 Seq. ID LIB3197-056-Q1-M1-H2 Method BLASTX NCBI GI g1944575 BLAST score 288 E value 3.0e-26 Match length 87 % identity 68 NCBI Description (Z94058) pectinesterase [Lycopersicon esculentum] Seq. No. 232537 Seq. ID LIB3197-056-Q1-M1-H3 Method BLASTX NCBI GI g3986289 BLAST score 485 E value 5.0e-49Match length 119 % identity NCBI Description (AB017357) L-Galactono-1,4-lactone dehydrogenase [Ipomoea batatas]

Seq. No. 232538

Seq. ID LIB3197-056-Q1-M1-H7

Method BLASTX
NCBI GI g549010
BLAST score 458
E value 6.0e-46
Match length 107



```
% identity
                    EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1)
NCBI Description
                     (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG)
                    >gi_322554_pir__S31328 omnipotent suppressor protein SUP1
                    homolog (clone G18) - Arabidopsis thaliana
                    >gi_16514_emb_CAA49172_ (X69375) similar to yeast omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi_1402882_emb_CAA66813_ (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis
                     thaliana] >gi_1495249_emb_CAA66118_ (X97486) eRF1-3
                     [Arabidopsis thaliana]
Seq. No.
                    232539
Seq. ID
                    LIB3197-056-Q1-M1-H8
Method
                    BLASTX
NCBI GI
                    q4218162
BLAST score
                    230
E value
                    3.0e-19
Match length
                     60
% identity
                     77
NCBI Description (AJ009723) MADS-box protein, GAGA2 [Gerbera hybrida]
Seq. No.
                    232540
Seq. ID
                    LIB3197-056-Q1-M1-H9
Method
                    BLASTX
NCBI GI
                    q3881978
                     378
BLAST score
                     1.0e-36
E value
Match length
                     99
                     38
% identity
NCBI Description (Y11348) annexin-like protein [Medicago sativa]
Seq. No.
                     232541
Seq. ID
                    LIB3197-057-Q1-M1-A1
Method
                    BLASTX
NCBI GI
                     q445613
BLAST score
                     431
E value
                     9.0e-61
Match length
                    150
                     72
% identity
NCBI Description ribosomal protein L7 [Solanum tuberosum]
Seq. No.
                     232542
Seq. ID
                    LIB3197-057-Q1-M1-A4
Method
                    BLASTX
NCBI GI
                     g280401
BLAST score
                    522
E value
                     3.0e-53
Match length
                    135
                     76
% identity
NCBI Description H+-transporting ATPase (EC 3.6.1.35) - curled-leaved
                     tobacco >gi 170206 (M27888) H+-translocating ATPase
```

[Nicotiana plumbaginifolia]

Seq. No. 232543

Seq. ID LIB3197-057-Q1-M1-A6

Method BLASTX



```
q4097579
NCBI GI
BLAST score
                  565
E value
                  2.0e-58
                  117
Match length
% identity
                  86
NCBI Description (U64922) NTGP1 [Nicotiana tabacum]
Seq. No.
                  232544
Seq. ID
                  LIB3197-057-Q1-M1-A7
Method
                  BLASTX
NCBI GI
                  q232029
BLAST score
                  144
E value
                  7.0e-13
Match length
                  119
% identity
                  42
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                  >gi 100154 pir S21989 translation elongation factor eEF-1
                  alpha chain - carrot >gi_18339_emb_CAA42843_ (X60302)
                  elongation factor 1A [Daucus carota]
Seq. No.
                  232545
Seq. ID
                  LIB3197-057-Q1-M1-A8
Method
                  BLASTX
NCBI GI
                  g2104529
BLAST score
                  529
E value
                  4.0e-54
Match length
                  135
% identity
                  78
NCBI Description (AF001308) putative hexose transporter [Arabidopsis
                  thaliana]
                  232546
Seq. No.
Seq. ID
                  LIB3197-057-Q1-M1-A9
Method
                  BLASTX
NCBI GI
                  g1076660
BLAST score
                  380
E value
                  1.0e-36
Match length
                  104
                  74
% identity
NCBI Description D13F(MYBST1) protein - potato >gi 786426 bbs 159122
                  (S74753) MybSt1=Myb-related transcriptional activator
                  {DNA-binding domain repeats} [Solanum tuberosum=potatoes,
                  leaf, Peptide, 342 aa] [Solanum tuberosum]
Seq. No.
                  232547
Seq. ID
                  LIB3197-057-Q1-M1-B1
Method
                  BLASTX
NCBI GI
                  g1839188
BLAST score
                  540
E value
                  2.0e-55
Match length
                  140
% identity
                  74
NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]
```

Seq. ID LIB3197-057-Q1-M1-B11

Method BLASTX



```
NCBI GI
                  q3182981
BLAST score
                  455
E value
                  2.0e-45
                  109
Match length
                  78
% identity
NCBI Description CELL ELONGATION PROTEIN DIMINUTO >gi 1695692 dbj BAA13096
                  (D86494) diminuto [Pisum sativum]
Seq. No.
                  232549
Seq. ID
                  LIB3197-057-Q1-M1-B6
Method
                  BLASTX
NCBI GI
                  g2829206
BLAST score
                  192
E value
                  9.0e-15
Match length
                  52
                  27
% identity
NCBI Description
                  (AF044205) proline-rich protein precursor [Gossypium
                  hirsutum]
                  232550
Seq. No.
Seq. ID
                  LIB3197-057-Q1-M1-B8
Method
                  BLASTX
NCBI GI
                  g3413167
BLAST score
                  448
E value
                  1.0e-44
                  88
Match length
% identity
                  98
NCBI Description (AJ010225) elongation factor 1-alpha [Cicer arietinum]
Seq. No.
                  232551
Seq. ID
                  LIB3197-057-Q1-M1-B9
Method
                  BLASTX
NCBI GI
                  q2130073
BLAST score
                  501
E value
                  9.0e-51
Match length
                  116
% identity
                  84
NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
                  cytosolic - rice >gi 786178 dbj BAA08845 (D50307) aldolase
                  C-1 [Oryza sativa] >gi 790970 dbj BAA08830 (D50301)
                  aldolase C-1 [Oryza sativa]
                  232552
Seq. No.
Seq. ID
                  LIB3197-057-Q1-M1-C1
Method
                  BLASTX
NCBI GI
                  q100488
BLAST score
                  197
                  2.0e-15
E value
Match length
                  65
% identity
                  52
NCBI Description TNP2 protein - garden snapdragon
Seq. No.
                  232553
```

Seq. ID LIB3197-057-Q1-M1-C10

Method BLASTX
NCBI GI g4115925
BLAST score 308



E value 3.0e-28 Match length 79 % identity 38

NCBI Description (AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi\_4539439\_emb\_CAB40027.1\_ (AL049523) RNA-binding protein

[Arabidopsis thaliana]

Seq. No. 232554

Seq. ID LIB3197-057-Q1-M1-C11

Method BLASTX
NCBI GI g2342724
BLAST score 554
E value 4.0e-57
Match length 135
% identity 79

NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]

Seq. No. 232555

Seq. ID LIB3197-057-Q1-M1-C12

Method BLASTX
NCBI GI g549063
BLAST score 387
E value 1.0e-37
Match length 113
% identity 67

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 232556

Seq. ID LIB3197-057-Q1-M1-C3

Method BLASTX
NCBI GI g3892051
BLAST score 133
E value 1.0e-17
Match length 57
% identity 81

NCBI Description (AC002330) predicted NADH dehydrogenase 24 kD subunit

[Arabidopsis thaliana]

Seq. No. 232557

Seq. ID LIB3197-057-Q1-M1-C6

Method BLASTX
NCBI GI g3757514
BLAST score 386
E value 2.0e-37
Match length 90
% identity 82

NCBI Description (AC005167) putative plasma membrane intrinsic protein

[Arabidopsis thaliana]

Seq. No. 232558

Seq. ID LIB3197-057-Q1-M1-C8

Method BLASTX NCBI GI g4455221



```
BLAST score
E value
                  4.0e-33
Match length
                  89
% identity
                  78
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  232559
Seq. ID
                  LIB3197-057-Q1-M1-D11
Method
                  BLASTX
NCBI GI
                  q3047085
BLAST score
                  447
E value
                  2.0e-44
Match length
                  132
% identity
NCBI Description (AF058914) No definition line found [Arabidopsis thaliana]
                  232560
Seq. No.
Seq. ID
                  LIB3197-057-Q1-M1-D12
Method
                  BLASTX
NCBI GI
                  q4490330
BLAST score
                  744
E value
                  3.0e-79
Match length
                  144
% identity
NCBI Description (AL035656) splicing factor-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  232561
Seq. ID
                  LIB3197-057-Q1-M1-D2
Method
                  BLASTX
NCBI GI
                  g4580394
BLAST score
                  267
E value
                  2.0e-23
Match length
                  123
% identity
                  42
NCBI Description (AC007171) putative fatty acid elongase [Arabidopsis
                  thaliana]
Seq. No.
                  232562
Seq. ID
                  LIB3197-057-Q1-M1-D4
Method
                  BLASTX
NCBI GI
                  g2462827
BLAST score
                  220
E value
                  5.0e-18
Match length
                  64
                  70
% identity
NCBI Description (AF000657) probable thiamin biosynthetic enzyme
                  [Arabidopsis thaliana]
                  232563
Seq. No.
Seq. ID
                  LIB3197-057-Q1-M1-D8
                  BLASTX
Method
```

NCBI GI g2062167
BLAST score 442
E value 7.0e-44
Match length 102
% identity 80



```
NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis
                  thaliana]
                  232564
Seq. No.
Seq. ID
                  LIB3197-057-Q1-M1-D9
Method
                  BLASTX
NCBI GI
                  q3249084
BLAST score
                  373
E value
                  8.0e-36
Match length
                  107
                  49
% identity
NCBI Description
                  (AC004473) Similar to red-1 (related to thioredoxin) gene
                  gb X92750 from Mus musculus. ESTs gb AA712687 and
                  gb Z37223 come from this gene [Arabidopsis thaliana]
Seq. No.
                  232565
                  LIB3197-057-Q1-M1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1644427
BLAST score
                  278
E value
                  1.0e-24
Match length
                  61
% identity
                  87
NCBI Description (U74610) glyoxalase II [Arabidopsis thaliana]
Seq. No.
                  232566
Seq. ID
                  LIB3197-057-Q1-M1-E11
Method
                  BLASTX
NCBI GI
                  g2146731
BLAST score
                  611
                  1.0e-63
E value
Match length
                  144
                  28
% identity
NCBI Description FK506-binding protein - Arabidopsis thaliana >qi 1354207
                  (U49453) rof1 [Arabidopsis thaliana]
Seq. No.
                  232567
Seq. ID
                  LIB3197-057-Q1-M1-E12
Method
                  BLASTX
NCBI GI
                  q3688600
BLAST score
                  244
                  1.0e-20
E value
Match length
                  120
% identity
                  46
NCBI Description (AB009030) beta-Amyrin Synthase [Panax ginseng]
Seq. No.
                  232568
Seq. ID
                  LIB3197-057-Q1-M1-E2
                  BLASTX
                  g2497753
BLAST score
                  324
E value
                  4.0e - 30
```

Method NCBI GI

Match length 93 % identity 57

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)

>gi 1321915 emb CAA65477 (X96716) lipid transfer protein

[Prunus dulcis]

Match length

NCBI Description

% identity

134

hirsutum]

```
Seq. No.
                  232569
Seq. ID
                  LIB3197-057-Q1-M1-E4
Method
                  BLASTX
NCBI GI
                  g416758
BLAST score
                  308
E value
                  3.0e-28
Match length
                  97
% identity
                  62
NCBI Description
                  SERINE CARBOXYPEPTIDASE PRECURSOR >gi 166674 (M81130)
                  carboxypeptidase Y-like protein [Arabidopsis thaliana]
                  >qi 445120 prf 1908426A carboxypeptidase Y [Arabidopsis
                  thaliana]
Seq. No.
                  232570
                  LIB3197-057-Q1-M1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2738949
BLAST score
                  623
E value
                  4.0e-65
Match length
                  127
                  89
% identity
NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x
                  ananassa]
Seq. No.
                  232571
                  LIB3197-057-Q1-M1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885343
BLAST score
                  190
                  2.0e-14
E value
                  78
Match length
% identity
                  42
NCBI Description (AC005623) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  232572
Seq. ID
                  LIB3197-057-Q1-M1-F10
                  BLASTX
Method
NCBI GI
                  q3395938
BLAST score
                  218
E value
                  1.0e-17
                  75
Match length
% identity
                  60
NCBI Description (AF076924) polypyrimidine tract-binding protein homolog
                  [Arabidopsis thaliana]
                  232573
Seq. No.
Seq. ID
                  LIB3197-057-Q1-M1-F11
Method
                  BLASTX
NCBI GI
                  q3169287
BLAST score
                  616
E value
                  3.0e-64
```

33513

(AF050673) vacuolar H+-ATPase catalytic subunit [Gossypium



```
Seq. No.
                  232574
Seq. ID
                  LIB3197-057-Q1-M1-F12
Method
                  BLASTX
NCBI GI
                  g1174592
BLAST score
                  608
E value
                  2.0e-63
Match length
                  113
                  99
% identity
NCBI Description TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
                  - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                  sativum]
Seq. No.
                  232575
Seq. ID
                  LIB3197-057-Q1-M1-F2
                  BLASTX
Method
NCBI GI
                  g3024909
BLAST score
                  158
E value
                  1.0e-10
Match length
                  141
% identity
                  33
NCBI Description HYPOTHETICAL 46.0 KD PROTEIN SLR0889
                  >gi 1652697_dbj_BAA17617_ (D90907) ABC1-like [Synechocystis
                  sp.]
                  232576
Seq. No.
Seq. ID
                  LIB3197-057-Q1-M1-F7
                  BLASTX
Method
NCBI GI
                  g2262107
BLAST score
                  182
                  1.0e-13
E value
Match length
                  42
% identity
                  81
NCBI Description (AC002343) Ser/Thr protein kinase isolog [Arabidopsis
                  thaliana]
                  232577
Seq. No.
Seq. ID
                  LIB3197-057-Q1-M1-G10
Method
                  BLASTX
NCBI GI
                  g1076560
BLAST score
                  390
E value
                  8.0e-38
Match length
                  93
% identity
NCBI Description cysteine proteinase inhibitor - castor bean
                  232578
Seq. No.
Seq. ID
                  LIB3197-057-Q1-M1-G11
Method
                  BLASTX
NCBI GI
                  g755150
BLAST score
                  395
E value
                  2.0e-38
Match length
                  113
% identity
                  51
NCBI Description (U13670) vacuolar H+-ATPase proteolipid (16 kDa) subunit
                  [Gossypium hirsutum]
```

NCBI GI

E value

BLAST score

q2388689

1.0e-13

184



```
LIB3197-057-Q1-M1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3641834
BLAST score
                  524
E value
                  2.0e-53
Match length
                  114
% identity
                  85
NCBI Description
                  (AJ007312) pyruvate dehydrogenase kinase [Arabidopsis
                  thaliana]
Seq. No.
                  232580
                  LIB3197-057-Q1-M1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3822036
BLAST score
                  215
E value
                  2.0e-17
Match length
                  115
% identity
                  45
NCBI Description (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]
Seq. No.
                  232581
Seq. ID
                  LIB3197-057-Q1-M1-G6
Method
                  BLASTX
NCBI GI
                  q4512653
BLAST score
                  370
E value
                  2.0e-35
Match length
                  87
% identity
NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]
Seq. No.
                  232582
                  LIB3197-057-Q1-M1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4204263
BLAST score
                  366
E value
                  4.0e-35
                  106
Match length
                  59
% identity
NCBI Description (AC005223) 40409 [Arabidopsis thaliana]
Seq. No.
                  232583
Seq. ID
                  LIB3197-057-Q1-M1-G9
                  BLASTX
Method
NCBI GI
                  g974782
BLAST score
                  235
                  8.0e-20
E value
Match length
                  102
                  50
% identity
NCBI Description (Z49150) cobalamine-independent methionine synthase
                  [Solenostemon scutellarioides]
                  232584
Seq. No.
Seq. ID
                  LIB3197-057-Q1-M1-H1
Method
                  BLASTX
```



```
79
Match length
% identity
                  52
NCBI Description (AF016633) GH1 protein [Glycine max]
Seq. No.
                  232585
Seq. ID
                  LIB3197-057-Q1-M1-H10
Method
                  BLASTX
NCBI GI
                  q2827529
BLAST score
                  249
E value
                  3.0e-21
Match length
                  115
                  45
% identity
NCBI Description (AL021633) putative protein [Arabidopsis thaliana]
Seq. No.
                  232586
                  LIB3197-057-Q1-M1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q232024
BLAST score
                  658
E value
                  3.0e-69
Match length
                  124
                  99
% identity
NCBI Description PROTEIN E6 >gi_421806_pir__A46130 fiber protein - upland
                  cotton >gi_2129498_pir__S65061 fiber protein E6 (clone
                  CKE6-1A) - upland cotton >gi_167323 (M92051) 5' start site
                  is putative; putative [Gossypium hirsutum] >gi_1000084
                   (U30505) E6 [Gossypium hirsutum]
                  232587
Seq. No.
Seq. ID
                  LIB3197-057-Q1-M1-H3
Method
                  BLASTX
NCBI GI
                  g4415996
BLAST score
                  484
E value
                  5.0e-49
Match length
                  97
% identity
                  95
NCBI Description (AF059290) beta-tubulin 4 [Eleusine indica]
Seq. No.
                  232588
Seq. ID
                  LIB3197-057-Q1-M1-H4
Method
                  BLASTX
NCBI GI
                  g4580460
BLAST score
                  324
E value
                  3.0e-30
Match length
                  87
% identity
                  76
NCBI Description
                  (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
                  thaliana]
```

Seq. ID

Method BLASTX
NCBI GI g135535
BLAST score 599
E value 2.0e-62
Match length 132
% identity 91

33516

LIB3197-057-Q1-M1-H5



NCBI Description T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) >gi 322602 pir JN0448 t-complex polypeptide Tcp-1 - Arabidopsis thaliana >gi\_217871\_dbj\_BAA01955\_ (D11351) t-complex polypeptide 1 homologue [Arabidopsis thaliana] >gi\_2326265\_dbj\_BAA21772\_ (D11352) CCT alpha/TCP-1 [Arabidopsis thaliana] 232590 Seq. No. Seq. ID LIB3197-057-Q1-M1-H6 Method BLASTX NCBI GI g1931647 BLAST score 320 E value 1.0e-29 Match length . 86 71 % identity NCBI Description (U95973) endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana] Seq. No. 232591 Seq. ID LIB3197-057-Q1-M1-H8 Method BLASTX NCBI GI g3687237 BLAST score 227 E value 7.0e-19 Match length 100 % identity 53 NCBI Description (AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana] Seq. No. 232592 LIB3197-058-Q1-M1-B1 Seq. ID BLASTX Method NCBI GI q1663706 BLAST score 192 E value 1.0e-14 92 Match length 47 % identity NCBI Description (D87685) similar to human transcription factor TFIIS (S34159). [Homo sapiens] 232593 Seq. No. Seq. ID LIB3197-058-Q1-M1-B2 Method BLASTX NCBI GI g4220476 BLAST score 200 E value 2.0e-16 Match length 87 % identity NCBI Description (AC006069) ribophorin I-like protein [Arabidopsis thaliana] Seq. No. 232594

Seq. ID LIB3197-058-Q1-M1-C3

Method BLASTX NCBI GI q3025299 BLAST score 149 E value 2.0e-09 Match length 116



% identity NCBI Description HYPOTHETICAL 62.3 KD PROTEIN T29M21.25 >gi 2088660 (AF002109) ABC1 isolog [Arabidopsis thaliana] Seq. No. 232595 Seq. ID LIB3197-058-Q1-M1-C7 Method BLASTX NCBI GI g113116 BLAST score 391 E value 6.0e - 38Match length 140 52 % identity NCBI Description ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME) >gi\_111396\_pir\_\_ A35007 ATP citrate (pro-S)-lyase (EC
4.1.3.8) - rat >gi\_203490 (J05210) ATP citrate-lyase [Rattus norvegicus] Seq. No. 232596 Seq. ID LIB3197-058-Q1-M1-D1 Method BLASTX NCBI GI g3193284 BLAST score 235 E value 9.0e-20 Match length 116 37 % identity NCBI Description (AF069298) No definition line found [Arabidopsis thaliana] Seq. No. 232597 Seq. ID LIB3197-058-Q1-M1-D2 Method BLASTX NCBI GI g4559310 BLAST score 151 E value 8.0e-10 Match length 133 % identity 29 NCBI Description (AF129131) putative Zic3 binding protein; CBP3 protein homolog [Xenopus laevis] 232598 Seq. No. Seq. ID LIB3197-058-Q1-M1-D3 Method BLASTX NCBI GI g3702962 BLAST score 309 E value 3.0e-28 Match length 61 % identity NCBI Description (AF079484) rac GTP binding protein Arac7 [Arabidopsis thaliana] Seq. No. 232599 Seq. ID LIB3197-058-Q1-M1-D9

Seq. ID LIB3197-058-Q1-M1-D9 Method BLASTX

NCBI GI g2444178
BLAST score 689
E value 7.0e-73
Match length 140
% identity 91



```
NCBI Description (U94784) unconventional myosin [Helianthus annuus]
                  232600
Seq. No.
Seq. ID
                  LIB3197-058-Q1-M1-E9
Method
                  BLASTX
NCBI GI
                  g125887
                  110
BLAST score
E value
                  1.0e-09
                  86
Match length
                  49
% identity
NCBI Description ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
                  >gi 82092 pir S04765 LAT52 protein precursor - tomato
                  >qi 295812 emb CAA33854 (X15855) LAT52 [Lycopersicon
                  esculentum]
                  232601
Seq. No.
Seq. ID
                  LIB3197-058-Q1-M1-F1
                  BLASTX
Method
NCBI GI
                  g1174592
BLAST score
                  548
E value
                  2.0e-56
Match length
                  120
% identity
                  86
NCBI Description TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
                  - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                  sativum]
Seq. No.
                  232602
Seq. ID
                  LIB3197-058-Q1-M1-F7
Method
                  BLASTX
NCBI GI
                  g4337175
BLAST score
                  433
E value
                  7.0e-43
                  123
Match length
% identity
                  67
                 (AC006416) ESTs gb T20589, gb T04648, gb AA597906,
NCBI Description
                  gb T04111, gb R84180, gb R65428, gb T44439, gb T76570,
                  gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
                  gb AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  232603
                  LIB3197-058-Q1-M1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g972511
BLAST score
                  141
                  1.0e-18
E value
Match length
                  60
                  87
% identity
NCBI Description (X90982) phosphoenolpyruvate carboxylase [Solanum
                  tuberosum]
```

Seq. ID LIB3197-058-Q1-M1-G1

Method BLASTX NCBI GI g1354849 BLAST score 293 E value 9.0e-33

Match length

% identity

69

58



```
Match length
                  131
% identity
                  42
NCBI Description (U57350) epoxide hydrolase [Nicotiana tabacum]
                  232605
Seq. No.
Seq. ID
                  LIB3197-058-Q1-M1-G2
Method
                  BLASTX
NCBI GI
                  q1351014
BLAST score
                  461
E value
                  3.0e-46
Match length
                  111
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj BAA07207 (D38010)
                  ribosomal protein S8 [Oryza sativa]
                  232606
Seq. No.
Seq. ID
                  LIB3197-058-Q1-M1-G7
Method
                  BLASTX
NCBI GI
                  g1486472
BLAST score
                  372
E value
                  1.0e-35
Match length
                  91
% identity
                  78
NCBI Description (X99853) oxoglutarate malate translocator [Solanum
                  tuberosum]
                  232607
Seq. No.
                  LIB3197-058-Q1-M1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128175
BLAST score
                  144
                  6.0e-09
E value
                  90
Match length
% identity
                  37
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                  232608
                  LIB3197-058-Q1-M1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g461736
BLAST score
                  560
E value
                  8.0e-58
Match length
                  118
                  95
% identity
NCBI Description MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR
                  >gi 478786 pir S29316 chaperonin 60 - cucurbit
                  >gi 12546 emb CAA50218 (X70868) chaperonin 60 [Cucurbita
                  sp.]
                  232609
Seq. No.
Seq. ID
                  LIB3197-058-Q1-M1-H3
                  BLASTX
Method
                  g2245132
NCBI GI
                  187
BLAST score
                  5.0e-14
E value .
```

% identity

50





```
NCBI Description (Z97344) syntaxin [Arabidopsis thaliana]
                  232610
Seq. No.
                  LIB3197-058-Q1-M1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2811278
BLAST score
                  328
                  6.0e-31
E value
                  78
Match length
                  81
% identity
NCBI Description (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                  232611
Seq. ID
                  LIB3197-058-Q1-M1-H8
Method
                  BLASTX
NCBI GI
                  g1848212
BLAST score
                  442
E value
                  6.0e-44
                  87
Match length
% identity
                  44
NCBI Description (Y11209) protein disulfide-isomerase precursor [Nicotiana
                  tabacum]
                  232612
Seq. No.
Seq. ID
                  LIB3197-058-Q1-M1-H9
Method
                  BLASTX
NCBI GI
                  g1706377
BLAST score
                  582
E value
                  2.0e-60
                  131
Match length
% identity
                  82
NCBI Description DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL
                  4-REDUCTASE) >qi 499018 emb CAA53578 (X75964)
                  dihydroflavonol reductase [Vitis vinifera]
                  232613
Seq. No.
                  LIB3197-059-Q1-M1-A1
Seq. ID
Method
                  BLASTX
                  q3075394
NCBI GI
BLAST score
                  454
                  2.0e-45
E value
Match length
                  98
% identity
NCBI Description
                  (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis
                  thaliana] >gi 3559809 emb CAA09311 (AJ010713) fiddlehead
                  protein [Arabidopsis Thalīana]
                  232614
Seq. No.
Seq. ID
                  LIB3197-059-Q1-M1-A10
Method
                  BLASTX
NCBI GI
                  g4539459
BLAST score
                  231
E value
                  3.0e-19
Match length
                  107
```

NCBI Description (AL049500) putative protein [Arabidopsis thaliana]



```
232615
Seq. No.
Seq. ID
                   LIB3197-059-Q1-M1-A11
Method
                   BLASTX
NCBI GI
                   g3036805
BLAST score
                   347
                   9.0e-33
E value
Match length
                   80
% identity
                   78
NCBI Description (AL022373) thaumatin-like protein [Arabidopsis thaliana]
Seq. No.
                   232616
                   LIB3197-059-Q1-M1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1743009
BLAST score
                   505
E value
                   3.0e-51
Match length
                   124
                   78
% identity
NCBI Description (Y10036) SNF1-related protein kinase [Cucumis sativus]
Seq. No.
                   232617
Seq. ID
                   LIB3197-059-Q1-M1-A6
Method
                   BLASTX
NCBI GI
                   q461735
BLAST score
                   608
E value
                   2.0e-63
Match length
                   141
% identity
                   84
NCBI Description MITOCHONDRIAL CHAPERONIN HSP60-1 PRECURSOR
                   >gi_478785_pir__S29315 chaperonin 60 - cucurbit
>gi_12544_emb_CAA50217_ (X70867) chaperonin 60 [Cucurbita
Seq. No.
                   232618
Seq. ID
                   LIB3197-059-Q1-M1-A7
Method
                   BLASTX
NCBI GI
                   g1854386
BLAST score
                   480
E value
                   2.0e-48
Match length
                   121
                   74
% identity
                   (AB001375) similar to soluble NSF attachment protein [Vitis
NCBI Description
                   vinifera]
Seq. No.
                   232619
Seq. ID
                   LIB3197-059-Q1-M1-A8
                   BLASTX
Method
NCBI GI
                   g464734
BLAST score
                   562
E value
                   2.0e-61
Match length
                   141
                   83
% identity
NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
```

HYDROLASE) (ADOHCYASE) >gi\_481237\_pir\_\_\$38379

adenosylhomocysteinase (EC $^{-}3.3.1.\overline{1}$ ) - Madagascar periwinkle >gi\_407412\_emb\_CAA81527\_ (Z26881) S-adenosyl-L-homocysteine

hydrolase [Catharanthus roseus]



```
232620
Seq. No.
                  LIB3197-059-Q1-M1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3643598
                  657
BLAST score
E value
                  4.0e-69
Match length
                  146
% identity
                  84
NCBI Description (AC005395) putative poly(A) polymerase [Arabidopsis
                  thaliana]
                  232621
Seq. No.
Seq. ID
                  LIB3197-059-Q1-M1-B4
                  BLASTX
Method
NCBI GI
                  g4567250
                  196
BLAST score
E value
                  5.0e-15
                  86
Match length
                  55
% identity
NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]
                  232622
Seq. No.
Seq. ID
                  LIB3197-059-Q1-M1-B7
Method
                  BLASTX
                  g3319355
NCBI GI
                  535
BLAST score
                  7.0e-55
E value
Match length
                  125
                  91
% identity
NCBI Description (AF077407) similar to chaperonin containing TCP-1 complex
                  gamma chain [Arabidopsis thaliana]
                  232623
Seq. No.
Seq. ID
                  LIB3197-059-Q1-M1-B8
                  BLASTX
Method
NCBI GI
                  q4432845
BLAST score
                  158
E value
                  1.0e-10
                  85
Match length
% identity
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                  232624
                  LIB3197-059-Q1-M1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q584867
BLAST score
                  166
E value
                  1.0e-11
Match length
                  113
                  33
% identity
NCBI Description CYTOCHROME P450 77A2 (CYPLXXVIIA2) (P-450EG5)
                  >gi 481959 pir S40266 gene CYP77A2 protein - eggplant
                  >gi_542071_pir__S41598 cytochrome P450 77A2 - eggplant
```

melongena]

>gi 438241 emb CAA50646 (X71655) CYP77A2 [Solanum



```
Seq. No.
                  232625
Seq. ID
                  LIB3197-059-Q1-M1-C1
Method
                  BLASTX
NCBI GI
                  g2894378
BLAST score
                  311
E value
                  2.0e-28
Match length
                  132
% identity
                  51
NCBI Description (Y14573) putative ribophorin I homologue [Hordeum vulgare]
Seq. No.
                  232626
Seq. ID
                  LIB3197-059-Q1-M1-C7
Method
                  BLASTX
NCBI GI
                  q3024991
BLAST score
                  215
E value
                  3.0e-17
Match length
                  128
                  35
% identity
NCBI Description HYPOTHETICAL AMINOTRANSFERASE YBDL >gi 1778518 (U82598)
                  hypothetical protein [Escherichia coli] >gi 1786816
                  (AE000165) putative aminotransferase [Escherichia coli]
                  >gi_4062217_dbj_BAA35230_ (D90701) Aspartate transaminase
                  (EC 2.6.1.1) [Escherichia coli]
Seq. No.
                  232627
Seq. ID
                  LIB3197-059-Q1-M1-D2
Method
                  BLASTX
NCBI GI
                  g3702333
BLAST score
                  169
E value
                  7.0e-12
                  96
Match length
                  41
% identity
NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  232628
Seq. ID
                  LIB3197-059-Q1-M1-D3
Method
                  BLASTX
NCBI GI
                  g1724102
BLAST score
                  554
E value
                  5.0e-57
Match length
                  121
% identity
                  84
NCBI Description (U79766) S-adenosyl-L-homocystein hydrolase; SAH
                  [Mesembryanthemum crystallinum]
                  232629
Seq. No.
                  LIB3197-059-Q1-M1-D7
Seq. ID
Method
                  BLASTX
                  g2119278
NCBI GI
BLAST score
                  636
E value
                  1.0e-66
```

Match length 118 % identity 97

NCBI Description tubulin beta-1 chain - rice

Seq. No. 232630

Seq. ID LIB3197-059-Q1-M1-E1



```
BLASTX
Method
NCBI GI
                  g2914703
BLAST score
                  169
E value
                  7.0e-12
Match length
                  91
                  57
% identity
NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]
Seq. No.
                  232631
Seq. ID
                  LIB3197-059-Q1-M1-E2
Method
                  BLASTX
NCBI GI
                  g2245094
BLAST score
                  176
E value
                  1.0e-12
                  78
Match length
% identity
                  53
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  232632
                  LIB3197-059-Q1-M1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3068714
BLAST score
                  581
E value
                  3.0e-60
Match length
                  133
% identity
                  32
NCBI Description (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                  232633
Seq. ID
                  LIB3197-059-Q1-M1-E8
Method
                  BLASTX
NCBI GI
                  g730463
BLAST score
                  270
E value
                  1.0e-23
Match length
                  83
% identity
                  60
NCBI Description 60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
                  >gi 630323 pir S44069 ribosomal protein L35a.e.c15 - yeast
                  (Saccharomyces cerevisiae) >gi 484241 (L23923) ribosomal
                  protein L37 [Saccharomyces cerevisiae]
                  >gi_1420537_emb_CAA99454_ (Z75142) ORF YOR234c
                  [Saccharomyces cerevisiae]
Seq. No.
                  232634
Seq. ID
                  LIB3197-059-Q1-M1-E9
                  {\tt BLASTX}
Method
                  g3122060
NCBI GI
BLAST score
                  416
E value
                  4.0e-41
Match length
                  81
% identity
                  99
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                  >gi 2598657 emb CAA10847 (AJ222579) elongation factor
                  1-alpha (EF1-a) [Vicia faba]
```

Seq. ID LIB3197-059-Q1-M1-F1



```
BLASTX
Method
NCBI GI
                   g4056469
BLAST score
                   586
E value
                   8.0e-61
Match length
                   116
                   98
% identity
```

(AC005990) Strong similarity to gb\_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb\_Z25826, gb\_R90191, gb\_N65697, gb\_AA713150, gb\_T46332, gb\_AA040967, NCBI Description

gb\_AA712956, gb\_T46403, gb\_T46050, gb\_AI100391 and

gb Z25043 come from t

Seq. No. 232636

Seq. ID LIB3197-059-Q1-M1-F2

Method BLASTX NCBI GI g2088651 BLAST score 168 E value 9.0e-12 Match length 75 % identity 39

NCBI Description (AF002109) hypersensitivity-related gene 201 isolog

[Arabidopsis thaliana]

232637 Seq. No.

LIB3197-059-Q1-M1-F3 Seq. ID

Method BLASTX NCBI GI g3600060 BLAST score 311 E value 2.0e-28 Match length 87 % identity 69

NCBI Description (AF080120) contains similarity to protein kinases (Pfam:

pkinase.hmm, score: 24.94) [Arabidopsis thaliana]

232638 Seq. No.

Seq. ID LIB3197-059-Q1-M1-F8

Method BLASTX NCBI GI g4138137 BLAST score 502 E value 5.0e-51 Match length 131 % identity 67

NCBI Description (AJ012796) ss-galactosidase [Lycopersicon esculentum]

Seq. No. 232639

Seq. ID LIB3197-059-Q1-M1-F9

Method BLASTX NCBI GI q3915699 BLAST score 578 8.0e-60 E value Match length 121 % identity

NCBI Description AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T

> PROTEIN) >gi\_541970\_pir\_ S40260 T-protein - garden pea >gi\_1362061\_pir\_\_S56661 glycine decarboxylase T protein precursor - garden pea >gi 438217 emb CAA81080 (Z25861)

T-protein [Pisum sativum] >gi 3021553 emb CAA10976



## (AJ222771) T protein [Pisum sativum]

```
Seq. No.
                  232640
                  LIB3197-059-Q1-M1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2288981
BLAST score
                  300
E value
                  3.0e-27
Match length
                  89
% identity
                  39
NCBI Description
                  (AC002335) calcium binding protein isolog [Arabidopsis
                  thaliana] >gi 3763938 (AC004450) putative calcium binding
                  protein [Arabidopsis thaliana]
Seq. No.
                  232641
                  LIB3197-059-Q1-M1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3702332
BLAST score
                  251
E value
                  1.0e-21
Match length
                  81
                  58
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.
                  232642
                  LIB3197-059-Q1-M1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3738297
BLAST score
                  271
E value
                  7.0e-24
                  92
Match length
% identity
                  28
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                  232643
Seq. ID
                  LIB3197-059-Q1-M1-G3
Method
                  BLASTX
NCBI GI
                  g1477428
BLAST score
                  615
E value
                  3.0e-64
                  140
Match length
                  85
% identity
NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]
Seq. No.
                  232644
Seq. ID
                  LIB3197-059-Q1-M1-G5
                  BLASTX
Method
NCBI GI
                  g3063710
BLAST score
                  498
                  2.0e-50
E value
Match length
                  144
                  66
% identity
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]
```

Seq. No. 232645

Seq. ID LIB3197-059-Q1-M1-G6

Method BLASTX

E value

Match length

% identity

2.0e-44

103

84



```
NCBI GI
                  g71634
BLAST score
                  472
E value
                  2.0e-47
Match length
                  88
                  100
% identity
NCBI Description actin 1 - rice
                  232646
Seq. No.
Seq. ID
                  LIB3197-059-Q1-M1-G7
Method
                  BLASTX
NCBI GI
                  g1495251
BLAST score
                  228
E value
                  6.0e-19
Match length
                  85
                  74
% identity
NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]
Seq. No.
                  232647
Seq. ID
                  LIB3197-059-Q1-M1-G8
Method
                  BLASTX
NCBI GI
                  g1174162
BLAST score
                  257
E value
                  3.0e-22
                  51
Match length
% identity
                  90
                  (U44976) ubiquitin-conjugating enzyme [Arabidopsis
NCBI Description
                  thaliana] >gi 3746915 (AF091106) E2
                  ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
Seq. No.
                  232648
Seq. ID
                  LIB3197-059-Q1-M1-G9
Method
                  BLASTX
NCBI GI
                  g3135693
BLAST score
                  217
E value
                  1.0e-17
Match length
                  43
% identity
NCBI Description (AF064201) glutathione S-transferase [Gossypium hirsutum]
Seq. No.
                  232649
Seq. ID
                  LIB3197-059-Q1-M1-H1
Method
                  BLASTX
NCBI GI
                  g3163946
BLAST score
                  644
                  1.0e-67
E value
Match length
                  144
% identity
                  88
NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]
                  232650
Seq. No.
Seq. ID
                  LIB3197-059-Q1-M1-H10
Method
                  BLASTX
NCBI GI
                  g1709761
BLAST score
                  346
```



NCBI Description PROTEASOME 27 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE COMPLEX 27 KD SUBUNIT) >gi\_1262146\_emb\_CAA65660\_ (X96974) proteasome subunit [Spinacia oleracea]

Seq. No. 232651

Seq. ID LIB3197-059-Q1-M1-H11

Method BLASTX
NCBI GI g3355468
BLAST score 305
E value 5.0e-52
Match length 123
% identity 82

NCBI Description (AC004218) putative ribosomal protein L35 [Arabidopsis

thalianal

Seq. No. 232652

Seq. ID LIB3197-059-Q1-M1-H2

Method BLASTX
NCBI GI g3413511
BLAST score 353
E value 2.0e-33
Match length 105
% identity 70

NCBI Description (AJ000265) glucose-6-phosphate isomerase [Spinacia

oleracea]

Seq. No. 232653

Seq. ID LIB3197-059-Q1-M1-H3

Method BLASTX
NCBI GI g267069
BLAST score 642
E value 2.0e-67
Match length 119
% identity 98

NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi 166914

(M84696) apha-2 tubulin [Arabidopsis thaliana] >gi\_166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No. 232654

Seq. ID LIB3197-059-Q1-M1-H6

Method BLASTX
NCBI GI g3885329
BLAST score 524
E value 1.0e-53
Match length 130
% identity 81

NCBI Description (AC005623) alien-like protein [Arabidopsis thaliana]

Seq. No. 232655

Seq. ID LIB3197-059-Q1-M1-H8

Method BLASTX
NCBI GI g2119278
BLAST score 584
E value 1.0e-60
Match length 107
% identity 97



```
NCBI Description
                  tubulin beta-1 chain - rice
Seq. No.
                   232656
Seq. ID
                   LIB3197-059-Q1-M1-H9
Method
                   BLASTX
NCBI GI
                   g3169287
BLAST score
                   166
E value
                   1.0e-11
Match length
                   52
% identity
                   65
NCBI Description
                   (AF050673) vacuolar H+-ATPase catalytic subunit [Gossypium
                   hirsutum]
                   232657
Seq. No.
Seq. ID
                   LIB3197-060-Q1-M1-A10
Method
                   BLASTX
NCBI GI
                   g1172872
BLAST score
                   310
E value
                   2.0e-28
Match length
                   132
% identity
                   56
                  CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
NCBI Description
                   precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_
                   (D13042) thiol protease [Arabidopsis thaliana]
                   >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible
                   cysteine proteinase RD19A precursor [Arabidopsis thaliana]
Seq. No.
                   232658
Seq. ID
                   LIB3197-060-Q1-M1-A11
Method
                   BLASTX
NCBI GI
                   g1076746
BLAST score
                   652
E value
                   3.0e-69
Match length
                   147
% identity
                   97
                   heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
                   232659
Seq. No.
Seq. ID
                   LIB3197-060-Q1-M1-A2
Method
                   BLASTX
NCBI GI
                   g586076
                   528
BLAST score
E value
                   5.0e-54
                   105
Match length
                   88
% identity
NCBI Description
                   TUBULIN BETA-1 CHAIN >gi 486734 pir S35142 tubulin beta
                   chain - white lupine >gi 402636 emb CAA49736 (X70184) Beta
                   tubulin 1 [Lupinus albus]
                   232660
Seq. No.
Seq. ID
                   LIB3197-060-Q1-M1-A3
```

BLASTX g1172872 BLAST score 264

Method

NCBI GI



```
E value
                   4.0e-23
Match length
                  116
                  50 -
% identity
                  CYSTEINE PROTEINASE RD19A PRECURSOR >gi 541856 pir JN0718
NCBI Description
                  drought-inducible cysteine proteinase (\overline{\text{EC}} 3.4.\overline{22}.-) RD19A
                  precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_
                   (D13042) thiol protease [Arabidopsis thaliana]
                  >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible
                  cysteine proteinase RD19A precursor [Arabidopsis thaliana]
Seq. No.
                  232661
                  LIB3197-060-Q1-M1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1055161
BLAST score
                  155
                  3.0e-10
E value
                  139
Match length
% identity
                  25
NCBI Description (U40029) similar to human 100 kDa coactivator (U22055)
                  [Caenorhabditis elegans]
                  232662
Seq. No.
Seq. ID
                  LIB3197-060-Q1-M1-B1
Method
                  BLASTX
NCBI GI
                  q2497543
BLAST score
                  328
                  7.0e-31
E value
Match length
                  84
                  77
% identity
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 542061 pir S41379
                  pyruvate kinase - common tobacco >gi 444023_emb_CAA82628
                  (Z29492) pyruvate kinase [Nicotiana Tabacum]
Seq. No.
                   232663
Seq. ID
                  LIB3197-060-Q1-M1-B10
Method
                  BLASTX
NCBI GI
                  q4204849
BLAST score
                  184
E value
                   1.0e-13
                  90
Match length
                   50
% identity
NCBI Description (U55875) protein kinase [Arabidopsis thaliana]
                  232664
Seq. No.
Seq. ID
                  LIB3197-060-Q1-M1-B11
Method
                  BLASTX
NCBI GI
                  g4337176
                  219
BLAST score
E value
                  1.0e-17
                  133
Match length
% identity
NCBI Description (AC006416) T31J12.4 [Arabidopsis thaliana]
```

Seq. ID LIB3197-060-Q1-M1-B2

Method BLASTX g3650032 NCBI GI



```
BLAST score
E value
                  2.0e-20
Match length
                  55
% identity
                  67
NCBI Description (AC005396) gibberellin-regulated protein GAST1-like
                  [Arabidopsis thaliana]
Seq. No.
                  232666
Seq. ID
                  LIB3197-060-Q1-M1-B5
Method
                  BLASTX
NCBI GI
                  g2384671
BLAST score
                  578
E value
                  8.0e-60
Match length
                  150
% identity
                  74
NCBI Description (AF012657) putative potassium transporter AtKT2p
                  [Arabidopsis thaliana]
Seq. No.
                  232667
Seq. ID
                  LIB3197-060-Q1-M1-B7
Method
                  BLASTX
NCBI GI
                  g1245343
BLAST score
                  226
E value
                  1.0e-18
Match length
                  65
% identity
                  62
NCBI Description (U50194) tripeptidylpeptidase II [Rattus norvegicus]
Seq. No.
                  232668
Seq. ID
                  LIB3197-060-Q1-M1-B8
Method
                  BLASTX
NCBI GI
                  g1777921
BLAST score
                  615
E value
                  3.0e-64
Match length
                  126
% identity
                  93
NCBI Description (U54774) glutamate decarboxylase [Nicotiana tabacum]
Seq. No.
                  232669
Seq. ID
                  LIB3197-060-Q1-M1-C10
Method
                  BLASTX
NCBI GI
                  g2832625
BLAST score
                  431
E value
                  1.0e-42
Match length
                  102
% identity
                  81
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                  232670
Seq. ID
                  LIB3197-060-Q1-M1-C11
                  BLASTX
Method
NCBI GI
                  g3023271
```

NCBI GI g3023273 BLAST score 691 E value 4.0e-73 Match length 140 % identity 95

NCBI Description GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)



(FALDH) (GSH-FDH)  $>gi_1675394$  (U77637) class III ADH enzyme [Oryza sativa]

Seq. No. 232671

Seq. ID LIB3197-060-Q1-M1-C2

Method BLASTX
NCBI GI g3334115
BLAST score 546
E value 4.0e-56
Match length 110
% identity 97

NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)

(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi\_2463664 (AF006489) adenine nucleotide translocator 1 [Gossypium

hirsutum]

Seq. No. 232672

Seq. ID LIB3197-060-Q1-M1-C3

Method BLASTX
NCBI GI g507275
BLAST score 178
E value 5.0e-13
Match length 105
% identity 40

NCBI Description (L34159) NADPH:quinone oxidoreductase/zeta crystallin [Lama

guanicoe]

Seq. No. 232673

Seq. ID LIB3197-060-Q1-M1-C5

Method BLASTX
NCBI GI g3269293
BLAST score 275
E value 3.0e-24
Match length 132
% identity 47

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

Seq. No. 3 232674

Seq. ID LIB3197-060-Q1-M1-C6

Method BLASTX
NCBI GI g1771162
BLAST score 515
E value 2.0e-52
Match length 130
% identity 82

NCBI Description (X98930) SBT2 [Lycopersicon esculentum]

>gi 3687307 emb CAA07000 (AJ006379) subtilisin-like

protease [Lycopersicon esculentum]

Seq. No. 232675

Seq. ID LIB3197-060-Q1-M1-C7

Method BLASTX
NCBI GI g1170567
BLAST score 635
E value 2.0e-67
Match length 143
% identity 92

% identity



```
NCBI Description MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)
                  >gi 1085960 pir S52648 INO1 protein - Citrus paradisi
                  >gi 602565 emb CAA83565 (Z32632) INO1 [Citrus x paradisi]
Seq. No.
                  232676
Seq. ID
                  LIB3197-060-Q1-M1-C8
Method
                  BLASTX
NCBI GI
                  g418854
BLAST score
                  688
E value
                  9.0e-73
Match length
                  138
% identity
                  18
NCBI Description ubiquitin precursor - parsley >gi 288112 emb CAA45621
                  (X64344) polyubiquitin [Petroselinum crispum]
                  >gi_288114_emb_CAA45622_ (X64345) polyubiquitin
                  [Petroselinum crispum]
                  232677
Seq. No.
Seq. ID
                  LIB3197-060-Q1-M1-C9
Method
                  BLASTX
NCBI GI
                  g1220196
BLAST score
                  518
E value
                  7.0e-53
Match length
                  119
% identity
                  80
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.
                  232678
Seq. ID
                  LIB3197-060-Q1-M1-D1
Method
                  BLASTX
NCBI GI
                  g463365
BLAST score
                  149
E value
                  4.0e-10
Match length
                  47
% identity
                  68
NCBI Description (U03702) ubiquitin [Affinetrina eburnea ]
                  232679
Seq. No.
Seq. ID
                  LIB3197-060-Q1-M1-D11
Method
                  BLASTX
NCBI GI
                  g3582436
BLAST score
                  477
E value
                  5.0e-48
Match length
                  142
% identity
                  67
NCBI Description (AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]
Seq. No.
                  232680
Seq. ID
                  LIB3197-060-Q1-M1-D3
Method
                  BLASTX
NCBI GI
                  g3668089
BLAST score
                  149
E value
                  1.0e-09
Match length
                  58
```

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]



232681

Seq. No.

```
Seq. ID
                  LIB3197-060-Q1-M1-D4
Method
                  BLASTX
NCBI GI.
                  g4191778
BLAST score
                  489
E value
                  2.0e-49
Match length
                  131
% identity
                  74
NCBI Description (AC005917) putative nucleosome assembly protein I
                  [Arabidopsis thaliana]
                  232682
Seq. No.
Seq. ID
                  LIB3197-060-Q1-M1-D5
Method
                  BLASTX
NCBI GI
                  g3702368
BLAST score
                  500
E value
                  1.0e-50
Match length
                  121
                  77
% identity
NCBI Description (AJ001855) alpha subunit of F-actin capping protein
                  [Arabidopsis thaliana]
Seq. No.
                  232683
Seq. ID
                  LIB3197-060-Q1-M1-D6
Method
                  BLASTX
NCBI GI
                  q3097321
BLAST score
                  180
E value
                  2.0e-13
Match length
                  79
% identity
                  44
NCBI Description (AB013289) Bd 30K [Glycine max]
Seq. No.
                  232684
Seq. ID
                  LIB3197-060-Q1-M1-D7
Method
                  BLASTX
NCBI GI
                  g466160
BLAST score
                  373
E value
                  8.0e-36
Match length
                  84
% identity
                  85
NCBI Description HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III
                  >gi 630771 pir S44903 ZK652.3 protein - Caenorhabditis
                  elegans >gi 289769 (L14429) putative [Caenorhabditis
                  elegans]
                  232685
Seq. No.
Seq. ID
                  LIB3197-060-Q1-M1-D8
Method
                  BLASTX
NCBI GI
                  g2244732
BLAST score
                  537
E value
                  5.0e-55
Match length
                  103
% identity
                  100
NCBI Description (D88413) endo-xyloglucan transferase [Gossypium hirsutum]
                  232686
Seq. No.
Seq. ID
                  LIB3197-060-Q1-M1-D9
```



```
Method
                  BLASTX
NCBI GI
                  q974782
BLAST score
                  493
E value
                  5.0e-50
Match length
                  99
                  99
% identity
                  (Z49150) cobalamine-independent methionine synthase
NCBI Description
                  [Solenostemon scutellarioides]
                  232687
Seq. No.
Seq. ID
                  LIB3197-060-Q1-M1-E1
Method
                  BLASTX
NCBI GI
                  a2459420
BLAST score
                  638
E value
                  6.0e-67
Match length
                  125
% identity
                  (AC002332) putative ribosomal protein L17 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  232688
                  LIB3197-060-Q1-M1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3859659
                  151
BLAST score
E value
                  9.0e-10
Match length
                  60
                  53
% identity
NCBI Description
                  (AL031394) putative potassium transporter AtKT5p (AtKT5)
                  [Arabidopsis thaliana]
Seq. No.
                  232689
Seq. ID
                  LIB3197-060-Q1-M1-E11
Method
                  BLASTX
NCBI GI
                  q1491615
BLAST score
                  252
E value
                  1.0e-21
Match length
                  113
% identity
                   45
                  (X99923) male sterility 2-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  232690
Seq. No.
Seq. ID
                  LIB3197-060-Q1-M1-E2
Method
                  BLASTX
NCBI GI
                  g3023815
BLAST score
                  370
E value
                  2.0e-35
                  108
Match length
% identity
                  69
                  GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM
NCBI Description
                   (G6PD) >gi 1362053 pir S57785 glucose-6-phosphate
                  1-dehydrogenase (EC 1.1.1.49) - alfalfa >gi 603219 (U18238)
                  glucose-6-phosphate dehydrogenase [Medicago sativa subsp.
```

sativa]



```
LIB3197-060-Q1-M1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2497492
BLAST score
                   240
E value
                   9.0e-26
Match length
                   121
% identity
                   55
NCBI Description
                   URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP
                   KINASE) >gi 1653646_dbj_BAA18558_ (D90915) uridine
                   monophosphate kinase [Synechocystis sp.]
Seq. No.
                   232692
Seq. ID
                   LIB3197-060-Q1-M1-E6
Method
                   BLASTX
NCBI GI
                   g2129578
BLAST score
                   227
E value
                   8.0e-19
Match length
                   63
                   75
% identity
NCBI Description
                   dTDP-glucose 4-6-dehydratases homolog - Arabidopsis
                   thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana]
                   >qi 1585435 prf 2124427B diamide resistance gene
                   [Arabidopsis thaliana]
Seq. No.
                   232693
Seq. ID
                   LIB3197-060-Q1-M1-E7
Method
                   BLASTX
NCBI GI
                   g2880051
BLAST score
                   167
E value
                   1.0e-11
Match length
                   64
% identity
                   53
NCBI Description (AC002340) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   232694
Seq. ID
                   LIB3197-060-Q1-M1-E8
Method
                   BLASTX
NCBI GI
                   g134891
BLAST score
                   142
                   9.0e-09
E value
                   99
Match length
                   35
% identity
NCBI Description SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT
                   (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA)
                   >gi 89066 pir A24570 signal recognition particle receptor
                   precursor - dog >gi 997 emb CAA26945 (X03184) signal
                   recognition particle receptor [Canis sp.]
                   >gi 224778 prf 1112224A signal recognition particle
                   receptor [Canis familiaris]
                   232695
Seq. No.
```

Seq. ID LIB3197-060-Q1-M1-F12

Method BLASTX NCBI GI g484656 BLAST score 599 E value 3.0e-62



```
Match length
% identity
                  80
                  monodehydroascorbate reductase (NADH) (EC 1.6.5.4) -
NCBI Description
                  cucumber >gi_452165_dbj_BAA05408_ (D26392)
                  monodehydroascorbate reductase [Cucumis sativus]
                  232696
Seq. No.
Seq. ID
                  LIB3197-060-Q1-M1-F4
Method
                  BLASTX
NCBI GI
                  g2493046
BLAST score
                  513
E value
                  3.0e-52
Match length
                  129
                  75
% identity
NCBI Description ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR
                  >gi_82297_pir__A41740 H+-transporting ATP synthase (EC
                  3.6.1.34) delta' chain precursor - sweet potato
                  >gi 217938 dbj BAA01511 (D10660) mitochondrial F1-ATPase
                  delta subunit [Ipomoea batatas]
Seq. No.
                  232697
Seq. ID
                  LIB3197-060-Q1-M1-F5
Method
                  BLASTX
NCBI GI
                  q4204260
BLAST score
                  196
                  5.0e-15
E value
Match length
                  60
% identity
                  60
NCBI Description (AC005223) 25568 [Arabidopsis thaliana]
                  232698
Seq. No.
Seq. ID
                  LIB3197-060-Q1-M1-F9
Method
                  BLASTX
NCBI GI
                  g3493172
BLAST score
                  520
                  4.0e-53
E value
Match length
                  112
% identity
                  91
NCBI Description (U89609) fiber annexin [Gossypium hirsutum]
Seq. No.
                  232699
Seq. ID
                  LIB3197-060-Q1-M1-G1
Method
                  BLASTX
NCBI GI
                  g3413167
BLAST score
                  166
E value
                  1.0e-11
Match length
                  34
% identity
                  97
NCBI Description (AJ010225) elongation factor 1-alpha [Cicer arietinum]
```

LIB3197-060-Q1-M1-G10 Seq. ID Method BLASTX

NCBI GI q1703380 BLAST score 704 E value 1.0e-74 Match length 136

% identity NCBI Description ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760) ADP-ribosylation factor [Oryza sativa] 232701 Seq. No. Seq. ID LIB3197-060-Q1-M1-G11 Method BLASTX NCBI GI q4104242 BLAST score 332 E value 5.0e - 3193 Match length 73 % identity NCBI Description (AF034266) palmitoyl-acyl carrier protein thioesterase [Gossypium hirsutum] 232702 Seq. No. Seq. ID LIB3197-060-Q1-M1-G12 BLASTX Method NCBI GI g4220532 BLAST score 144 E value 5.0e-09 Match length 53 % identity 62 NCBI Description (AL035356) putative protein [Arabidopsis thaliana] 232703 Seq. No. Seq. ID LIB3197-060-Q1-M1-G2 BLASTX Method g2894612 426 5.0e-42 111 71 NCBI Description (AL021889) putative protein [Arabidopsis thaliana] 232704 Seq. No.

NCBI GI BLAST score E value Match length % identity

Seq. ID LIB3197-060-Q1-M1-G4

BLASTX Method NCBI GI q4101626 BLAST score 528 E value 5.0e-54 122 Match length 78 % identity

NCBI Description (AF005096) desaturase/cytochrome b5 protein [Ricinus

communis]

232705 Seq. No.

Seq. ID LIB3197-060-Q1-M1-G8

Method BLASTX NCBI GI q2407800 BLAST score 402 E value 3.0e-39 Match length 89 % identity 91

NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No. 232706



```
Seq. ID
                    LIB3197-060-Q1-M1-G9
 Method
                   BLASTX
 NCBI GI
                    g267069
 BLAST score
                    616
 E value
                    3.0e-64
 Match length
                    114
 % identity
                    99
 NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
                    tubulin alpha chain - Arabidopsis thaliana >gi 166914
                    (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                    (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                    232707
 Seq. No.
 Seq. ID
                    LIB3197-060-Q1-M1-H1
 Method
                    BLASTX
 NCBI GI
                    g4539408
 BLAST score
                    287
 E value
                    1.0e-25
                    74
 Match length
                    73
 % identity
 NCBI Description (ALO49524) putative alpha NAC [Arabidopsis thaliana]
 Seq. No.
                    232708
 Seq. ID
                    LIB3197-060-Q1-M1-H10
 Method
                    BLASTX
NCBI GI
                    q4512671
 BLAST score
                    299
                    4.0e-27
 E value
 Match length
                    74
                    73
 % identity
 NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    232709
 Seq. ID
                    LIB3197-060-Q1-M1-H11
 Method
                   BLASTX
 NCBI GI
                    q3041738
 BLAST score
                    431
 E value
                    1.0e-42
 Match length
                    146
 % identity
                    60
 NCBI Description T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA)
                    (HIV-1 NEF INTERACTING PROTEIN) >gi 2559010 (AF026292)
                    chaperonin containing t-complex polypeptide 1, eta subunit;
                    CCT-eta [Homo sapiens]
                    232710
  Seq. No.
                    LIB3197-060-Q1-M1-H6
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2118222
 BLAST score
                    364
                    9.0e-35
 E value
                    87
 Match length
                    54
  % identity
 NCBI Description H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
```

33540

thaliana]

(clone AVA-P4) - Arabidopsis thaliana >gi\_926935 (L44584) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis



```
Seq. No.
                    232711
Seq. ID
                    LIB3197-060-Q1-M1-H7
Method
                    BLASTX
NCBI GI
                    g1174592
BLAST score
                    540
E value
                    2.0e-55
Match length
                    103
% identity
                    99
                    TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin
NCBI Description
                    - garden pea >gi 525332 (U12589) alpha-tubulin [Pisum
                    sativum]
Seq. No.
                    232712
                    LIB3197-060-Q1-M1-H8
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1172556
BLAST score
                    390
E value
                    8.0e-38
Match length
                    91
                    79
% identity
                    36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
NCBI Description
                    (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                    (POM 36) >gi_629729_pir__S46925 porin II, 36K - potato >gi_1076681_pir__B55364 porin (clone pPOM 36.2) - potato mitochondrion >gi_515360_emb_CAA56600_ (X80387) 36kDA porin
                    II [Solanum tuberosum]
Seq. No.
                    232713
Seq. ID
                    LIB3272-001-P1-K1-A10
Method
                    BLASTX
NCBI GI
                    g421923
BLAST score
                    386
E value
                    2.0e-37
Match length
                    94
                    70
% identity
                    pathogenesis-related protein P23 - tomato (fragment)
NCBI Description
                    >gi 542031 pir PQ0742 pathogenesis-related protein P23
                    precursor - tomato (fragment) >gi 19315 emb_CAA50059
                    (X70787) pathogenesis-related protein PR P23 [Lycopersicon
                    esculentum]
                    232714
Seq. No.
                    LIB3272-001-P1-K1-A11
Seq. ID
Method
                    BLASTX
NCBI GI
                    g4218122
BLAST score
                    332
                    5.0e-31
E value
                    120
Match length
                    57
% identity
NCBI Description (AL035353) putative protein [Arabidopsis thaliana]
                    232715
Seq. No.
Seq. ID
                    LIB3272-001-P1-K1-A4
```

Method BLASTX NCBI GI g3287824 BLAST score 524



1.0e-53 E value Match length 100 99 % identity (+)-DELTA-CADINENE SYNTHASE ISOZYME XC1 (D-CADINENE NCBI Description SYNTHASE) >gi 2147015 pir S68365 (+)-delta-cadinene synthase isozyme XC1 - Gossypium arboreum >gi 1045312 (U23206) (+)-delta-cadinene synthase isozyme XC1 [Gossypium arboreum] 232716 Seq. No. Seq. ID LIB3272-001-P1-K1-A6 Method BLASTX NCBI GI g2194122 BLAST score 195 E value 6.0e-15 Match length 133 41 % identity NCBI Description (AC002062) No definition line found [Arabidopsis thaliana] Seq. No. 232717 Seq. ID LIB3272-001-P1-K1-A7 Method BLASTX NCBI GI g3080435 BLAST score 244 E value 1.0e-20 Match length 101 % identity 51 NCBI Description (AL022605) putative protein [Arabidopsis thaliana] 232718 Seq. No. LIB3272-001-P1-K1-A9 Seq. ID Method BLASTX NCBI GI q3885884 BLAST score 581 3.0e-60 E value Match length 114 93 % identity NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa] Seq. No. 232719 Seq. ID LIB3272-001-P1-K1-B1 Method BLASTX NCBI GI q3420055 BLAST score 407 E value 8.0e-40 Match length 100 % identity 78 NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana] 232720 Seq. No. LIB3272-001-P1-K1-B10 Seq. ID Method BLASTX

NCBI GI q3738331 BLAST score 251 E value 2.0e-21 Match length 55 % identity 76

Seq. ID



```
NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]
                    232721
 Seq. No.
                    LIB3272-001-P1-K1-B3
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q3522952
 BLAST score
                    424
 E value
                    8.0e-42
 Match length
                    125
                    66
 % identity
 NCBI Description (AC004411) putative alcohol dehydrogenase [Arabidopsis
                    thaliana]
                    232722
 Seq. No.
 Seq. ID
                    LIB3272-001-P1-K1-B4
                    BLASTX
 Method
 NCBI GI
                    g529353
 BLAST score
                    295
 E value
                    1.0e-26
 Match length
                    101
 % identity
                    54
 NCBI Description (U12757) diphenol oxidase [Acer pseudoplatanus]
 Seq. No.
                    232723
                    LIB3272-001-P1-K1-B8
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2662343
 BLAST score
                    566
 E value
                    2.0e-58
 Match length
                    112
 % identity
                    96
 NCBI Description (D63581) EF-1 alpha [Oryza sativa]
 Seq. No.
                    232724
 Seq. ID
                    LIB3272-001-P1-K1-B9
 Method
                    BLASTX
 NCBI GI
                    g3395430
 BLAST score
                    144
 E value
                    5.0e-09
 Match length
                    115
 % identity
                    34
 NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                    232725
                    LIB3272-001-P1-K1-C1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g832876
 BLAST score
                    553
 E value
                    6.0e-57
 Match length
                    120
 % identity
                    90
* NCBI Description
                   (L41345) ascorbate free radical reductase [Solanum
                    lycopersicum] >gi 1097368 prf 2113407A ascorbate free
                    radical reductase [Lycopersicon esculentum]
 Seq. No.
                    232726
```

33543

LIB3272-001-P1-K1-C10

```
Method
                  BLASTX
NCBI GI
                  g3738332
BLAST score
                  322
E value
                  6.0e-30
Match length
                  125
% identity
                  55
NCBI Description (AC005170) putative eukaryotic initiation factor
                  [Arabidopsis thaliana]
Seq. No.
                  232727
Seq. ID
                  LIB3272-001-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g3559811
BLAST score
                  391
E value
                  6.0e-38
Match length
                  109
% identity
                  67
NCBI Description (AJ010735) gr1-protein [Arabidopsis thaliana]
Seq. No.
                  232728
Seq. ID
                  LIB3272-001-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g2661021
BLAST score
                  603
E value
                  7.0e-63
Match length
                  115
                  97
% identity
NCBI Description (AF035255) catalase [Glycine max]
Seq. No.
                  232729
Seq. ID
                  LIB3272-001-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g1170747
BLAST score
                  338
                  9.0e-32
E value
Match length
                  79
                  84
% identity
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEAS-A >qi 167345
                  (M88324) late embryogenesis-abundant protein [Gossypium
                  hirsutum] >gi 167347 (M37697) Lea5-A late
```

embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 232730

Seq. ID LIB3272-001-P1-K1-C6

Method BLASTX NCBI GI q3913194 BLAST score 310 E value 2.0e-28 Match length 93 % identity 56

NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE 3 (CAD) >gi 548323 (L36456)

cinnamyl-alcohol dehydrogenase [Stylosanthes humilis]

Seq. No. 232731

Seq. ID LIB3272-001-P1-K1-C7

Method BLASTX NCBI GI q2245087

33544



```
BLAST score
                    9.0e-18
 E value
 Match length
                   131
                    42
 % identity
 NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
                    232732
 Seq. No.
 Seq. ID
                    LIB3272-001-P1-K1-C8
 Method
                    BLASTX
 NCBI GI
                    g2984709
 BLAST score
                    442
 E value
                    6.0e-44
 Match length
                   91
                    90
 % identity
 NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                    232733
 Seq. No.
 Seq. ID
                    LIB3272-001-P1-K1-D1
 Method
                   BLASTX
 NCBI GI
                    g4539386
 BLAST score
                    311
 E value
                    1.0e-28
 Match length
                   134
                    25
 % identity
 NCBI Description (AL035526) extensin-like protein [Arabidopsis thaliana]
 Seq. No.
                    232734
 Seq. ID
                    LIB3272-001-P1-K1-D11
 Method
                   BLASTX
 NCBI GI
                    g3869088
 BLAST score
                    570
 E value
                    6.0e-59
                   109
 Match length
 % identity
                    100
 NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
                    232735
 Seq. No.
 Seq. ID
                    LIB3272-001-P1-K1-D3
 Method
                    BLASTX
 NCBI GI
                    g3420051
 BLAST score
                    611
 E value
                    1.0e-63
 Match length
                   110
 % identity
                    96
 NCBI Description (AC004680) unknown protein [Arabidopsis thaliana]
                    232736
· Seq. No.
                    LIB3272-001-P1-K1-D4
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q1172955
 BLAST score
                    210
 E value
                    1.0e-16
 Match length
                    66
```

Match length 66 % identity 59

NCBI Description 50S RIBOSOMAL PROTEIN L13 >gi\_1075232\_pir\_\_G64123 ribosomal

protein L13 (rpL13) homolog - Haemophilus influenzae

(strain Rd KW20) >gi 1574283 (U32823) ribosomal protein L13



## (rpL13) [Haemophilus influenzae Rd]

```
232737
Seq. No.
Seq. ID
                  LIB3272-001-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g3158376
BLAST score
                  478
E value
                  4.0e-48
Match length
                  126
% identity
                  76
NCBI Description (AF035385) unknown [Arabidopsis thaliana]
                  232738
Seq. No.
Seq. ID
                  LIB3272-001-P1-K1-D6
                  BLASTX
Method
NCBI GI
                  g4567307
BLAST score
                  207
E value
                  2.0e-16
Match length
                  102
% identity
                  45
NCBI Description (AC005956) putative zinc finger protein [Arabidopsis
                  thaliana]
                  232739
Seq. No.
                  LIB3272-001-P1-K1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g131772
BLAST score
                  288
E value
                  7.0e-26
                  74
Match length
                  81
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
                  >gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) -
                  maize
                  232740
Seq. No.
Seq. ID
                  LIB3272-001-P1-K1-D9
                  BLASTX
Method
NCBI GI
                  g3915873
BLAST score
                  714
E value
                  8.0e-76
Match length
                  136
% identity
                  96
NCBI Description SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)
                  (NODULIN-100) >gi 2606081 (AF030231) sucrose synthase
                  [Glycine max]
                  232741
Seq. No.
Seq. ID
                  LIB3272-001-P1-K1-E1
                  BLASTX
Method
                  q3063396
NCBI GI
BLAST score
                  525
E value
                  1.0e-53
Match length
                  118
% identity
                  84
NCBI Description (AB012947) vcCyP [Vicia faba]
```



```
Seq. No.
                   232742
Seq. ID
                   LIB3272-001-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g602076
BLAST score
                   645
E value
                   9.0e-68
Match length
                   130
% identity
                   23
NCBI Description (X77456) pentameric polyubiquitin [Nicotiana tabacum]
                   232743
Seq. No.
Seq. ID
                   LIB3272-001-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   q549063
BLAST score
                   396
E value
                   2.0e-38
Match length
                   103
                   76
% identity
NCBI Description
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
                   232744
Seq. No.
                   LIB3272-001-P1-K1-E3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4220534
BLAST score
                   481
E value
                   2.0e-48
                   135
Match length
                   70
% identity
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
                   232745
Seq. No.
Seq. ID
                   LIB3272-001-P1-K1-E4
                   BLASTX
Method
NCBI GI
                   q3834310
BLAST score
                   526
E value
                   9.0e-54
                   100
Match length
% identity
                  (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
NCBI Description
                   gb_D83004 from Homo sapiens. ESTs gb T88233, gb_Z24464,
                   gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122
                   come from this gene. [Arabidopsis thaliana]
Seq. No.
                   232746
                   LIB3272-001-P1-K1-E5
Seq. ID
Method
                   BLASTX
                   q1657948
NCBI GI
BLAST score
                   414
```

1.0e-40 E value 109 Match length % identity 75

NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]

Seq. No. 232747

Method

NCBI GI

BLAST score

BLASTX

356

q4455323



```
Seq. ID
                     LIB3272-001-P1-K1-E6
  Method
                     BLASTX
  NCBI GI
                     g4510346
  BLAST score
                     168
  E value
                     8.0e-12
  Match length
                     38
  % identity
                     87
  NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]
                     232748
  Seq. No.
  Seq. ID
                     LIB3272-001-P1-K1-E7
                     BLASTX
  Method
  NCBI GI
                     q3868758
  BLAST score
                     445
  E value
                     3.0e-44
  Match length
                     108
                     75
  % identity
  NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
  Seq. No.
                     232749
  Seq. ID
                     LIB3272-001-P1-K1-E9
  Method
                     BLASTX
  NCBI GI
                     q1174592
BLAST score
                     713
  E value
                     1.0e-75
  Match length
                     135
  % identity
                     98
                     TUBULIN ALPHA-1 CHAIN >gi_2119270 pir__S60233 alpha-tubulin
  NCBI Description
                     - garden pea >gi_525332 (U12589) alpha-tubulin [Pisum
                     sativum]
  Seq. No.
                     232750
  Seq. ID
                     LIB3272-001-P1-K1-F1
  Method
                     BLASTX
  NCBI GI
                     q4337046
  BLAST score
                     308
  E value
                     3.0e-28
  Match length
                     118
  % identity
                     57
NCBI Description (AF124162) molybdopterin synthase sulphurylase [Nicotiana
                     plumbaginifolia]
  Seq. No.
                     232751
  Seq. ID
                     LIB3272-001-P1-K1-F11
  Method
                     BLASTX
  NCBI GI
                     q3420239
  BLAST score
                     333
  E value
                     3.0e-31
  Match length
                     63
  % identity
                     100
  NCBI Description (AF059484) actin [Gossypium hirsutum]
  Seq. No.
                     232752
  Seq. ID
                     LIB3272-001-P1-K1-F12
```



```
E value
                    7.0e - 34
 Match length
                    94
  % identity
                    71
                    (AL035525) aminopeptidase-like protein [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    232753
 Seq. ID
                    LIB3272-001-P1-K1-F2
 Method
                    BLASTX
 NCBI GI
                    q1694976
 BLAST score
                    403
 E value
                    2.0e-39
 Match length
                    112
  % identity
                    68
 NCBI Description
                    (Y09482) HMG1 [Arabidopsis thaliana]
                    >gi 2832361 emb CAA74402 (Y14073) HMG protein [Arabidopsis
                    thaliana]
 Seq. No.
                    232754
                    LIB3272-001-P1-K1-F3
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q4204303
 BLAST score
                    462
 E value
                    3.0e-46
 Match length
                    95
% identity
                    87
 NCBI Description
                   (AC003027) lcl prt seq No definition line found
                    [Arabidopsis thaliana]
 Seq. No.
                    232755
                    LIB3272-001-P1-K1-F6
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1945611
 BLAST score
                    282
 E value
                    3.0e-25
 Match length
                    127
  % identity
                    45
                    (AB003103) 26S proteasome subunit p55 [Homo sapiens]
 NCBI Description
                    >gi 4506221 ref NP 002807.1_pPSMD12_ proteasome (prosome,
                    macropain) 26S subunit, non-ATPase,
                    232756
 Seq. No.
 Seq. ID
                    LIB3272-001-P1-K1-F8
 Method
                    BLASTX
 NCBI GI
                    g167367
 BLAST score
                    640
 E value
                    4.0e-67
 Match length
                    120
                    98
  % identity
 NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                    232757
 Seq. No.
 Seq. ID
                    LIB3272-001-P1-K1-F9
```

Method BLASTX NCBI GI q1524121 BLAST score 508 1.0e-51 E value



```
Match length
                   117
% identity
                   79
NCBI Description
                  (X96539) malate dehydrogenase [Mesembryanthemum
                  crystallinum]
                   232758
Seq. No.
Seq. ID
                  LIB3272-001-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q4098521
BLAST score
                  481
E value
                   2.0e-48
Match length
                  103
                   90
% identity
                  (U79160) HMG-CoA synthase [Arabidopsis thaliana]
NCBI Description
                   >gi 4098523 (U79161) HMG-CoA synthase [Arabidopsis
                  thaliana]
                   232759
Seq. No.
                  LIB3272-001-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3080428
BLAST score
                   321
E value
                   9.0e-30
Match length
                   98
                   56
% identity
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
                   232760
Seq. No.
                  LIB3272-001-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3668089
BLAST score
                   255
                   5.0e-22
E value
                  84
Match length
% identity
                   54
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
                   232761
Seq. No.
Seq. ID
                   LIB3272-001-P1-K1-G4
Method
                  BLASTX
NCBI GI
                   g322598
BLAST score
                   266
E value
                   3.0e-23
                  124
Match length
% identity
                   44
NCBI Description St12p protein - Arabidopsis thaliana
                   232762
Seq. No.
Seq. ID
                  LIB3272-001-P1-K1-G5
                  BLASTX
Method
NCBI GI
                   g3643602
BLAST score
                   318
```

E value 2.0e-29 Match length 114 % identity 59

(AC005395) putative tonoplast intrinsic protein NCBI Description

[Arabidopsis thaliana]



```
232763
Seq. No.
Seq. ID
                   LIB3272-001-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g267082
BLAST score
                   632
E value
                   3.0e-66
Match length
                   118
% identity
                   98
NCBI Description
                   TUBULIN BETA-8 CHAIN >gi 320189 pir JQ1592 tubulin beta-8
                   chain - Arabidopsis thaliana >gi 166908 (M84705) beta-8
                   tubulin [Arabidopsis thaliana]
Seq. No.
                   232764
                   LIB3272-001-P1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3878594
BLAST score
                   109
E value
                   3.0e-10
Match length
                   106
                   34
% identity
NCBI Description
                   (Z81102) Similarity to Mouse CMP-sialic acid transporter
                   (TR:Q61420) [Caenorhabditis elegans] >gi_3881872_emb_CAB05329 (Z82288) Similarity to Mouse
                   CMP-sialic acid transporter (TR:Q61420) [Caenorhabditis
                   elegans]
                   232765
Seq. No.
Seq. ID
                   LIB3272-001-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g2493131
BLAST score
                   503
E value
                   4.0e-51
Match length
                   106
% identity
                   95
                   VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B
NCBI Description
                   SUBUNIT) >gi 167108 (L11862) vacuolar ATPase B subunit
                   [Hordeum vulgare]
Seq. No.
                   232766
Seq. ID
                   LIB3272-001-P1-K1-G9
                   {\tt BLASTX}
Method
NCBI GI
                   g3901014
BLAST score
                   235
                   1.0e-19
E value
                   55
Match length
                   76
% identity
NCBI Description (AJ130886) metallothionein-like protein class II [Fagus
                   sylvatica]
Seq. No.
                   232767
                   LIB3272-001-P1-K1-H10
Seq. ID
```

Method BLASTX
NCBI GI g4521249
BLAST score 442
E value 6.0e-44
Match length 111



```
% identity
NCBI Description
                  (AB013912) DNA helicase [Mus musculus]
                   232768
Seq. No.
                  LIB3272-001-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g629597
BLAST score
                  214
E value
                   3.0e-31
Match length
                   93
% identity
                   78
NCBI Description
                  proline-rich protein - rape >gi_545029_bbs_142669 (S68113)
                  proline-rich SAC51 [Brassica napus=oilseed rape, pods,
                  Peptide, 147 aa] [Brassica napus]
                   232769
Seq. No.
                  LIB3272-001-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g167367
BLAST score
                   368
E value
                   3.0e-35
Match length
                  101
% identity
                   71
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                   232770
Seq. ID
                  LIB3272-001-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g3135997
BLAST score
                  191
E value
                  2.0e-14
Match length
                  120
% identity
                   33
NCBI Description (AL023589) hypothetical protein [Schizosaccharomyces pombe]
                  232771
Seq. No.
Seq. ID
                  LIB3272-001-P1-K1-H9
                  BLASTX
Method
NCBI GI
                  g4335758
BLAST score
                  284
E value
                  2.0e-25
Match length
                  99
                   63
% identity
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]
                   232772
Seq. No.
Seq. ID
                  LIB3272-002-P1-K1-A1
Method
                  BLASTX
```

NCBI GI g3738325 BLAST score 292 E value 2.0e-26 Match length 86 % identity

NCBI Description (AC005170) putative CaMB-channel protein [Arabidopsis

thaliana]

Seq. No. 232773



LIB3272-002-P1-K1-A12 Seq. ID Method BLASTX NCBI GI g3077640 BLAST score 353 E value 2.0e-33 Match length 128 % identity 54 NCBI Description (AJ223151) O-methyltransferase [Prunus dulcis] Seq. No. 232774 Seq. ID LIB3272-002-P1-K1-A3 Method BLASTX NCBI GI q4539334 BLAST score 261 E value 1.0e-22 Match length 86 % identity 60 NCBI Description (AL035539) putative protein [Arabidopsis thaliana] 232775 Seq. No. LIB3272-002-P1-K1-A4 Seq. ID Method BLASTX NCBI GI q4455206 BLAST score 390 E value 6.0e-39 Match length 126 % identity NCBI Description (AL035440) putative beta-1, 3-glucanase [Arabidopsis thaliana] Seq. No. 232776 Seq. ID LIB3272-002-P1-K1-A5 Method BLASTX NCBI GI q2052029 BLAST score 479 E value 3.0e-48Match length 120 % identity 72 NCBI Description (Y10820) glutathione transferase [Glycine max] Seq. No. 232777 LIB3272-002-P1-K1-A6 Seq. ID Method BLASTX NCBI GI g2459417 BLAST score 503 E value 4.0e-51 Match length 109 % identity 85 NCBI Description (AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana] 232778 Seq. No.

Seq. ID LIB3272-002-P1-K1-A9

Method BLASTX NCBI GI g1694976 BLAST score 409 E value 5.0e-40



Match length 115 % identity NCBI Description

(Y09482) HMG1 [Arabidopsis thaliana]

>gi 2832361\_emb\_CAA74402\_ (Y14073) HMG protein [Arabidopsis

thaliana]

Seq. No. Seq. ID

232779

LIB3272-002-P1-K1-B10

Method BLASTX NCBI GI q4467145 BLAST score 297 E value 6.0e-27 Match length 70 80 % identity

NCBI Description (AL035540) farnesylated protein (ATFP6) [Arabidopsis

thalianal

Seq. No.

232780

LIB3272-002-P1-K1-B11 Seq. ID

Method BLASTX NCBI GI g3924597 BLAST score 207 2.0e-16 E value Match length 113 % identity 37

NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.

232781 Seq. ID LIB3272-002-P1-K1-B12

Method BLASTX NCBI GI g1944319 BLAST score 317 E value 2.0e-29 Match length 121 54

% identity

(D31700) cysteine proteinase inhibitor [Glycine max] NCBI Description >gi 1944342 dbj BAA19610 (D64115) cysteine proteinase

inhibitor [Glycine max]

Seq. No.

Seq. ID LIB3272-002-P1-K1-B2

232782

Method BLASTX NCBI GI q4262149 BLAST score 405 E value 1.0e-39 Match length 89 % identity 83

NCBI Description (AC005275) putative xyloglucan endotransglycosylase

[Arabidopsis thaliana]

Seq. No. 232783

Seq. ID LIB3272-002-P1-K1-B4

Method BLASTX NCBI GI q2980793 BLAST score 547 E value 3.0e-56 Match length 135

33554



% identity NCBI Description (AL022197) putative protein [Arabidopsis thaliana] 232784 Seq. No. Seq. ID LIB3272-002-P1-K1-B5 Method BLASTX NCBI GI g4056502 BLAST score 432 E value 9.0e-43Match length 103 % identity 83 (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana] NCBI Description 232785 Seq. No. LIB3272-002-P1-K1-B7 Seq. ID Method BLASTX NCBI GI g1173256 BLAST score 633 E value 3.0e-66 Match length 123 % identity 98 NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi 629496 pir S45026 ribosomal protein S4 - upland cotton >gi 488739 emb CAA55882 (X79300) ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum] Seq. No. 232786 Seq. ID LIB3272-002-P1-K1-C10 Method BLASTX NCBI GI g2160166 BLAST score 466 9.0e-47E value Match length 135 % identity 62 NCBI Description (AC000132) No definition line found [Arabidopsis thaliana] Seq. No. 232787 Seq. ID LIB3272-002-P1-K1-C12 Method BLASTX NCBI GI g2351380 BLAST score 235 E value 1.0e-19 Match length 96 % identity 54 NCBI Description (U54559) translation initiation factor eIF3 p40 subunit [Homo sapiens] >gi 4503515 ref NP 003747.1 pEIF3S3 UNKNOWN

Seq. No. 232788 Seq. ID LIB3272-002-P1-K1-C5

Method BLASTX NCBI GI g1326338 BLAST score 178 E value 4.0e-13 Match length 85 % identity

NCBI Description (U58746) R05G6.4 gene product [Caenorhabditis elegans]



```
Seq. No.
                  232789
Seq. ID
                  LIB3272-002-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g4538905
BLAST score
                  585
E value
                  1.0e-60
Match length
                  132
                  83
% identity
NCBI Description (AL049482) putative protein [Arabidopsis thaliana]
                  232790
Seq. No.
Seq. ID
                  LIB3272-002-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q2827558
BLAST score
                  159
E value
                  1.0e-10
                  53
Match length
                  53
% identity
NCBI Description (AL021635) putative DNA binding protein [Arabidopsis
                  thaliana]
                  232791
Seq. No.
Seq. ID
                  LIB3272-002-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2213590
BLAST score
                  186
E value
                  6.0e-14
                  78
Match length
% identity
                  41
NCBI Description (AC000348) T7N9.10 [Arabidopsis thaliana]
Seq. No.
                  232792
Seq. ID
                  LIB3272-002-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g4455208
                  555
BLAST score
E value
                  3.0e-57
Match length
                  134
% identity
                  81
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  232793
Seq. ID
                  LIB3272-002-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  q4204303
BLAST score
                  596
                  5.0e-62
E value
Match length
                  129
% identity
                  82
NCBI Description (AC003027) lcl prt seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  232794
```

Seq. No. 232794 Seq. ID LIB32

Seq. ID LIB3272-002-P1-K1-D12

Method BLASTX NCBI GI g3023815 BLAST score 516



```
E value
                   1.0e-52
Match length
                   129
                   75
% identity
                   GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM
NCBI Description
                   (G6PD) >gi_1362053_pir__S57785 glucose-6-phosphate
1-dehydrogenase (EC 1.1.1.49) - alfalfa >gi_603219 (U18238)
                   glucose-6-phosphate dehydrogenase [Medicago sativa subsp.
                   sativa]
                   232795
Seq. No.
Seq. ID
                   LIB3272-002-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   q3036840
BLAST score
                   318
E value
                   2.0e-29
Match length
                   128
% identity
                   48
                  (AJ222967) cystinosin [Homo sapiens]
NCBI Description
                   >gi 3036851 emb CAA75882 (Y15924) cystinosin [Homo
                   sapiens]
                   232796
Seq. No.
Seq. ID
                   LIB3272-002-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   q2738949
BLAST score
                   586
E value
                   8.0e-61
Match length
                   118
% identity
                   92
NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x
                   ananassa]
Seq. No.
                   232797
Seq. ID
                   LIB3272-002-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   g2739004
BLAST score
                   352
E value
                   2.0e-33
Match length
                   138
% identity
                   52
NCBI Description (AF022461) CYP82Clp [Glycine max]
Seq. No.
                   232798
Seq. ID
                   LIB3272-002-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   q2062155
BLAST score
                   523
                   2.0e-53
E value
Match length
                   135
% identity
NCBI Description (AC001645) mitochondrial processing peptidase alpha subunit
                   precusor isolog [Arabidopsis thaliana]
```

Seq. No. 232799

Seq. ID LIB3272-002-P1-K1-E12

Method BLASTX NCBI GI g832876



```
BLAST score
_ E value
                     2.0e-56
                     119
  Match length
                     90
  % identity
                    (L41345) ascorbate free radical reductase [Solanum
  NCBI Description
                     lycopersicum] >gi_1097368_prf__2113407A ascorbate free
                    radical reductase [Lycopersicon esculentum]
                    232800
  Seq. No.
                    LIB3272-002-P1-K1-E2
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g2149955
  BLAST score
                    565
  E value
                    2.0e-58
                    119
  Match length
                     91
  % identity
  NCBI Description (U97023) putative aquaporin-1 [Phaseolus vulgaris]
  Seq. No.
                     232801
  Seq. ID
                    LIB3272-002-P1-K1-E3
  Method
                    BLASTX
  NÇBI GI
                    g2435604
  BLAST score
                    117
  E value
                     5.0e-09
  Match length
                    65
  % identity
                     48
  NCBI Description (AF026213) strong similarity to Saccharomyces cerevisiae
                    endosomal P24A protein (SP:P32802) [Caenorhabditis elegans]
                     232802
  Seq. No.
  Seq. ID
                    LIB3272-002-P1-K1-E4
                    {\tt BLASTX}
  Method
  NCBI GI
                     q4468046
  BLAST score
                    303
  E value
                    1.0e-27
  Match length
                    113
  % identity
  NCBI Description (X69192) catechol methyltransferase [Vanilla planifolia]
  Seq. No.
                    232803
                    LIB3272-002-P1-K1-E5
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q480450
  BLAST score
                    418
  E value
                     4.0e-41
  Match length
                    114
                     75
  % identity
  NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
                    thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid
                    reductoisomerase [Arabidopsis thaliana]
  Seq. No.
                     232804
  Seq. ID
                    LIB3272-002-P1-K1-E6
```

Method BLASTX NCBI GI q2344897 BLAST score 217 E value 1.0e-17



```
Match length
                   59
% identity
Seq. No.
                   232805
Seq. ID
```

NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

LIB3272-002-P1-K1-E8

Method BLASTX NCBI GI g3643609 BLAST score 399 E value 7.0e-39 Match length 132 % identity 62

NCBI Description (AC005395) putative Cys3His zinc finger protein

[Arabidopsis thaliana]

Seq. No. 232806

Seq. ID LIB3272-002-P1-K1-E9

Method BLASTX NCBI GI g543867 BLAST score 436 E value 3.0e-43Match length 115 81 % identity

NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR

>gi\_1076684\_pir\_\_A47493 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor - sweet potato

>gi\_303626 dbj BAA03526 (D14699) F1-ATPase gammma subunit

[Ipomoea batatas]

232807 Seq. No.

Seq. ID LIB3272-002-P1-K1-F1

Method BLASTX NCBI GI g4539435 BLAST score 161 E value 5.0e-11 Match length 49 % identity 65

NCBI Description (AL049523) putative protein [Arabidopsis thaliana]

Seq. No. 232808

Seq. ID LIB3272-002-P1-K1-F11

Method BLASTX NCBI GI g549063 BLAST score 351 E value 3.0e-33 Match length 108 % identity 65

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi 1072464 pir A38958 IgE-dependent histamine-releasing factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 232809

Seq. ID LIB3272-002-P1-K1-F12

Method BLASTX NCBI GI q1706547 BLAST score 454



E value 2.0e-45
Match length 136
% identity 65
NCBI Description GLUCAN

Description GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM

PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi\_2129912\_pir\_\_S65077 beta-1,3-glucanase class I precursor - Para rubber tree >gi\_1184668 (U22147)

beta-1,3-glucanase [Hevea brasiliensis]

Seq. No.

232810

Seq. ID LIB3272-002-P1-K1-F2

Method BLASTX
NCBI GI g3913633
BLAST score 363
E value 1.0e-34
Match length 113
% identity 66

NCBI Description HYPOTHETICAL PROTEIN F8A5.25 >gi 2462742 (AC002292) Unknown

protein [Arabidopsis thaliana]

Seq. No.

232811

Seq. ID LIB3272-002-P1-K1-F3

Method BLASTX
NCBI GI g2501647
BLAST score 476
E value 6.0e-48
Match length 127
% identity 75

NCBI Description UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD)

>gi\_1362120\_pir\_\_S55732 uroporphyrinogen decarboxylase -

common tobacco >gi\_1009429\_emb\_CAA58040\_ (X82833) uroporphyrinogen decarboxylase [Nicotiana tabacum]

Seq. No.

232812

Seq. ID LIB3272-002-P1-K1-F4

Method BLASTX
NCBI GI g2244806
BLAST score 257
E value 3.0e-22
Match length 92
% identity 55

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.

232813

Seq. ID LIB3272-002-P1-K1-F5 Method BLASTX

Method BLASTX
NCBI GI g549063
BLAST score 506
E value 2.0e-51
Match length 117
% identity 82

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi 1072464 pir A38958 IgE-dependent histamine-releasing

factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626)

21kd polypeptide [Oryza sativa]



232814 Seq. No. Seq. ID LIB3272-002-P1-K1-F7 Method BLASTX NCBI GI g3158376 BLAST score 473 1.0e-47 E value Match length 125 76 % identity NCBI Description (AF035385) unknown [Arabidopsis thaliana] Seq. No. 232815 LIB3272-002-P1-K1-F8 Seq. ID Method BLASTX NCBI GI g1917019 BLAST score 549 E value 2.0e-56 Match length 114 90 % identity NCBI Description (U92045) ribosomal protein S6 RPS6-1 [Zea mays] Seq. No. 232816 LIB3272-002-P1-K1-F9 Seq. ID Method BLASTX NCBI GI g2911362 BLAST score 245 E value 1.0e-22 Match length 118 % identity 58 NCBI Description (AF041045) NADPH HC toxin reductase [Zea mays] Seq. No. 232817 Seq. ID LIB3272-002-P1-K1-G1 Method BLASTX NCBI GI g3694872 BLAST score 461 E value 4.0e-46 Match length 112 % identity 78 NCBI Description (AF092547) profilin [Ricinus communis] Seq. No. 232818 Seq. ID LIB3272-002-P1-K1-G10 Method BLASTX NCBI GI g3668089 BLAST score 217 E value 1.0e-17 Match length 80 47 % identity NCBI Description (AC004667) unknown protein [Arabidopsis thaliana] Seq. No. 232819

Seq. ID LIB3272-002-P1-K1-G11

BLASTX Method NCBI GI g2662343 BLAST score 601 E value 1.0e-62 Match length 117

33561



```
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                  232820
Seq. ID
                  LIB3272-002-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g729470
BLAST score
                   497
E value
                   2.0e-50
Match length
                  122
% identity
                  80
NCBI Description
                  MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
                   (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
                  >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2)
                  precursor, mitochondrial - potato >gi_297798_emb_CAA79702_
                   (Z21493) mitochondrial formate dehydrogenase precursor
                   [Solanum tuberosum]
                  232821
Seq. No.
Seq. ID
                  LIB3272-002-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q218157
BLAST score
                  594
E value
                  9.0e-62
                  134
Match length
% identity
                  88
                 (D13512) cytoplasmic aldolase [Oryza sativa]
NCBI Description
                  232822
Seq. No.
Seq. ID
                  LIB3272-002-P1-K1-G5
Method
                  BLASTX
NCBI GI
                   g886100
BLAST score
                   454
E value
                   2.0e-45
Match length
                  97
% identity
                   88
NCBI Description
                  (U27347) putative water channel protein; plasmalemma
                   intrinsic protein; similar to Arabidopsis Pip2a gene
                  product, PIR Accession Number S44084 [Glycine max]
Seq. No.
                   232823
Seq. ID
                  LIB3272-002-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g3420004
BLAST score
                  243
E value
                   1.0e-20
Match length
                  118
```

43 % identity (AF000305) steroid sulfotransferase 1 [Brassica napus] NCBI Description

Seq. No. 232824

Seq. ID LIB3272-002-P1-K1-G9

BLASTX Method NCBI GI g1076510 BLAST score 635 E value 1.0e-66 Match length 136



% identity peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean NCBI Description >gi 829119 emb CAA52414 (X74403) cyclophilin [Phaseolus vulgaris] 232825 Seq. No. LIB3272-002-P1-K1-H10 Seq. ID Method BLASTX NCBI GI g3668089 BLAST score 182 2.0e-13 E value

% identity 42 NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 232826

Match length

Seq. ID LIB3272-002-P1-K1-H11

86

Method BLASTX NCBI GI g120669 BLAST score 484 E value 6.0e-49Match length 120 78 % identity

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 232827

Seq. ID LIB3272-002-P1-K1-H12

Method BLASTX NCBI GI q4454097 BLAST score 273 E value 4.0e-24 Match length 66

% identity 82

NCBI Description (X85206) hybrid proline-rich protein [Catharanthus roseus]

Seq. No. 232828

Seq. ID LIB3272-002-P1-K1-H2

BLASTX Method NCBI GI g1169782 BLAST score 255 E value 5.0e-22101 Match length

57 % identity

NCBI Description FUSCA PROTEIN FUS6 >gi 432446 (L26498) FUS6 [Arabidopsis

thaliana]

Seq. No. 232829

LIB3272-002-P1-K1-H3 Seq. ID

Method BLASTX NCBI GI q1170747 BLAST score 296 8.0e-27 E value Match length 72



% identity

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345

(M88324) late embryogenesis-abundant protein [Gossypium

hirsutum] >gi 167347 (M37697) Lea5-A late

embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 232830

Seq. ID LIB3272-002-P1-K1-H4

Method BLASTX NCBI GI q2160166 BLAST score 469 E value 4.0e-47 Match length 128 % identity 66

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 232831

Seq. ID LIB3272-002-P1-K1-H5

Method BLASTX NCBI GI g3643609 BLAST score 431 E value 1.0e-42 Match length 134 % identity 64

NCBI Description (AC005395) putative Cys3His zinc finger protein

[Arabidopsis thaliana]

232832 Seq. No.

Seq. ID LIB3272-002-P1-K1-H7

Method BLASTX NCBI GI g3834312 BLAST score 529 E value 4.0e-54 Match length 129 % identity 72

NCBI Description (AC005679) Strong similarity to glycoprotein EP1 gb L16983

Daucus carota and a member of S locus glycoprotein  $\overline{f}$ amily

PF 00954. ESTs gb AA067487, gb Z35737, gb Z30815, gb Z35350, gb AA713171, gb AI100553, gb Z34248,

gb AA728536, gb Z30816 an

Seq. No. 232833

Seq. ID LIB3272-002-P1-K1-H8

85

Method BLASTX NCBI GI q3915095 BLAST score 510 E value 7.0e-52 Match length 118

% identity NCBI Description TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID

> 4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73) >gi\_1526537\_dbj\_BAA13414 (D87520) cytochrome P450

(CYP73A14) [Glycyrrhiza echinata]

Seq. No. 232834

Seq. ID LIB3272-003-P1-K1-A1

Method BLASTX



```
NCBI GI
                    q4220481
 BLAST score
                    194
                    8.0e-15
 E value
 Match length
                    53
  % identity
                    70
 NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
                    232835
 Seq. No.
  Seq. ID
                    LIB3272-003-P1-K1-A11
                    BLASTX
 Method
 NCBI GI
                    q2842486
 BLAST score
                    249
                    1.0e-23
 E value
 Match length
                    104
  % identity
                    62
 NCBI Description (AL021749) putative protein [Arabidopsis thaliana]
 Seq. No.
                    232836
 Seq. ID
                    LIB3272-003-P1-K1-A3
 Method
                    BLASTX
 NCBI GI
                    g3915847
 BLAST score
                    656
 E value
                    5.0e-69
                    133
 Match length
                    95
  % identity
 NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
                    40S ribosomal protein S2 [Arabidopsis thaliana]
                    232837
 Seq. No.
 Seq. ID
                    LIB3272-003-P1-K1-A4
 Method
                    BLASTX
 NCBI GI
                    q2924521
 BLAST score
                    192
                    1.0e-14
 E value
                   109
 Match length
 % identity
                    43
 NCBI Description (AL022023) putative protein [Arabidopsis thaliana]
 Seq. No.
                    232838
 Seq. ID
                    LIB3272-003-P1-K1-A9
 Method
                    BLASTX
                    q3694872
 NCBI GI
 BLAST score
                    496
 E value
                    3.0e-50
 Match length
                    118
  % identity
                    79
 NCBI Description (AF092547) profilin [Ricinus communis]
 Seq. No.
                    232839
 Seq. ID
                    LIB3272-003-P1-K1-B1
 Method
                    BLASTX
 NCBI GI
                    q464707
 BLAST score
                    574
 E value
                    2.0e-59
 Match length
                    117
 % identity
                    96
```

NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal



protein S18.A - Arabidopsis thaliana

>gi\_405613\_emb\_CAA80684\_ (Z23165) ribosomal protein S18A
[Arabidopsis thaliana] >gi\_434343\_emb\_CAA82273\_ (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi\_434345\_emb\_CAA82274\_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi\_434906\_emb\_CAA82275\_ (Z28962)

S18 ribosomal protein [Arabidopsis thaliana]

>gi\_2505871\_emb\_CAA72909\_ (Y12227) ribosomal protein S18A
[Arabidopsis thaliana] >gi\_3287678 (AC003979) Match to
ribosomal S18 gene mRNA gb\_Z28701, DNA gb\_Z23165 from A.
thaliana. ESTs gb\_T21121, gb\_Z17755, gb\_R64776 and
gb\_R30430 come from this gene. [Arabidopsis thaliana]

>gi\_4538910\_emb\_CAB39647.1\_ (AL049482) S18.A ribosomal
protein [Arabidopsis thaliana]

Seq. No. 232840 Seq. ID LIB3272-003-P1-K1-B10

Method BLASTX
NCBI GI g508304
BLAST score 223
E value 3.0e-18

Match length 76 % identity 59

NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 232841

Seq. ID LIB3272-003-P1-K1-B12

Method BLASTX
NCBI GI g3176684
BLAST score 380
E value 1.0e-36
Match length 131
% identity 57

NCBI Description (AC003671) Contains similarity to equilibratiave nucleoside

transporter 1 gb\_U81375 from Homo sapiens. ESTs gb\_N65317, gb\_T20785, gb\_AA586285 and gb\_AA712578 come from this gene.

[Arabidopsis thaliana]

Seq. No. 232842

Seq. ID LIB3272-003-P1-K1-B2

Method BLASTX
NCBI GI g2760084
BLAST score 217
E value 2.0e-23
Match length 92
% identity 20

NCBI Description (Y16045) leucine-rich repeat protein [Arabidopsis thaliana]

Seq. No. 232843

Seq. ID LIB3272-003-P1-K1-B4

Method BLASTX
NCBI GI g3927825
BLAST score 513
E value 3.0e-52
Match length 100

% identity 95

NCBI Description (AC005727) putative dTDP-glucose 4-6-dehydratase

NCBI GI

BLAST score



## [Arabidopsis thaliana]

```
Seq. No.
                  232844
Seq. ID
                  LIB3272-003-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g2407790
BLAST score
                  417
E value
                  5.0e-41
Match length
                  135
% identity
                  16
NCBI Description (AF019910) grr1 [Glycine max]
Seq. No.
                  232845
Seq. ID
                  LIB3272-003-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2914698
BLAST score
                  196
E value
                  4.0e-15
Match length
                  101
% identity
                  46
NCBI Description (AC003974) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  232846
Seq. ID
                  LIB3272-003-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g1166450
BLAST score
                  299
E value
                  4.0e-27
Match length
                  67
% identity
                  79
NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]
Seq. No.
                  232847
Seq. ID
                  LIB3272-003-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g3860247
BLAST score
                  550
E value
                  1.0e-56
Match length
                  114
% identity
                  88
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.
                  232848
Seq. ID
                  LIB3272-003-P1-K1-C3
Method
                  {\tt BLASTX}
NCBI GI
                  g4220481
BLAST score
                  154
E value
                  3.0e-10
                  43
Match length
% identity
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.
                  232849
Seq. ID
                  LIB3272-003-P1-K1-C4
Method
                  BLASTX
```

g1703108

508



```
1.0e-51
E value
Match length
                    93
                    100
% identity
                    ACTIN 2/7 >gi 2129525 pir S71210 actin 2 - Arabidopsis thaliana >gi 2129528 pir S68107 actin 7 - Arabidopsis thaliana >gi 1049307 (U37281) actin-2 [Arabidopsis
NCBI Description
                    thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis
                    thaliana]
Seq. No.
                    232850
Seq. ID
                    LIB3272-003-P1-K1-C5
Method
                    BLASTX
NCBI GI
                    q4263517
BLAST score
                    407
E value
                    8.0e-40
Match length
                    128
% identity
                    64
                   (AC004044) similar to PHZF, catalyzing the hydroxylation of
NCBI Description
                    phenazine-1-carboxylic acid to
                    2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis
                    thaliana]
Seq. No.
                    232851
Seq. ID
                    LIB3272-003-P1-K1-C6
Method
                    BLASTX
NCBI GI
                    q729668
BLAST score
                    329
E value
                    1.0e-30
Match length
                    76
% identity
                    86
                    HISTONE H1 >gi 2147479 pir S65059 histone H1,
NCBI Description
                    drought-inducible - Lycopersicon pennellii >gi 436823
                    (U01890) Solanum pennellii histone H1 [Solanum pennellii]
Seq. No.
                    232852
Seq. ID
                    LIB3272-003-P1-K1-C9
Method
                    BLASTX
NCBI GI
                    g1129145
BLAST score
                    591
E value
                    2.0e-61
                    129
Match length
% identity
                    87
NCBI Description (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]
Seq. No.
                    232853
Seq. ID
                    LIB3272-003-P1-K1-D1
                    BLASTX
Method
NCBI GI
                    q1928981
BLAST score
                    549
E value
                    2.0e-56
```

Match length 114 % identity 95

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

232854 Seq. No.

Seq. ID LIB3272-003-P1-K1-D10



```
BLASTX
Method
NCBI GI
                   q4049341
BLAST score
                   440
E value
                   2.0e-61
Match length
                   137
% identity
                   85
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
Seq. No.
                   232855
Seq. ID
                   LIB3272-003-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   g1166450
BLAST score
                   300
E value
                   3.0e-27
Match length
                   66
% identity
                   80
NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]
Seq. No.
                   232856
Seq. ID
                   LIB3272-003-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   g1351408
BLAST score
                   572
E value
                   4.0e-59
Match length
                   136
% identity
                   78
NCBI Description VACUOLAR PROCESSING ENZYME PRECURSOR (VPE)
                   >gi_1076563_pir__S51117 cystein proteinase - sweet orange
                   >gi_633185_emb_CAA87720_ (Z47793) cystein proteinase (by
similarity) [Citrus sinensis] >gi_1588548_prf__2208463A
                   vascular processing protease [Citrus sinensis]
Seq. No.
                   232857
Seq. ID
                   LIB3272-003-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   g2792297
BLAST score
                   261
E value
                   1.0e-22
                   77
Match length
                   58
% identity
NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa]
Seq. No.
                   232858
Seq. ID
                   LIB3272-003-P1-K1-D8
Method
                   {\tt BLASTX}
NCBI GI
                   g1362055
BLAST score
                   246
E value
                   5.0e-21
                   59
Match length
% identity
                   78
NCBI Description phosphogluconate dehydrogenase (decarboxylating) (EC
                   1.1.1.44) - alfalfa >gi 603221 (U18239) 6-phosphogluconate
                   dehydrogenase [Medicago sativa subsp. sativa]
```

Seq. No.

Seq. ID LIB3272-003-P1-K1-E1

232859

Method BLASTX

33569



```
NCBI GI
                  q585241
BLAST score
                  237
E value
                  7.0e-20
Match length
                  61
                  77
% identity
                  HISTONE H1 >gi 629668 pir S45662 histone H1 - tomato
NCBI Description
                  >gi 424100 (U03391) histone H1 [Lycopersicon esculentum]
Seq. No.
                  232860
Seq. ID
                  LIB3272-003-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g1173256
BLAST score
                  626
E value
                  2.0e-65
Match length
                  123
% identity
                  98
                 40S RIBOSOMAL PROTEIN S4 >gi 629496 pir S45026 ribosomal
NCBI Description
                  protein S4 - upland cotton >gi 488739 emb CAA55882
                  (X79300) ribosomal protein, small subunit 4e (RS4e)
                  [Gossypium hirsutum]
Seq. No.
                  232861
                  LIB3272-003-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2160166
BLAST score
                  332
E value
                  5.0e-31
Match length
                  131
                  57
% identity
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
                  232862
Seq. No.
Seq. ID
                  LIB3272-003-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q3006145
BLAST score
                  379
E value
                  1.0e-36
Match length
                  131
                  35
% identity
NCBI Description (AL022299) ABC transporter [Schizosaccharomyces pombe]
                  232863
Seq. No.
Seq. ID
                  LIB3272-003-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  q3861068
BLAST score
                  176
E value
                  1.0e-12
Match length
                  60
% identity
NCBI Description (AJ235272) unknown [Rickettsia prowazekii]
Seq. No.
                  232864
                  LIB3272-003-P1-K1-E9
Seq. ID
```

Method BLASTX NCBI GI q456568 BLAST score 737 E value 2.0e-78



Match length 137 % identity 98

NCBI Description (L29077) ubiquitin conjugating enzyme [Pisum sativum]

Seq. No. 232865

Seq. ID LIB3272-003-P1-K1-F1

Method BLASTX
NCBI GI g2507421
BLAST score 486
E value 4.0e-49
Match length 101
% identity 92

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi\_1800277 (U81042) translation initiation factor [Arabidopsis

thaliana] >gi\_4490709\_emb\_CAB38843.1\_ (AL035680) translation initiation factor [Arabidopsis thaliana]

Seq. No. 232866

Seq. ID LIB3272-003-P1-K1-F10

Method BLASTX
NCBI GI g1703129
BLAST score 635
E value 1.0e-66
Match length 120
% identity 100

NCBI Description ACTIN 11 >gi 2129522 pir S68109 actin 11 - Arabidopsis

thaliana >gi 1002533 (U27981) actin-11 [Arabidopsis

thaliana]

Seq. No. 232867

Seq. ID LIB3272-003-P1-K1-F11

Method BLASTX
NCBI GI g2493146
BLAST score 400
E value 5.0e-39
Match length 114
% identity 51

NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi\_755148

(U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit [Gossypium hirsutum] >gi\_4519415\_dbj\_BAA75542.1\_ (AB024275)

vacuolar H+-ATPase c subunit [Citrus unshiu]

Seq. No. 232868

Seq. ID LIB3272-003-P1-K1-F12

Method BLASTX
NCBI GI g3851636
BLAST score 573
E value 3.0e-59
Match length 138
% identity 80

NCBI Description (AF098519) unknown [Avicennia marina] >gi\_4128206

(AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No. 232869

Seq. ID LIB3272-003-P1-K1-F2

Method BLASTX NCBI GI q3694872



BLAST score 500 E value 1.0e-50 Match length 119 % identity 79

NCBI Description (AF092547) profilin [Ricinus communis]

Seq. No.

Seq. ID LIB3272-003-P1-K1-F3

232870

Method BLASTX
NCBI GI g1709498
BLAST score 383
E value 1.0e-44
Match length 123
% identity 71

NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR

>gi\_1362001\_pir\_\_S57524 osmotin precursor - Arabidopsis
thaliana >gi 887390 emb\_CAA61411\_ (X89008) osmotin

[Arabidopsis thaliana]

Seq. No. 232871

Seq. ID LIB3272-003-P1-K1-F4

Method BLASTX
NCBI GI g3600030
BLAST score 299
E value 4.0e-27
Match length 106
% identity 54

NCBI Description (AF080119) contains similarity to ankyrin repeats (Pfam:

ank.hmm, score: 13.93, 14.93 and 27.78) [Arabidopsis

thaliana]

Seq. No. 232872

Seq. ID LIB3272-003-P1-K1-F6

Method BLASTX
NCBI GI g112925
BLAST score 169
E value 7.0e-12
Match length 108
% identity 40

NCBI Description 41-2 PROTEIN ANTIGEN PRECURSOR >gi 320938 pir A45503 41-2

protein antigen precursor - Plasmodium falciparum >gi\_160039 (J04656) 41-2 protein antigen [Plasmodium

falciparum]

Seq. No. 232873

Seq. ID LIB3272-003-P1-K1-F7

Method BLASTX
NCBI GI g2760084
BLAST score 223
E value 2.0e-24
Match length 92
% identity 21

NCBI Description (Y16045) leucine-rich repeat protein [Arabidopsis thaliana]

Seq. No. 232874

Seq. ID LIB3272-003-P1-K1-F8

Method BLASTX

33572



```
q3894159
NCBI GI
                   271
BLAST score
E value
                   7.0e - 32
Match length
                   125
% identity
                   55
                  (AC005312) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   232875
                   LIB3272-003-P1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q129837
BLAST score
                   156
                   2.0e-10
E value
                   97
Match length
                   41
% identity
                  LIGNIN FORMING ANIONIC PEROXIDASE PRECURSOR
NCBI Description
                   >gi_100356_pir__A39889 peroxidase (EC 1.11.1.7) - common
                   tobacco >g\overline{i}_17\overline{03}16 (J02979) lignin-forming peroxidase
                   precursor (EC 1.11.1.7) [Nicotiana tabacum]
                   >gi 225796_prf__1313381A lignin-forming peroxidase
                   [Nicotiana sp.]
                   232876
Seq. No.
                   LIB3272-003-P1-K1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3687237
                   267
BLAST score
                   2.0e-23
E value
                   135
Match length
                   47
% identity
NCBI Description
                  (AC005169) putative Cys3His zinc-finger protein
                   [Arabidopsis thaliana]
                   232877
Seq. No.
                   LIB3272-003-P1-K1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2245131
BLAST score
                   169
                   7.0e-12
E value
                   75
Match length
                   52
% identity
NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   232878
                   LIB3272-003-P1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g729470
BLAST score
                   493
                   7.0e-50
E value
Match length
                   121
                   79
% identity
```

NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)

>gi\_542089\_pir\_\_JQ2272 formate dehydrogenase (EC 1.2.1.2)
precursor, mitochondrial - potato >gi\_297798\_emb\_CAA79702\_
(Z21493) mitochondrial formate dehydrogenase precursor

[Solanum tuberosum]



```
Seq. No.
                   232879
Seq. ID
                   LIB3272-003-P1-K1-H1
Method
                   BLASTX
NCBI GI
                   g3123515
BLAST score
                   497
                   1.0e-56
E value
Match length
                   124
% identity
                  (Y08761) Mago Nashi-like protein [Euphorbia lagascae]
NCBI Description
                   232880
Seq. No.
                   LIB3272-003-P1-K1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2499945
BLAST score
                   391
E value
                   6.0e-38
Match length
                   122
                   61
% identity
                   URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
NCBI Description
                   PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                   DECARBOXYLASE >gi_1076363_pir__S46440 orotate
phosphoribosyltransferase (EC 2.4.2.10) /
                   orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) -
                   Arabidopsis thaliana >gi 443818 emb CAA50686 (X71842)
                   pyrE-F [Arabidopsis thaliana]
                   232881
Seq. No.
                   LIB3272-003-P1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3413716
BLAST score
                   277
                   1.0e-24
E value
Match length
                   118
% identity
                   56
                   (AC004747) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3643589 (AC005395) unknown protein [Arabidopsis
                   thaliana]
Seq. No.
                   232882
Seq. ID
                   LIB3272-003-P1-K1-H3
                   {\tt BLASTX}
Method
                   g2459417
NCBI GI
BLAST score
                   404
E value
                   2.0e-39
Match length
                   139
% identity
                   60
NCBI Description (AC002332) putative pre-mRNA splicing factor PRP19
                   [Arabidopsis thaliana]
                   232883
Seq. No.
Seq. ID
                   LIB3272-003-P1-K1-H4
Method
                   BLASTX
```

Method BLASTX
NCBI GI g3549679
BLAST score 159
E value 9.0e-11
Match length 41



```
% identity
 NCBI Description (AL031394) putative protein [Arabidopsis thaliana]
 Seq. No.
                    232884
 Seq. ID
                    LIB3272-003-P1-K1-H8
 Method
                    BLASTX
 NCBI GI
                    g1173209
 BLAST score
                    604
 E value
                    6.0e-63
 Match length
                    121
 % identity
                    99
                   40S RIBOSOMAL PROTEIN S16 >qi 541835 pir S41193 ribosomal
 NCBI Description
                    protein S16 protein - upland cotton
                    >gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit
                    [Gossypium hirsutum]
                    232885
 Seq. No.
                    LIB3272-003-P1-K1-H9
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4097579
 BLAST score
                    412
 E value
                    2.0e-40
 Match length
                    87
 % identity
 NCBI Description (U64922) NTGP1 [Nicotiana tabacum]
                    232886

✓ Seq. No.

 Seq. ID
                    LIB3272-004-P1-K1-A1
 Method
                    BLASTX
 NCBI GI
                    g2388575
 BLAST score
                    285
 E value
                    2.0e-25
 Match length
                    112
 % identity
                    47
 NCBI Description (AC000098) YUP8H12.18 [Arabidopsis thaliana]
                    232887
 Seq. No.
 Seq. ID
                    LIB3272-004-P1-K1-A11
 Method
                    BLASTX
 NCBI GI
                    g2341034
 BLAST score
                    551
                    1.0e-56
 E value
                    112
 Match length
                    97
 % identity
 NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]
                    232888
 Seq. No.
                    LIB3272-004-P1-K1-A3
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    q629483
 BLAST score
                    377
 E value
                    3.0e-36
 Match length
                    134
 % identity
                    57
 NCBI Description gene 1-Sc3 protein - European white birch
```

33575

>gi\_534898\_emb\_CAA54696\_ (X77601) 1 Sc-3 [Betula pendula]
>gi\_1584322 prf 2122374C allergen Bet v 1-Sc3 [Betula



## pendula]

Seq. No. 232889 LIB3272-004-P1-K1-A4 Seq. ID Method BLASTX NCBI GI g3335366 BLAST score 433 E value 7.0e-43Match length 114 % identity 71 NCBI Description (AC003028) unknown protein [Arabidopsis thaliana] Seq. No. 232890 Seq. ID LIB3272-004-P1-K1-A5 Method BLASTX NCBI GI g1136741 BLAST score 347 E value 9.0e-33 Match length 96 % identity 67 NCBI Description (D42052) predicted protein of 548 amino acids [Homo sapiens] Seq. No. 232891 Seq. ID LIB3272-004-P1-K1-A6 Method BLASTX NCBI GI q3080428 BLAST score 311 E value 1.0e-28 Match length 98 54 % identity NCBI Description (AL022604) putative protein [Arabidopsis thaliana] Seq. No. 232892 Seq. ID LIB3272-004-P1-K1-A7 Method BLASTX NCBI GI g3868758 BLAST score 162 E value 2.0e-11 Match length 38 74 % identity NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa] 232893 Seq. No. Seq. ID LIB3272-004-P1-K1-A8  ${\tt BLASTX}$ Method NCBI GI g2493144 BLAST score 224 E value 1.0e-18 Match length 66 % identity 73 NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi\_2118221\_pir\_\_S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain

thaliana]

(clone AVA-P2) - Arabidopsis thaliana >gi\_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis



Seq. No. 232894

Seq. ID LIB3272-004-P1-K1-A9

Method BLASTX
NCBI GI g3377797
BLAST score 468
E value 6.0e-47
Match length 127
% identity 72

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No. 232895

Seq. ID LIB3272-004-P1-K1-B1

Method BLASTX
NCBI GI g4235430
BLAST score 224
E value 9.0e-34
Match length 108
% identity 75

NCBI Description (AF098458) latex-abundant protein [Hevea brasiliensis]

Seq. No. 232896

Seq. ID LIB3272-004-P1-K1-B11

Method BLASTX
NCBI GI g129881
BLAST score 688
E value 9.0e-73
Match length 141
% identity 93

NCBI Description PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE

ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))

(PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)

(PPI-PFK) >gi\_482294\_pir\_\_A36094

pyrophosphate--fructose-6-phosphate 1-phosphotransferase

(EC 2.7.1.90) alpha chain - potato (cv. Kennebec) >gi 169538 (M55190) pyrophosphate-fructose 6-phosphate 1-phosphotransferase alpha-subunit [Solanum tuberosum]

Seq. No. 232897

Seq. ID LIB3272-004-P1-K1-B12

Method BLASTX
NCBI GI g3158474
BLAST score 478
E value 4.0e-48
Match length 116
% identity 83

NCBI Description (AF067184) aquaporin 1 [Samanea saman]

Seq. No. 232898

Seq. ID LIB3272-004-P1-K1-B2

Method BLASTX NCBI GI g3747050 BLAST score 417



```
E value
                  5.0e-41
Match length
                  103
                  78
% identity
NCBI Description (AF093540) ribosomal protein L26 [Zea mays]
                  232899
Seq. No.
                  LIB3272-004-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4220481
BLAST score
                  285
E value
                  2.0e-25
Match length
                  77
                  71
% identity
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
                  232900
Seq. No.
                  LIB3272-004-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4033431
BLAST score
                  625
E value
                  2.0e-65
Match length
                  139
% identity
                  87
NCBI Description PROBABLE PYRUVATE KINASE, CYTOSOLIC ISOZYME (PK)
                  >gi_2982467_emb_CAA18231_ (AL022223) pyruvate kinase like
                  protein [Arabidopsis thaliana]
                  232901
Seq. No.
Seq. ID
                  LIB3272-004-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g167367
BLAST score
                  537
E value
                  4.0e-55
Match length
                  136
% identity
                  77
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                  232902
Seq. No.
Seq. ID
                  LIB3272-004-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g3759184
BLAST score
                  270
E value
                  9.0e-24
                  106
Match length
% identity
                  54
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
                  232903
Seq. No.
Seq. ID
                  LIB3272-004-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g3334349
BLAST score
                  533
                  1.0e-54
E value
Match length
                  115
% identity
                  86
```

>gi\_2564215 emb CAA05162 (AJ002062) glycyl-tRNA synthetase

NCBI Description GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS)

NCBI Description



## [Arabidopsis thaliana]

```
Seq. No.
                   232904
Seq. ID
                   LIB3272-004-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   g2791834
BLAST score
                   578
E value
                   7.0e-60
Match length
                   115
% identity
                   96
                  (AF041463) elongation factor 1-alpha [Manihot esculenta]
NCBI Description
                   232905
Seq. No.
Seq. ID
                   LIB3272-004-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g2341034
BLAST score
                   535
E value
                   8.0e-55
Match length
                   109
% identity
                   97
NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]
Seq. No.
                   232906
Seq. ID
                   LIB3272-004-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   q549063
BLAST score
                   361
E value
                   2.0e-34
Match length
                   112
% identity
                    64
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
Seq. No.
                   232907
Seq. ID
                   LIB3272-004-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g1076316
BLAST score
                   260
E value
                   1.0e-22
                   69
Match length
% identity
                    59
                   drought-induced protein Di19 - Arabidopsis thaliana
NCBI Description
                   >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis
                   thaliana]
                   232908
Seq. No.
Seq. ID
                   LIB3272-004-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g4185140
BLAST score
                   406
E value
                   1.0e-39
Match length
                   88
% identity
                    91
```

(snRNP-E) [Arabidopsis thaliana]

(AC005724) putative small nuclear ribonucleoprotein E

Match length

% identity

108

18



```
Seq. No.
                  232909
                  LIB3272-004-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g125606
BLAST score
                  479
E value
                  3.0e-48
Match length
                  104
% identity
                  87
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 100463 pir S12248
NCBI Description
                  pyruvate kinase (EC 2.7.1.40) - potato
                  >gi 22576 emb CAA37727 (X53688) pyruvate kinase [Solanum
                  tuberosum]
Seq. No.
                  232910
                  LIB3272-004-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1107526
BLAST score
                  500
E value
                  1.0e-50
Match length
                  124
                  76
% identity
NCBI Description (X87931) SIEP1L protein [Beta vulgaris]
Seq. No.
                  232911
Seq. ID
                  LIB3272-004-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q441457
BLAST score
                  585
E value
                  1.0e-60
Match length
                  112
                  97
% identity
NCBI Description (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
                  esculentum]
                  232912
Seq. No.
Seq. ID
                  LIB3272-004-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q1718097
                  258
BLAST score
E value
                  2.0e-22
Match length
                  74
                  64
% identity
NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
                   (41 KD ACCESSORY PROTEIN) (DVA41) >gi 626048 pir A55016
                  lysosomal membrane protein DVA41 - slime mold
                   (Dictyostelium discoideum) >gi 532733 (U13150) vacuolar
                  ATPase subunit DVA41 [Dictyostelium discoideum]
Seq. No.
                  232913
                  LIB3272-004-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4115337
BLAST score
                  533
E value
                  1.0e-54
```

% identity



```
NCBI Description (L81141) ubiquitin [Pisum sativum]
                  232914
Seq. No.
Seq. ID
                  LIB3272-004-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g2961372
BLAST score
                  640
E value
                  4.0e-67
Match length
                  126
                  93
% identity
                  (AL022141) putative ribosomal protein L8 [Arabidopsis
NCBI Description
                  thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal
                  protein L2 [Arabidopsis thaliana]
Seq. No.
                  232915
Seq. ID
                  LIB3272-004-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g1684855
BLAST score
                  447
E value
                  1.0e-44
                  90
Match length
                  21
% identity
NCBI Description (U77939) ubiquitin-like protein [Phaseolus vulgaris]
Seq. No.
                  232916
Seq. ID
                  LIB3272-004-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g3264767
BLAST score
                  399
                  7.0e-39
E value
Match length
                  125
% identity
                  60
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
Seq. No.
                  232917
Seq. ID
                  LIB3272-004-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g1709498
BLAST score
                  545
E value
                  5.0e-56
Match length
                  120
% identity
NCBI Description
                 OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                  >gi 1362001 pir S57524 osmotin precursor - Arabidopsis
                  thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
                  [Arabidopsis thaliana]
Seq. No.
                  232918
Seq. ID
                  LIB3272-004-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g167367
BLAST score
                  467
E value
                  8.0e-47
Match length
                  121
```

NCBI Description (L08199) peroxidase [Gossypium hirsutum]

% identity



```
Seq. No.
                   232919
 Seq. ID
                   LIB3272-004-P1-K1-E11
 Method
                   BLASTX
 NCBI GI
                   g3687235
 BLAST score
                   431
 E value
                   1.0e-42
Match length
                   130
 % identity
                   68
NCBI Description
                  (AC005169) putative copia-like transposable element
                   [Arabidopsis thaliana]
 Seq. No.
                   232920
                   LIB3272-004-P1-K1-E12
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2129630
 BLAST score
                   235
 E value
                   1.0e-19
Match length
                   86
 % identity
                   45
 NCBI Description lamin - Arabidopsis thaliana >gi_1262754_emb_CAA65750
                   (X97023) lamin [Arabidopsis thaliana] >gi 3395760 (U77721)
                   unknown [Arabidopsis thaliana]
Seq. No.
                   232921
 Seq. ID
                   LIB3272-004-P1-K1-E2
Method
                   BLASTX
 NCBI GI
                   q549750
 BLAST score
                   149
E value
                   1.0e-09
Match length
                   136
 % identity
                   31
 NCBI Description HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION
                   >gi 539221 pir S38045 hypothetical protein YKL207w - yeast
                   (Saccharomyces cerevisiae) >gi_486369_emb_CAA82052_
                   (Z28207) ORF YKL207w [Saccharomyces cerevisiae]
 Seq. No.
                   232922
 Seq. ID
                   LIB3272-004-P1-K1-E3
 Method
                   BLASTX
 NCBI GI
                   g2352492
 BLAST score
                   631
 E value
                   4.0e-66
                   142
 Match length
                   82
 % identity
 NCBI Description
                  (AF005047) transport inhibitor response 1 [Arabidopsis
                   thaliana] >gi 2352494 (AF005048) transport inhibitor
                   response 1 [Arabidopsis thaliana]
                   232923
 Seq. No.
 Seq. ID
                   LIB3272-004-P1-K1-E6
 Method
                   BLASTX
 NCBI GI
                   q3947719
 BLAST score
                   249
 E value
                   3.0e-21
 Match length
                   53
```

NCBI Description (AJ012653) ribosomal protein S28 [Prunus persica]



>gi\_3947721\_emb\_CAA10102 (AJ012654) ribosomal protein S28
[Prunus persica] >gi\_3947723\_emb\_CAA10103\_ (AJ012655)
ribosomal protein S28 [Prunus persica]

Seq. No. 232924

Seq. ID LIB3272-004-P1-K1-F10

Method BLASTX
NCBI GI g3033391
BLAST score 270
E value 2.0e-31
Match length 136
% identity 52

NCBI Description (AC004238) putative amino acid transporter [Arabidopsis

thalianal

Seq. No. 232925

Seq. ID LIB3272-004-P1-K1-F2

Method BLASTX
NCBI GI g3176708
BLAST score 171
E value 2.0e-12
Match length 76
% identity 45

NCBI Description (AC002392) putative proline-rich protein APG [Arabidopsis

thaliana]

Seq. No. 232926

Seq. ID LIB3272-004-P1-K1-F3

Method BLASTX
NCBI GI g2662310
BLAST score 472
E value 2.0e-47
Match length 132
% identity 70

NCBI Description (AB009307) bpw1 [Hordeum vulgare]

Seq. No. 232927

Seq. ID LIB3272-004-P1-K1-F4

Method BLASTX
NCBI GI g120669
BLAST score 451
E value 6.0e-45
Match length 108
% identity 80

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 232928

Seq. ID LIB3272-004-P1-K1-F5

Method BLASTX
NCBI GI g465820
BLAST score 377
E value 3.0e-36
Match length 105



% identity NCBI Description HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III >gi\_280536\_pir\_\_S28301 hypothetical protein C40H1.6 -Caenorhabditis elegans >gi\_3874819\_emb\_CAA79557\_ (Z19154) C40H1.6 [Caenorhabditis elegans] 232929

Seq. No. Seq. ID LIB3272-004-P1-K1-F6 Method BLASTX NCBI GI q2980793 BLAST score 524 E value 2.0e-53 Match length 134 72 % identity

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 232930 Seq. ID LIB3272-004-P1-K1-F7 Method BLASTX NCBI GI q1843527 482 1.0e-48

BLAST score E value Match length 127 % identity 43

NCBI Description (U73747) annexin [Gossypium hirsutum]

Seq. No. 232931

Seq. ID LIB3272-004-P1-K1-F8

Method BLASTX NCBI GI g115473 BLAST score 500 E value 1.0e-50 Match length 130 % identity 69

NCBI Description CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE

> DEHYDRATASE) >gi 170219 (M94135) chloroplast carbonic anhydrase [Nicotiana tabacum] >gi\_445610\_prf\_1909357A

carbonic anhydrase [Nicotiana tabacum]

Seq. No. 232932

Seq. ID LIB3272-004-P1-K1-G11

Method BLASTX NCBI GI g1076316 BLAST score 373 E value 8.0e-36 Match length 115 % identity 58

NCBI Description drought-induced protein Di19 - Arabidopsis thaliana

>gi\_469110\_emb\_CAA55321\_ (X78584) Di19 [Arabidopsis

thaliana]

Seq. No. 232933

Seq. ID LIB3272-004-P1-K1-G12

Method BLASTX NCBI GI q3510540 BLAST score 507 E value 2.0e-51

% identity



```
123
Match length
% identity
                   72
NCBI Description (AF038815) expansin [Prunus armeniaca]
                   232934
Seq. No.
Seq. ID
                   LIB3272-004-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   g2494625
BLAST score
                   214
E value
                   3.0e-17
Match length
                   84
                   50
% identity
NCBI Description HYPOTHETICAL PROTEIN KIAA0107 >gi 285951 dbj BAA03497
                   (D14663) KIAA0107 [Homo sapiens]
                   232935
Seq. No.
Seq. ID
                   LIB3272-004-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   g1709498
BLAST score
                   488
E value
                   2.0e-49
Match length
                   113
% identity
                   80
                  OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
NCBI Description
                   >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
                   [Arabidopsis thaliana]
Seq. No.
                   232936
Seq. ID
                   LIB3272-004-P1-K1-G6
                   BLASTX
Method
NCBI GI
                   g3080398
BLAST score
                   217
E value
                   2.0e-17
                   112
Match length
                   41
% identity
NCBI Description (AL022603) putative protein [Arabidopsis thaliana]
Seq. No.
                   232937
Seq. ID
                   LIB3272-004-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   q285286
BLAST score
                   415
E value
                   9.0e-41
                   138
Match length
% identity
                   57
NCBI Description flavonol 4'-sulfotransferase - Flaveria chloraefolia
Seq. No.
                   232938
                   LIB3272-004-P1-K1-G8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3334147
BLAST score
                   547
E value
                   3.0e-56
Match length
                   129
```

33585

NCBI Description ENDOCHITINASE 1 PRECURSOR >gi 1469788 (U60197) class I



## chitinase [Gossypium hirsutum]

```
232939
Seq. No.
Seq. ID
                  LIB3272-004-P1-K1-G9
                  BLASTX
Method
NCBI GI
                  q2827552
BLAST score
                  158
                  1.0e-10
E value
Match length
                  58
                  57
% identity
NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]
                  232940
Seq. No.
                  LIB3272-004-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245089
BLAST score
                  157
                  2.0e-10
E value
Match length
                  103
% identity
                  39
                 (Z97343) asparagine--tRNA ligase homolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  232941
                  LIB3272-004-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2760347
BLAST score
                  529
E value
                  3.0e-54
Match length
                  108
% identity
                  17
NCBI Description (U84968) ubiquitin [Arabidopsis thaliana]
Seq. No.
                  232942
Seq. ID
                  LIB3272-004-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g577301
BLAST score
                  180
E value
                  3.0e-13
Match length
                  130
                  33
% identity
NCBI Description (D42044) The ha3523 gene product is related to S.cerevisiae
                  gene product located in chromosome III. [Homo sapiens]
Seq. No.
                  232943
Seq. ID
                  LIB3272-004-P1-K1-H3
                  BLASTX
Method
NCBI GI
                  q542200
BLAST score
                  448
E value
                  1.0e-44
                  137
Match length
% identity
                  66
                 hypothetical protein - garden asparagus
NCBI Description
                  >gi 452714 emb CAA54526_ (X77320) unknown [Asparagus
```

Seq. No. 232944

officinalis]



```
LIB3272-004-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4105269
BLAST score
                  250
                  2.0e-21
E value
                  128
Match length
                  43
% identity
                  (AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase
NCBI Description
                  [Rattus norvegicus]
Seq. No.
                  232945
                  LIB3272-004-P1-K1-H5
Seq. ID
Method
                  BLASTX
                  g3915039
NCBI GI
BLAST score
                  171
                  3.0e-12
E value
                  79
Match length
                  48
% identity
NCBI Description SUGAR CARRIER PROTEIN C >gi_169718 (L08196) sugar carrier
                  protein [Ricinus communis]
                  232946
Seq. No.
Seq. ID
                  LIB3272-004-P1-K1-H8
Method
                  BLASTX
                  q3608412
NCBI GI
BLAST score
                  644
                  1.0e-67
E value
Match length
                  140
                  87
% identity
NCBI Description (AF079355) protein phosphatase-2c [Mesembryanthemum
                  crystallinum]
Seq. No.
                   232947
Seq. ID
                  LIB3272-004-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g4522004
BLAST score
                  450
                   7.0e-45
E value
Match length
                  136
% identity
                   68
NCBI Description (AC007069) putative histidine kinase, sensory transduction
                   [Arabidopsis thaliana]
                   232948
Seq. No.
Seq. ID
                  LIB3272-005-P1-K1-A1
Method
                  BLASTX
NCBI GI
                   g285741
BLAST score
                   485
E value
                   6.0e-49
                  139
Match length
% identity
                   61
NCBI Description (D14550) EDGP precursor [Daucus carota]
                  232949
Seq. No.
Seq. ID
                  LIB3272-005-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g2160166
```

BLAST score

Match length

% identity

E value

443

143

61

5.0e-44



```
BLAST score
                  1.0e-43
E value
Match length
                  134
% identity
                  62
                  (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                  232950
Seq. No.
                  LIB3272-005-P1-K1-A12
Seq. ID
Method
                  BLASTX
                  g3882081
NCBI GI
BLAST score
                  611
                  1.0e-63
E value
Match length
                  125
                   38
% identity
                  (AJ012552) polyubiquitin [Vicia faba]
NCBI Description
                  232951
Seq. No.
                  LIB3272-005-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2464905
BLAST score
                  542
                   1.0e-55
E value
Match length
                  145
                   72
% identity
                  (Z99708) minor allergen [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   232952
                  LIB3272-005-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1143511
BLAST score
                   694
                   2.0e-73
E value
Match length
                   126
                   98
% identity
NCBI Description
                  (Z47076) Ser/Thr protein phosphatase homologous to PPX
                   [Malus domestica] >gi_1586034_prf__2202340A Ser/Thr protein
                   phosphatase [Malus domestica]
                   232953
Seq. No.
Seq. ID
                   LIB3272-005-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   g3641837
                   376
BLAST score
E value
                   5.0e-41
Match length
                   139
% identity
                   71
                  (AL023094) Nonclathrin coat protein gamma - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   232954
Seq. No.
                   LIB3272-005-P1-K1-A9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1346809
```



```
NCBI Description PATHOGEN-RELATED PROTEIN >gi 499074 emb CAA34641 (X16648)
                  pathogenesis related protein [Hordeum vulgare]
Seq. No.
                  232955
Seq. ID
                  LIB3272-005-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g1173187
BLAST score
                  579
E value
                  5.0e-60
Match length
                  115
                  95
% identity
                 40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673
NCBI Description
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                  strawberry >gi 643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
Seq. No.
                  232956
Seq. ID
                  LIB3272-005-P1-K1-B12
```

Method BLASTX NCBI GI g2493131 BLAST score 470 E value 3.0e-47Match length 101 % identity 94 NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B

SUBUNIT) >gi 167108 (L11862) vacuolar ATPase B subunit

[Hordeum vulgare]

Seq. No. 232957 Seq. ID LIB3272-005-P1-K1-B3 Method BLASTX NCBI GI g1710780 BLAST score 420 E value 2.0e-41 Match length 119

% identity 69

NCBI Description 40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433 (X96613) cytoplasmic ribosomal protein S7 [Podospora

anserina]

232958 Seq. No.

Seq. ID LIB3272-005-P1-K1-B4

Method BLASTX NCBI GI q4567279 BLAST score 585 E value 1.0e-60 Match length 135 % identity

NCBI Description (AC006841) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 232959

Seq. ID LIB3272-005-P1-K1-B7

Method BLASTX NCBI GI q3334147 BLAST score 541 E value 2.0e-55



```
Match length
                  82
% identity
                  ENDOCHITINASE 1 PRECURSOR >gi 1469788 (U60197) class I
NCBI Description
                  chitinase [Gossypium hirsutum]
                  232960
Seq. No.
                  LIB3272-005-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3393062
BLAST score
                  442
E value
                  6.0e-44
Match length
                  116
                  67
% identity
                  (Y17386) putative In2.1 protein [Triticum aestivum]
NCBI Description
Seq. No.
                  232961
                  LIB3272-005-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2979555
BLAST score
                  366
                   5.0e-35
E value
Match length
                  138
% identity
                  54
NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]
                  232962
Seq. No.
                  LIB3272-005-P1-K1-C4
Seq. ID
Method
                  BLASTX
                  g3980393
NCBI GI
BLAST score
                  400
                   5.0e-39
E value
Match length
                  130
                   58
% identity
                  (AC004561) putative glutathione S-transferase [Arabidopsis
NCBI Description
                   thaliana]
                   232963
Seq. No.
Seq. ID
                  LIB3272-005-P1-K1-C5
Method
                  BLASTX
                   g1928981
NCBI GI
BLAST score
                   600
                   2.0e-62
E value
                  126
Match length
                   63
% identity
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                   oleracea var. botrytis]
                   232964
Seq. No.
Seq. ID
                   LIB3272-005-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   g126770
BLAST score
                   614
E value
                   3.0e-70
Match length
                   140
% identity
                   97
```

NCBI Description MALATE SYNTHASE, GLYOXYSOMAL >gi\_68218\_pir\_\_SYCNMU malate synthase (EC 4.1.3.2) - upland cotton



>gi\_18507\_emb\_CAA36546\_ (X52305) malate synthase (AA 1-567)
[Gossypium hirsutum]

Seq. No. 232965

Seq. ID LIB3272-005-P1-K1-C7

Method BLASTX
NCBI GI g729470
BLAST score 656
E value 5.0e-69
Match length 139
% identity 91

NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR

(NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)

>gi\_542089\_pir\_\_JQ2272 formate dehydrogenase (EC 1.2.1.2)
precursor, mitochondrial - potato >gi\_297798\_emb\_CAA79702\_
(Z21493) mitochondrial formate dehydrogenase precursor

[Solanum tuberosum]

Seq. No. 232966

Seq. ID LIB3272-005-P1-K1-C9

Method BLASTX
NCBI GI g2662341
BLAST score 723
E value 7.0e-77
Match length 141
% identity 99

NCBI Description (D63580) EF-1 alpha [Oryza sativa]

>gi\_2662345\_dbj\_BAA23659\_ (D63582) EF-1 alpha [Oryza
sativa] >gi\_2662347\_dbj\_BAA23660\_ (D63583) EF-1 alpha

[Oryza sativa]

Seq. No. 232967

Seq. ID LIB3272-005-P1-K1-D2

Method BLASTX
NCBI GI g115492
BLAST score 388
E value 3.0e-38
Match length 76
% identity 42

NCBI Description CALMODULIN-RELATED PROTEIN >gi\_169205 (M80831)

calmodulin-related protein [Petunia hybrida]

Seq. No. 232968

Seq. ID LIB3272-005-P1-K1-D3

Method BLASTX
NCBI GI g3451072
BLAST score 543
E value 9.0e-56
Match length 119
% identity 81

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 232969

Seq. ID LIB3272-005-P1-K1-D4

Method BLASTX NCBI GI g2832623 BLAST score 278



```
4.0e-25
E value
Match length
                   66
% identity
                   82
                   (AL021711) protein kinase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   232970
Seq. No.
Seq. ID
                   LIB3272-005-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   g1702983
BLAST score
                   356
E value
                   8.0e-34
Match length
                   111
% identity
                   59
                   AUXIN-REPRESSED 12.5 KD PROTEIN >gi 99855_pir__S11850
NCBI Description
                   hypothetical protein - garden strawberry
                   >gi_22573_emb_CAA36676_ (X52429) 12.5 kDa protein [Fragaria
x ananassa] >gi_927034 (L44142) auxin-repressed protein
                   [Fragaria ananassa]
Seq. No.
                   232971
Seq. ID
                   LIB3272-005-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   q456568
BLAST score
                   710
E value
                   2.0e-75
Match length
                   134
% identity
                   96
NCBI Description (L29077) ubiquitin conjugating enzyme [Pisum sativum]
                   232972
Seq. No.
                   LIB3272-005-P1-K1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g82512
                   267
BLAST score
E value
                   5.0e-24
                   60
Match length
% identity
                    46
NCBI Description
                   ubiquitin precursor - rice (fragment)
                   >gi 218189 dbj BAA02241 (D12776) poly-ubiquitin [Oryza
                   satīva]
                   232973
Seq. No.
Seq. ID
                   LIB3272-005-P1-K1-E10
                   BLASTX
Method
NCBI GI
                   g1076316
BLAST score
                   146
                   3.0e-09
E value
                   57
Match length
% identity
                    46
```

NCBI Description

ion drought-induced protein Di19 - Arabidopsis thaliana >gi 469110 emb CAA55321 (X78584) Di19 [Arabidopsis

thaliana]

Seq. No. 232974

Seq. ID LIB3272-005-P1-K1-E11

Method BLASTX

Match length

% identity



```
q3328240
NCBI GI
BLAST score
                  358
                  5.0e - 34
E value
Match length
                  122
% identity
                  55
                  (AF064775) early nodule-specific protein [Medicago
NCBI Description
                  truncatula]
                  232975
Seq. No.
                  LIB3272-005-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4545231
BLAST score
                  558
                  2.0e-57
E value
Match length
                  107
% identity
                  100
                  (AF116243) RAS-related GTP-binding protein [Gossypium
NCBI Description
                  hirsutum]
                  232976
Seq. No.
                  LIB3272-005-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3334756
BLAST score
                   553
                   6.0e-57
E value
Match length
                   112
% identity
                   94
NCBI Description (Y16672) putative arginine/serine-rich splicing factor
                   [Medicago sativa]
Seq. No.
                   232977
                   LIB3272-005-P1-K1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1352663
BLAST score
                   732
E value
                   6.0e-78
                   137
Match length
                   96
% identity
                   SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-3 CATALYTIC
NCBI Description
                   SUBUNIT >gi 1076388 pir__S52659 phosphoprotein phosphatase
                   (EC 3.1.3.16) 2A isoform 3 - Arabidopsis thaliana
                   >gi 466441 (M96841) Ser/Thr protein phosphatase
                   [Arabidopsis thaliana]
                   >gi_4559341_gb_AAD23003.1_AC007087 22 (AC007087)
                   serine/threonine protein phosphatase PP2A-3 catalytic
                   subunit [Arabidopsis thaliana]
                   >gi_4567320_gb_AAD23731.1_AC005956_20 (AC005956)
                   serine/threonine protein phosphatase [Arabidopsis thaliana]
                   232978
Seq. No.
                   LIB3272-005-P1-K1-E4
Seq. ID
                   BLASTX
Method
                   g1914685
NCBI GI
                   323
BLAST score
E value
                   5.0e-33
```



```
(Y12014) RAD23 protein, isoform II [Daucus carota]
NCBI Description
                   232979
Seq. No.
Seq. ID
                   LIB3272-005-P1-K1-E7
Method
                   BLASTX
                   q2760837
NCBI GI
                   193
BLAST score
E value
                   1.0e-14
Match length
                   131
% identity
                   35
                  (AC003105) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   232980
Seq. ID
                  LIB3272-005-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   g1843527
BLAST score
                   480
                   2.0e-48
E value
Match length
                   124
                   43
% identity
NCBI Description (U73747) annexin [Gossypium hirsutum]
                   232981
Seq. No.
                   LIB3272-005-P1-K1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3158476
                   570
BLAST score
                   6.0e-59
E value
Match length
                   126
% identity
NCBI Description (AF067185) aquaporin 2 [Samanea saman]
Seq. No.
                   232982
Seq. ID
                   LIB3272-005-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   g464707
BLAST score
                   218
E value
                   1.0e-17
Match length
                   56
                   79
% identity
                  40S RIBOSOMAL PROTEIN-S18 >gi_480908_pir__S37496 ribosomal
NCBI Description
                   protein S18.A - Arabidopsis thaliana
                   >gi 405613 emb CAA80684 (Z23165) ribosomal protein S18A
                   [Arabidopsis thaliana] >gi 434343 emb CAA82273 (Z28701)
                   S18 ribosomal protein [Arabidopsis thaliana]
                   >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
                   [Arabidopsis thaliana] >gi 434906 emb CAA82275 (Z28962)
                   S18 ribosomal protein [Arabidopsis thaliana]
                   >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A
                   [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to
                   ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
                   gb R30430 come from this gene. [Arabidopsis thaliana]
                   >gī 4538910 emb CAB39647.1_ (AL049482) S18.A ribosomal
```

Seq. No. 232983

protein [Arabidopsis thaliana]



```
LIB3272-005-P1-K1-F12
Seq. ID
                BLASTX
Method
NCBI GI
                  g1928981
                  585
BLAST score
                  1.0e-60
E value
Match length
                  125
% identity
                  63
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                  oleracea var. botrytis]
                  232984
Seq. No.
Seq. ID
                  LIB3272-005-P1-K1-F3
                  BLASTX
Method
NCBI GI
                  g1173209
BLAST score
                  269
                  8.0e-24
E value
                  77
Match length
                  73
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal
                  protein S16 protein - upland cotton
                  >gi 439654 emb CAA53567 (X75954) RS16 protein, 40S subunit
                  [Gossypium hirsutum]
                  232985
Seq. No.
Seq. ID
                  LIB3272-005-P1-K1-F5
                  BLASTX
Method
NCBI GI
                  g3641312
BLAST score
                  597
E value
                  4.0e-62
                  131
Match length
% identity
                  85
NCBI Description (AF087412) AJH2 [Arabidopsis thaliana]
Seq. No.
                  232986
                  LIB3272-005-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g401329
BLAST score
                  159
E value
                  1.0e-10
Match length
                  110
                  33
% identity
NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT C (V-ATPASE C SUBUNIT)
                  >qi 542836 pir JN0907 H+-transporting ATPase (EC 3.6.1.35)
                  chain C, vacuolar - human >gi 37643 emb CAA48903 (X69151)
                  vacuolar proton-ATPase [Homo sapiens]
                  >gi 4502315 ref NP 001686.1 pATP6D ATPase, H+
                  transporting, lysosomal (vacuolar proton pump) 42kD
Seq. No.
                  232987
                  LIB3272-005-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3510254
BLAST score
                  596
E value
                  6.0e-62
Match length
                  138
                  86
% identity
```

NCBI Description (AC005310) putative zinc transporter [Arabidopsis thaliana]

Seq. No.

Seq. ID Method

232993

BLASTX

LIB3272-005-P1-K1-G7



```
232988
Seq. No.
                  LIB3272-005-P1-K1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2388689
BLAST score
                  209
                  7.0e-24
E value
Match length
                  73
% identity
                  84
NCBI Description (AF016633) GH1 protein [Glycine max]
                  232989
Seq. No.
Seq. ID
                  LIB3272-005-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g541816
BLAST score
                  510
                  7.0e-52
E value
Match length
                  139
% identity
                  71
NCBI Description protein kinase - common ice plant >gi_457689_emb_CAA82990
                  (Z30329) protein kinase [Mesembryanthemum crystallinum]
                  232990
Seq. No.
                  LIB3272-005-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1621268
BLAST score
                  273
E value
                  4.0e-24
Match length
                  129
% identity
                  52
NCBI Description (Z81012) unknown [Ricinus communis]
                  232991
Seq. No.
Seq. ID
                  LIB3272-005-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g3386621
BLAST score
                  651
E value
                  2.0e-68
                  137
Match length
% identity
                  91
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
                  232992
Seq. No.
Seq. ID
                  LIB3272-005-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g1710780
                  229
BLAST score
E value
                  4.0e-19
Match length
                  77
% identity
                  62
                  40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433
NCBI Description
                  (X96613) cytoplasmic ribosomal protein S7 [Podospora
                  anserina]
```



```
NCBI GI
                   g3237190
                  221
BLAST score
                   5.0e-18
E value
Match length
                  86
                  50
% identity
NCBI Description (AB014760) cystein proteinase inhibitor [Cucumis sativus]
Seq. No.
                  232994
                  LIB3272-005-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g167367
BLAST score
                  551
                  1.0e-56
E value
                  137
Match length
                  79
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                  232995
Seq. No.
                  LIB3272-005-P1-K1-G9
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3548810
BLAST score
                   300
                   3.0e-27
E value
Match length
                  118
% identity
                   47
NCBI Description (AC005313) putative chloroplast nucleoid DNA binding
                  protein [Arabidopsis thaliana]
Seq. No.
                   232996
                  LIB3272-005-P1-K1-H11
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2970051
BLAST score
                   287
E value
                   9.0e-26
                   90
Match length
                   63
% identity
NCBI Description (AB012110) ARG10 [Vigna radiata]
Seq. No.
                   232997
Seq. ID
                   LIB3272-005-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   g2244766
BLAST score
                   267
E value
                   2.0e-23
                   118
Match length
% identity
                   45
NCBI Description (Z97335) glucosyltransferase [Arabidopsis thaliana]
Seq. No.
                   232998
                   LIB3272-005-P1-K1-H2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1172811
BLAST score
                   313
E value
                   2.0e-29
Match length
                   106
                   62
% identity
```

NCBI Description 60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34)



>gi\_1076751\_pir\_\_S49575 ribosomal protein L10.e, cytosolic - rice >gi\_575355\_emb\_CAA57339\_ (X81691) putative tumor suppresser [Oryza sativa]

 Seq. No.
 232999

 Seq. ID
 LIB3272-005-P1-K1-H4

 Method
 BLASTX

 NCBI GI
 q549063

NCBI GI g549063 BLAST score 502 E value 6.0e-51 Match length 116 % identity 82

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 233000

Seq. ID LIB3272-005-P1-K1-H5

Method BLASTX
NCBI GI g3377797
BLAST score 575
E value 2.0e-59
Match length 140
% identity 79

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No. 233001

Seq. ID LIB3272-005-P1-K1-H6

Method BLASTX
NCBI GI g1418990
BLAST score 251
E value 2.0e-21
Match length 73

% identity 59

NCBI Description (Z75524) unknown [Lycopersicon esculentum]

Seq. No. 233002

Seq. ID LIB3272-005-P1-K1-H7

Method BLASTX
NCBI GI g1199778
BLAST score 429
E value 2.0e-42
Match length 117
% identity 72

NCBI Description (D83225) peroxidase [Populus nigra]

Seq. No. 233003

Seq. ID LIB3272-005-P1-K1-H8

Method BLASTX
NCBI GI g2499710
BLAST score 646
E value 8.0e-68



```
Match length
% identity
                  90
                  PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
NCBI Description
                  (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                  >gi 1438075 (L33686) phospholipase D [Ricinus communis]
                  233004
Seq. No.
Seq. ID
                  LIB3272-005-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g82308
BLAST score
                  677
E value
                  2.0e-71
Match length
                  130
                  91
% identity
NCBI Description myb protein 308 - garden snapdragon
Seq. No.
                  233005
                  LIB3272-006-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2146746
BLAST score
                  253
E value
                  7.0e-22
Match length
                  90
% identity
                  58
NCBI Description protein kinase (EC 2.7.1.-) - Arabidopsis thaliana
                  >gi 166819 (L05562) protein kinase [Arabidopsis thaliana]
                  233006
Seq. No.
                  LIB3272-006-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g70644
BLAST score
                  515
E value
                  1.0e-52
Match length
                  111
% identity
                  18
NCBI Description ubiquitin precursor - common sunflower (fragment)
                  233007
Seq. No.
Seq. ID
                  LIB3272-006-P1-K1-A7
                  BLASTX
Method
NCBI GI
                  g2894607
BLAST score
                  258
E value
                  2.0e-22
Match length
                  54
% identity
                  87
NCBI Description (AL021889) NAM (no apical meristem) - like protein
                   [Arabidopsis thaliana]
                  233008
Seq. No.
Seq. ID
                  LIB3272-006-P1-K1-A8
                  BLASTX
Method
NCBI GI
                  g1170747
BLAST score
                  206
E value
                  2.0e-16
Match length
                  43
% identity
                   98
```

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi\_167345



(M88324) late embryogenesis-abundant protein [Gossypium hirsutum] >gi\_167347 (M37697) Lea5-A late

embryogenesis-abundant protein [Gossypium hirsutum]

233009 Seq. No. LIB3272-006-P1-K1-B10 Seq. ID Method BLASTX NCBI GI g3128228 BLAST score 550 E value 1.0e-56 Match length 117 % identity 89

NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi 3337376 (AC004481) putative ribosomal protein

L18A [Arabidopsis thaliana]

 Seq. No.
 233010

 Seq. ID
 LIB3272-006-P1-K1-B3

 Method
 BLASTX

Method BLASTX
NCBI GI g4455206
BLAST score 371
E value 1.0e-35
Match length 129
% identity 60

NCBI Description (AL035440) putative beta-1, 3-glucanase [Arabidopsis

thaliana]

Seq. No. 233011

Seq. ID LIB3272-006-P1-K1-B9

Method BLASTX
NCBI GI g543711
BLAST score 500
E value 1.0e-50
Match length 112
% identity 90

NCBI Description 14-3-3-LIKE PROTEIN S94 >gi\_419796\_pir\_S30927 14-3-3

protein homolog - rice >gi\_303859\_dbj\_BAA03711\_ (D16140)

brain specific protein [Oryza sativa]

Seq. No. 233012

Seq. ID LIB3272-006-P1-K1-C2

Method BLASTX
NCBI GI g508304
BLAST score 273
E value 4.0e-24
Match length 65
% identity 78

NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 233013

Seq. ID LIB3272-006-P1-K1-C3

Method BLASTX
NCBI GI g167367
BLAST score 606
E value 4.0e-63
Match length 132
% identity 89

Seq. No.

233019





```
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                   233014
                   LIB3272-006-P1-K1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3549691
                   595
BLAST score
E value
                   7.0e-62
Match length
                   134
                   76
% identity
NCBI Description (AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]
                   233015
Seq. No.
Seq. ID
                   LIB3272-006-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g1351222
BLAST score
                   402
E value
                   1.0e-44
Match length
                   103
% identity
                   89
                   TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi 945087
NCBI Description
                   (U31097) transcription factor TFIIB [Glycine max]
Seq. No.
                   233016
Seq. ID
                   LIB3272-006-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   g1171035
BLAST score
                   164
E value
                   2.0e-11
Match length
                   74
% identity
                    42
                   METALLOTHIONEIN-LIKE PROTEIN TYPE 2 PKIWI504
NCBI Description
                   >gi_1086021_pir__S48038 metallothionein-like protein - kiwi fruit >gi_450245 (L27813) metallothionein-like protein
                    [Actinidia deliciosa]
                    233017
Seq. No.
                   LIB3272-006-P1-K1-D1
Seq. ID
                   BLASTX
Method
NCBI GI
                    g3868758
BLAST score
                    346
                    1.0e-32
E value
                   107
Match length
% identity
                    62
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
                    233018
Seq. No.
Seq. ID
                   LIB3272-006-P1-K1-D10
                   BLASTX
Method
NCBI GI
                    q3021348
BLAST score
                    255
                    4.0e-40
E value
                    108
Match length
% identity
NCBI Description (AJ004961) ribosomal protein L18 [Cicer arietinum]
```

Match length

% identity

113

52



```
LIB3272-006-P1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q114420
BLAST score
                   634
E value
                   2.0e-66
Match length
                   132
% identity
                   94
NCBI Description
                   ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
                   >gi_100882_pir__S11491 H+-transporting ATP synthase (EC
                   3.6.1.34) beta chain, mitochondrial - maize
                   >gi 22173 emb CAA38140 (X54233) ATPase F1 subunit protein
                   [Zea mays] >gi 897618 (M36087) F-1-ATPase subunit 2 [Zea
                   mays]
Seq. No.
                   233020
Seq. ID
                   LIB3272-006-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   g1709498
BLAST score
                   513
E value
                   3.0e-52
Match length
                   113
% identity
NCBI Description
                   OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                   >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis
thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
                   [Arabidopsis thaliana]
Seq. No.
                   233021
                   LIB3272-006-P1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3450842
BLAST score
                   142
                   9.0e-09
E value
Match length
                   110
% identity
                   30
NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza
                   sativa]
                   233022
Seq. No.
                   LIB3272-006-P1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3329368
BLAST score
                   181
E value
                   3.0e-21
Match length
                   125
% identity
                   42
NCBI Description (AF031244) nodulin-like protein [Arabidopsis thaliana]
                   233023
Seq. No.
Seq. ID
                   LIB3272-006-P1-K1-D6
                   BLASTX
Method
NCBI GI
                   g1168728
BLAST score
                   321
E value
                   9.0e-30
```

NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi 598071 (L37883)

Seq. No.

233029



## cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]

```
233024
Seq. No.
                  LIB3272-006-P1-K1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3759184
                  257
BLAST score
                  3.0e-22
E value
Match length
                  111
% identity
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
                  233025
Seq. No.
Seq. ID
                  LIB3272-006-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g122003
                  316
BLAST score
                  3.0e-29
E value
                  88
Match length
                  72
% identity
NCBI Description HISTONE H2A >gi_82089_pir__JQ1182 histone H2A.1 - tomato
                  233026
Seq. No.
                  LIB3272-006-P1-K1-E2
Seq. ID
Method
                  BLASTX
                  q1928981
NCBI GI
BLAST score
                  582
                  2.0e-60
E value
                  123
Match length
                  63
% identity
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                  oleracea var. botrytis]
                  233027
Seq. No.
                  LIB3272-006-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1172441
BLAST score
                  204
E value
                   5.0e-16
Match length
                  75
% identity
                   61
                  POSSIBLE TRANSCRIPTION FACTOR POSF21 >gi_99685_pir__S21883
NCBI Description
                   DNA-binding protein POSF21 - Arabidopsis thaliana
                   >gi 16429 emb CAA43366_ (X61031) posF21 [Arabidopsis
                   thaliana]
Seq. No.
                   233028
                  LIB3272-006-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3142634
                  203
BLAST score
E value
                   4.0e-16
                  69
Match length
                   61
% identity
NCBI Description (AF063665) small nuclear ribonucleoprotein N [Mus musculus]
```



```
LIB3272-006-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128186
BLAST score
                  164
                  2.0e-11
E value
Match length
                  104
                  38
% identity
NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  233030
                  LIB3272-006-P1-K1-F10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3377797
BLAST score
                  468
E value
                  4.0e-47
Match length
                  102
% identity
                  89
                  (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
                  233031
Seq. No.
Seq. ID
                  LIB3272-006-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q1170747
BLAST score
                  321
                  9.0e-30
E value
                  77
Match length
                  82
% identity
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
NCBI Description
                  (M88324) late embryogenesis-abundant protein [Gossypium
                  hirsutum] >gi 167347 (M37697) Lea5-A late
                  embryogenesis-abundant protein [Gossypium hirsutum]
                  233032
Seq. No.
Seq. ID
                  LIB3272-006-P1-K1-F2
Method
                  BLASTX
                  g1076660
NCBI GI
BLAST score
                  316
                  4.0e-29
E value
                  92
Match length
                  73
% identity
NCBI Description D13F(MYBST1) protein - potato >gi 786426 bbs 159122
                  (S74753) MybSt1=Myb-related transcriptional activator
                  {DNA-binding domain repeats} [Solanum tuberosum=potatoes,
                  leaf, Peptide, 342 aa] [Solanum tuberosum]
Seq. No.
                  233033
                  LIB3272-006-P1-K1-F4
```

Seq. ID

Method BLASTX g2459448 NCBI GI 217

BLAST score E value 4.0e-24 Match length 113 % identity 49



(ACO02332) putative cinnamoyl-CoA reductase [Arabidopsis NCBI Description thaliana]

233034 Seq. No.

LIB3272-006-P1-K1-F5 Seq. ID

Method BLASTX NCBI GI g3769472 BLAST score 429 E value 2.0e-42 Match length 105

% identity 68

(AF064732) putative phospholipase A2 [Dianthus NCBI Description

caryophyllus]

Seq. No. 233035

LIB3272-006-P1-K1-F6 Seq. ID

Method BLASTX NCBI GI g549063 BLAST score 466 E value 9.0e-47 Match length 107 % identity 82

TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) NCBI Description

>gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626)

21kd polypeptide [Oryza sativa]

233036 Seq. No.

LIB3272-006-P1-K1-F7 Seq. ID

Method BLASTX NCBI GI g2970051 BLAST score 196 E value 4.0e-15 70 Match length

% identity 57

NCBI Description (AB012110) ARG10 [Vigna radiata]

233037 Seq. No.

Seq. ID LIB3272-006-P1-K1-F8

BLASTX Method g2499610 NCBI GI BLAST score 489 2.0e-49 E value Match length 128 % identity 77

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 6 (MAP KINASE 6)

(ATMPK6) >qi 629547 pir S40472 mitogen-activated protein

kinase 6 (EC 2.7.1.-) - Arabidopsis thaliana

>gi 457404 dbj BAA04869 (D21842) MAP kinase [Arabidopsis thaliana] >gi 2281091 (AC002333) MAP Kinase 6 [Arabidopsis

thaliana]

Seq. No. 233038

Seq. ID LIB3272-006-P1-K1-F9

Method BLASTX g4415942 NCBI GI BLAST score 433

BLAST score

Match length

E value

329 1.0e-30

122



```
7.0e-43
E value
Match length
                   133
% identity
                   64
NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   233039
                   LIB3272-006-P1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2191150
BLAST score
                   211
E value
                   2.0e-21
Match length
                   88
% identity
                   68
NCBI Description
                  (AF007269) similar to mitochondrial carrier family
                   [Arabidopsis thaliana]
Seq. No.
                   233040
                   LIB3272-006-P1-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g322596
BLAST score
                   376
E value
                   3.0e-36
                   79
Match length
% identity
                   92
NCBI Description serine/threonine protein kinase (EC 2.7.-.-) AK21 -
                   Arabidopsis thaliana >gi_166600 (M93023) SNF1-related
                   protein kinase [Arabidopsis thaliana]
                   >gi_1742969_emb_CAA64384_ (X94757) ser/thr protein kinase
                   [Arabidopsis thaliana]
                   233041
Seq. No.
Seq. ID
                   LIB3272-006-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   g1332579
BLAST score
                   514
                   2.0e-52
E value
Match length
                   118
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
                   233042
Seq. No.
                   LIB3272-006-P1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g730456
BLAST score
                   488
E value
                   2.0e-49
                   115
Match length
                   75
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S19
                   233043
Seq. No.
Seq. ID
                   LIB3272-006-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   g2462762
```

NCBI Description



```
% identity
                  (AC002292) Highly similar to auxin-induced protein
NCBI Description
                  (aldo/keto reductase family) [Arabidopsis thaliana]
                  233044
Seq. No.
                  LIB3272-006-P1-K1-G5
Seq. ID
                  BLASTX
Method
                  q3059131
NCBI GI
BLAST score
                  304
                  9.0e-28
E value
                  95
Match length
                  58
% identity
NCBI Description (AJ000478) cytochrome P450 [Helianthus tuberosus]
                  233045
Seq. No.
                  LIB3272-006-P1-K1-G7
Seq. ID
                  BLASTX
Method
                  g1332579
NCBI GI
                  531
BLAST score
                  4.0e-60
E value
Match length
                  132
                  10
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
                  233046
Seq. No.
                  LIB3272-006-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3860259
                  159
BLAST score
                   4.0e-13
E value
Match length
                  102
                  49
% identity
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
                   233047
Seq. No.
Seq. ID
                  LIB3272-006-P1-K1-G9
Method
                  BLASTX
NCBI GI
                   g2739046
BLAST score
                   374
E value
                   6.0e - 36
Match length
                   112
% identity
                   62
NCBI Description (AF024652) polyphosphoinositide binding protein Ssh2p
                   [Glycine max]
                   233048
Seq. No.
                   LIB3272-006-P1-K1-H1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3128228
                   214
BLAST score
                   2.0e-17
E value
                   67
Match length
                   67
% identity
                   (AC004077) putative ribosomal protein L18A [Arabidopsis
```

L18A [Arabidopsis thaliana]

thaliana] >gi\_3337376 (AC004481) putative ribosomal protein



```
233049
Seq. No.
                  LIB3272-006-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3142300
BLAST score
                  258
                  1.0e-22
E value
Match length
                  84
                  61
% identity
                  (AC002411) Contains similarity to pre-mRNA processing
NCBI Description
                  protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908
                  and gb_T88158, gb_N38703 and gb_AA651043 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  233050
                  LIB3272-006-P1-K1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3242079
BLAST score
                  218
                  6.0e-18
E value
Match length
                  67
% identity
NCBI Description (AJ006984) proline-rich protein [Capsicum annuum]
Seq. No.
                  233051
                  LIB3272-006-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3337350
                  259
BLAST score
E value
                  1.0e-22
Match length
                  104
% identity
                   52
NCBI Description (AC004481) putative permease [Arabidopsis thaliana]
Seq. No.
                   233052
                  LIB3272-006-P1-K1-H4
Seq. ID
                  BLASTX
Method
                   g1928981
NCBI GI
                   451
BLAST score
E value
                   5.0e-45
Match length
                   114
                   79
% identity
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                   oleracea var. botrytis]
Seq. No.
                   233053
                   LIB3272-006-P1-K1-H5
Seq. ID
                   BLASTX
Method
                   q3928543
NCBI GI
BLAST score
                   153
E value
                   5.0e-10
                   124
Match length
% identity
                  (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
```

33608

233054

LIB3272-006-P1-K1-H7

Seq. No.

Seq. ID

Method BLASTX NCBI GI g2764941 BLAST score 222 E value 3.0e-18 Match length 72 % identity 58 NCBI Description thaliana] 233055 Seq. No. Method BLASTX g2160166 123 1.0e-09 66 % identity 58

(X98255) transcriptionally stimulated by gibberellins; expressed in meristematic region, and style [Arabidopsis

Seq. ID LIB3272-007-P1-K1-A1

NCBI GI BLAST score E value Match length

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 233056

Seq. ID LIB3272-007-P1-K1-A12

Method BLASTX NCBI GI g3158376 BLAST score 328 E value 9.0e-31 95 Match length % identity 68

NCBI Description (AF035385) unknown [Arabidopsis thaliana]

Seq. No. 233057

Seq. ID LIB3272-007-P1-K1-A2

Method BLASTX NCBI GI g4510363 BLAST score 249 3.0e-21 E value 58 Match length 81 % identity

NCBI Description (AC007017) putative DNA-binding protein [Arabidopsis

thaliana]

233058 Seq. No.

Seq. ID LIB3272-007-P1-K1-A4

Method BLASTX NCBI GI g2494905 BLAST score 153 4.0e-10 E value

Match length 85 % identity 45

NCBI Description MICROTUBULE-ASSOCIATED PROTEIN YTM1 >gi 2132107 pir S67174

hypothetical protein YOR272w - yeast (Saccharomyces

cerevisiae) >gi 1279699\_emb\_CAA61778\_ (X89633) hypothetical

protein [Saccharomyces cerevisiae]

>gi 1420610 emb CAA99497\_ (Z75180) ORF YOR272w [Saccharomyces cerevisiae] >gi 1928989 (U92821)

microtubule-associated protein [Saccharomyces cerevisiae]



```
233059
Seq. No.
                   LIB3272-007-P1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g464986
                   366
BLAST score
                   3.0e - 35
E value
                   69
Match length
                   97
% identity
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                   >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana
                   >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                   enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana]
                   >gi 600391_emb_CAA51201_ (X72626) ubiquitin conjugating
                    enzyme E2 [Arabidopsis thaliana]
                    >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein
                    ligase UBC9 [Arabidopsis thaliana]
Seq. No.
                    233060
                   LIB3272-007-P1-K1-A7
Seq. ID
                   BLASTX
Method
                    g4538993
NCBI GI
BLAST score
                    521
                    3.0e-53
E value
Match length
                    127
                    75
% identity
NCBI Description (AL049481) putative host response protein [Arabidopsis
                    thaliana]
                    233061
Seq. No.
                    LIB3272-007-P1-K1-A9
Seq. ID
Method
                    BLASTX
NCBI GI
                    q2499946
BLAST score
                    575
E value
                    2.0e-59
                    134
Match length
% identity
                    URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
NCBI Description
                    PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                    DECARBOXYLASE >gi 747980 (U22260) UMP synthase [Nicotiana
                    tabacum]
                    233062
Seq. No.
                    LIB3272-007-P1-K1-B1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g927575
BLAST score
                    405
E value
                    1.0e-39
                    90
Match length
                    77
% identity
NCBI Description (U12926) alpha galactosidase [Glycine max]
```

Seq. No. 233063

Seq. ID LIB3272-007-P1-K1-B10

Method BLASTX

% identity



```
NCBI GI
                   q3914467
BLAST score
                   165
                   1.0e-11 ·
E value
                   79
Match length
% identity
                   51
                   26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
NCBI Description
                   >qi 1864003 dbj BAA19252 (AB001422) 21D7 [Nicotiana
                   tabacum]
Seq. No.
                   233064
                   LIB3272-007-P1-K1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4098129
BLAST score
                   481
E value
                   1.0e-48
Match length
                   93
% identity
                   94
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
Seq. No.
                   233065
                   LIB3272-007-P1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q167367
BLAST score
                   354
E value
                   9.0e - 38
Match length
                   92
                   92
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                   233066
Seq. No.
                   LIB3272-007-P1-K1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1171577
BLAST score
                   401
E value
                   3.0e-39
Match length
                   118
                   67
% identity
NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]
Seq. No.
                   233067
Seq. ID
                   LIB3272-007-P1-K1-B3
                   BLASTX
Method
NCBI GI
                   g3738285
BLAST score
                   197
E value
                   3.0e-15
Match length
                   80
                   50
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
                   233068
Seq. No.
Seq. ID
                   LIB3272-007-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   g730241
BLAST score
                   225
E value
                   1.0e-18
Match length
                   94
```



NCBI Description DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) >gi\_473947\_dbj\_BAA06126\_ (D29643) similar to Canis oligosaccharyltransferase 48 kDa subunit (M98392). [Homo sapiens] 233069 Seq. No. Seq. ID LIB3272-007-P1-K1-B7 BLASTX Method NCBI GI q1173104 BLAST score 494 5.0e-50 E value Match length 121 70 % identity RIBONUCLEASE 2 PRECURSOR >qi 289210 (M98336) ribonuclease NCBI Description [Arabidopsis thaliana] >gi 2642160 (AC003000) ribonuclease, RNS2 [Arabidopsis thaliana] 233070 Seq. No. LIB3272-007-P1-K1-C1 Seq. ID Method BLASTX NCBI GI q419778 BLAST score 458 E value 5.0e-46Match length 104 % identity 84 ferredoxin--nitrite reductase (EC 1.7.7.1) nir-1 - common NCBI Description tobacco (fragment) >gi\_542053\_pir\_\_S23769
ferredoxin--nitrite reductase (EC 1.7.7.1) - common tobacco (fragment) >gi\_445049\_prf\_\_1908371A nitrite reductase [Nicotiana tabacum] 233071 Seq. No. Seq. ID LIB3272-007-P1-K1-C10 Method BLASTX NCBI GI q4210948 BLAST score 428 E value 2.0e-42 Match length 83 % identity 99 NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis] Seq. No. 233072 Seq. ID LIB3272-007-P1-K1-C11 Method BLASTX q3551954 169 4.0e-12

NCBI GI BLAST score E value Match length 78 % identity 45

(AF082030) senescence-associated protein 5 [Hemerocallis NCBI Description

hybrid cultivar]

233073 Seq. No.

Seq. ID LIB3272-007-P1-K1-C2

Method BLASTX



NCBI GI g3881649 BLAST score 466 E value 1.0e-46 Match length 88 % identity 89

NCBI Description (Z70757) Similarity to yeast hypothetical protein PIR accession number S52511; cDNA EST EMBL:D73067 comes from this gene; cDNA EST EMBL:D74461 comes from this gene; cDNA

EST EMBL: D76044 comes from this gene; cDNA EST yk504c7.3

Seq. No. 233074

Seq. ID LIB3272-007-P1-K1-C3

Method BLASTX
NCBI GI g2462762
BLAST score 404
E value 2.0e-39
Match length 132
% identity 61

NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 233075

Seq. ID LIB3272-007-P1-K1-C9

Method BLASTX
NCBI GI g1220180
BLAST score 275
E value 2.0e-24
Match length 111

% identity 52

NCBI Description (Z69996) dormancy related protein [Trollius ledebourii]

Seq. No. 233076

Seq. ID LIB3272-007-P1-K1-D10

Method BLASTX
NCBI GI g1946371
BLAST score 322
E value 4.0e-30
Match length 82

% identity 73

NCBI Description (U93215) regulatory protein Viviparous-1 isolog

[Arabidopsis thaliana]

Seq. No. 233077

Seq. ID LIB3272-007-P1-K1-D11

Method BLASTX
NCBI GI g113621
BLAST score 238
E value 2.0e-20
Match length 54
% identity 87

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi\_68196\_pir\_\_ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi\_168420 (M16220) aldolase [Zea mays] >gi\_295850\_emb\_CAA31366\_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi\_225624\_prf\_\_1307278A

cytoplasmic aldolase [Zea mays]

Match length

% identity

73



```
Seq. No.
                  233078
Seq. ID
                  LIB3272-007-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q2811025
BLAST score
                  187
                  3.0e-14
E value
Match length
                  70
% identity
                  60
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607_
                  (AB002695) aspartic endopeptidase [Cucurbita pepo]
Seq. No.
                  233079
                  LIB3272-007-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g113621
BLAST score
                  264
                  2.0e-23
E value
Match length
                  60
% identity
                  88
NCBI Description
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
                  >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
                  4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
                  [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
                  bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A
                  cytoplasmic aldolase [Zea mays]
                  233080
Seq. No.
Seq. ID
                  LIB3272-007-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g533086
BLAST score
                  315
E value
                  2.0e-29
Match length
                  82
% identity
                  71
NCBI Description (U07605) precursor delta-9-stearoyl-acyl carrier protein
                  desaturase [Thunbergia alata]
                  233081
Seq. No.
Seq. ID
                  LIB3272-007-P1-K1-D7
                  BLASTX
Method
NCBI GI
                  g3924596
BLAST score
                  476
E value
                  6.0e-48
Match length
                  126
% identity
                  75
NCBI Description (AF069442) putative phospho-ser/thr phosphatase
                  [Arabidopsis thaliana]
                  233082
Seq. No.
Seq. ID
                  LIB3272-007-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g1345673
BLAST score
                  388
E value
                  8.0e-38
```

NCBI Description CATALASE ISOZYME 1 >gi\_862452\_dbj BAA09506 (D55645)



## catalase [Cucurbita pepo]

```
Seq. No.
                  233083
                  LIB3272-007-P1-K1-E2
Seq. ID
Method
                  BLASTX
                  g3915826
NCBI GI
BLAST score
                  411
E value
                  2.0e-40
Match length
                  92
% identity
                  83
NCBI Description 60S RIBOSOMAL PROTEIN L5
Seq. No.
                  233084
                  LIB3272-007-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q126770
BLAST score
                  480
E value
                  1.0e-48
Match length
                  93
                  97
% identity
NCBI Description MALATE SYNTHASE, GLYOXYSOMAL >gi_68218_pir__SYCNMU malate
                  synthase (EC 4.1.3.2) - upland cotton
                  >gi_18507_emb_CAA36546_ (X52305) malate synthase (AA 1-567)
                  [Gossypium hirsutum]
                  233085
Seq. No.
                  LIB3272-007-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g232029
BLAST score
                  373
E value
                  4.0e-36
Match length
                  74
% identity
                  99
NCBI Description
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                  >gi_100154_pir__S21989 translation elongation factor eEF-1
                  alpha chain - carrot >gi 18339 emb CAA42843 (X60302)
                  elongation factor 1A [Daucus carota]
                  233086
Seq. No.
Seq. ID
                  LIB3272-007-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g4204265
BLAST score
                  396
                  1.0e-38
E value
Match length
                  93
% identity
                  77
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]
Seq. No.
                  233087
Seq. ID
                  LIB3272-007-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g549063
BLAST score
                  394
E value
                  2.0e-38
Match length
                  92
% identity
                  82
```

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)



233088

>gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626) 21kd polypeptide [Oryza sativa]

LIB3272-007-P1-K1-F11 Seq. ID Method BLASTX q3980393 NCBI GI BLAST score 374 6.0e-36 E value Match length 120 59 % identity

Seq. No.

(AC004561) putative glutathione S-transferase [Arabidopsis NCBI Description

thaliana]

233089 Seq. No.

LIB3272-007-P1-K1-F12 Seq. ID

Method BLASTX q4510363 NCBI GI BLAST score 212 2.0e-17 E value 45 Match length % identity 96

(AC007017) putative DNA-binding protein [Arabidopsis NCBI Description

thaliana]

233090 Seq. No.

LIB3272-007-P1-K1-F8 Seq. ID

BLASTX Method NCBI GI g3776005 BLAST score 153 E value 2.0e-10 Match length 67

57 % identity

NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

233091 Seq. No.

LIB3272-007-P1-K1-F9 Seq. ID

BLASTX Method NCBI GI g4006957 232 BLAST score 2.0e-19 E value 92 Match length % identity 48

(AJ006910) pollen allergen Betv1, isoform at45 [Betula NCBI Description

pendula]

233092 Seq. No.

LIB3272-007-P1-K1-G11 Seq. ID

BLASTX Method NCBI GI g3860247 BLAST score 203 E value 3.0e-16 44 Match length 82 % identity

NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

```
233093
Seq. No.
Seq. ID
                  LIB3272-007-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q547713
BLAST score
                  263
                  4.0e-23
E value
                  55
Match length
                  80
% identity
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E)
NCBI Description
                  (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-(ISO)4F 25 KD
                  SUBUNIT) (EIF-(ISO)4F P28 SUBUNIT) >gi_322866_pir__B44452
                  translation initiation factor eIF-4F isozyme form subunit
                  p28 - wheat >gi_170751 (M95818) initiation factor (iso)4F
                  p28 subunit [Triticum aestivum]
                  233094
Seq. No.
                  LIB3272-007-P1-K1-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4510363
BLAST score
                  336
                  9.0e-32
E value
                  69
Match length
                  94
% identity
                  (AC007017) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  233095
                  LIB3272-007-P1-K1-H10
Seq. ID
                  BLASTX
Method
                  q4567314
NCBI GI
BLAST score
                  495
                   4.0e-50
E value
                  109
Match length
                  83
% identity
NCBI Description (AC005956) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   233096
                  LIB3272-007-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g167367
BLAST score
                   679
                   9.0e-72
E value
                  127
Match length
                   98
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                   233097
                  LIB3272-007-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1173234
BLAST score
                   314
                   6.0e-29
E value
                  71
Match length
                   87
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S25 >gi 481909 pir S40089 ribosomal
```

33617

ribosomal protein S25 [Lycopersicon esculentum]

protein S25 - tomato >gi 435679 emb CAA54132 (X76714)



233098

>gi\_1584836\_prf\_\_2123431A ribosomal protein S25
[Lycopersicon esculentum]

 Seq. ID
 LIB3272-007-P1-K1-H5

 Method
 BLASTX

 NCBI GI
 g2809255

 BLAST score
 738

 E value
 1.0e-78

 Match length
 144

 % identity
 90

Seq. No.

NCBI Description (AC002560) F21B7.24 [Arabidopsis thaliana]

Seq. No. 233099

Seq. ID LIB3272-007-P1-K1-H6

Method BLASTX
NCBI GI g3928543
BLAST score 196
E value 2.0e-15
Match length 85
% identity 46

NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 233100

Seq. ID LIB3272-007-P1-K1-H8

Method BLASTX
NCBI GI g3928099
BLAST score 291
E value 3.0e-26
Match length 131
% identity 24

NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 233101

Seq. ID LIB3272-008-P1-K1-A10

Method BLASTX
NCBI GI g3881724
BLAST score 164
E value 3.0e-11
Match length 52
% identity 56

NCBI Description (Z69385) Similarity to Yeast JTA107 protein (PIR Acc. No.

S55137); cDNA EST yk290e3.3 comes from this gene; cDNA EST yk290e3.5 comes from this gene [Caenorhabditis elegans]

Seq. No. 233102

Seq. ID LIB3272-008-P1-K1-A2

Method BLASTX
NCBI GI g4262234
BLAST score 390
E value 7.0e-38
Match length 120
% identity 65

NCBI Description (AC006200) unknown protein [Arabidopsis thaliana]

Seq. No. 233103



```
LIB3272-008-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2149127
BLAST score
                   300
E value
                   2.0e-27
Match length
                   108
                   56
% identity
                   (U81293) UDP-glucose:indole-3-acetate
NCBI Description
                  beta-D-glucosyltransferase [Arabidopsis thaliana]
Seq. No.
                   233104
                   LIB3272-008-P1-K1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3337356
BLAST score
                   566
                   2.0e-58
E value
Match length
                   118
                   93
% identity
                  (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
                   233105
Seq. No.
Seq. ID
                   LIB3272-008-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   g2245136
BLAST score
                   446
                   2.0e-44
E value
Match length
                   120
% identity
                   68
                   (Z97344) trehalose-6-phosphate synthase homolog
NCBI Description
                   [Arabidopsis thaliana]
                   233106
Seq. No.
Seq. ID
                   LIB3272-008-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   g3738301
BLAST score
                   395
E value
                   2.0e-38
Match length
                   104
% identity
                   64
NCBI Description
                   (AC005309) putative zinc-finger protein [Arabidopsis
                   thaliana] >gi_4249397 (AC006072) putative zinc-finger
                   protein (B-box zinc finger domain) [Arabidopsis thaliana]
Seq. No.
                   233107
Seq. ID
                   LIB3272-008-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   g1001309
BLAST score
                   216
E value
                   2.0e-17
Match length
                   125
                   35
% identity
                 (D64006) aspartate aminotransferase [Synechocystis sp.]
NCBI Description
```

Seq. No. 233108

Seq. ID LIB3272-008-P1-K1-B12

Method BLASTX



NCBI GI g730463 BLAST score 322 E value 8.0e-30 Match length 105 % identity 59

NCBI Description 60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)

>gi\_630323\_pir\_\_S44069 ribosomal protein L35a.e.c15 - yeast
(Saccharomyces cerevisiae) >gi\_484241 (L23923) ribosomal

protein L37 [Saccharomyces cerevisiae]

>gi\_1420537\_emb\_CAA99454\_ (Z75142) ORF YOR234c

[Saccharomyces cerevisiae]

Seq. No. 233109

Seq. ID LIB3272-008-P1-K1-B3

Method BLASTX
NCBI GI g4512653
BLAST score 505
E value 2.0e-51
Match length 142
% identity 53

NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]

Seq. No. 233110

Seq. ID LIB3272-008-P1-K1-B5

Method BLÄSTX
NCBI GI g2465008
BLAST score 327
E value 2.0e-30
Match length 138
% identity 47

NCBI Description (AJ001445) ripening-induced protein [Fragaria vesca]

Seq. No. 233111

Seq. ID LIB3272-008-P1-K1-C1

Method BLASTX
NCBI GI g417060
BLAST score 282
E value 2.0e-45
Match length 103
% identity 87

NCBI Description GLUTAMINE SYNTHETASE NODULE ISOZYME (GLUTAMATE--AMMONIA

LIGASE) (GS) >gi\_170637 (M94765) glutamine synthetase [Vigna aconitifolia] >gi 1094850 prf 2106409A Gln

synthetase [Vigna aconitifolia]

Seq. No. 233112

Seq. ID LIB3272-008-P1-K1-C10

Method BLASTX
NCBI GI g2130073
BLAST score 507
E value 2.0e-51
Match length 112
% identity 89

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,

cytosolic - rice >gi\_786178\_dbj\_BAA08845\_ (D50307) aldolase

C-1 [Oryza sativa] >gi\_790970\_dbj\_BAA08830\_ (D50301)

aldolase C-1 [Oryza sativa]

Seq. No.

Seq. ID

233118

LIB3272-008-P1-K1-C8



```
233113
Seq. No.
                   LIB3272-008-P1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244846
                   463
BLAST score
                   2.0e-46
E value
                   118
Match length
                   73
 % identity
                  (Z97337) ferredoxin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   233114
                   LIB3272-008-P1-K1-C12
Seq. ID
Method
                   BLASTX
                   g3395673
NCBI GI
BLAST score
                   450
                   7.0e-45
E value
Match length
                   116
                   74
 % identity
NCBI Description
                  (AB016623) RWC-3 [Oryza sativa]
                   233115
Seq. No.
                   LIB3272-008-P1-K1-C2
Seq. ID
                   BLASTX
Method
                   g3024017
NCBI GI
BLAST score
                  - 509
                   9.0e-52
E value
                   99
Match length
                   97
 % identity
 NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)
                   (EIF-4C) >gi 2565421 (AF026804) eukaryotic translation
                   initiation factor eIF-1A [Onobrychis viciifolia]
                   233116
 Seq. No.
 Seq. ID
                   LIB3272-008-P1-K1-C4
 Method
                   BLASTX
 NCBI GI
                   g1518540
 BLAST score
                   512
 E value
                   4.0e-52
 Match length
                   108
 % identity
                   92
 NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
 Seq. No.
                   233117
                   LIB3272-008-P1-K1-C5
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q2129915
 BLAST score
                   186
 E value
                   4.0e-14
                   72
 Match length
                   51
% identity
                   ferredoxin precursor - sweet orange
 NCBI Description
                   >gi 1360725 emb CAA87068 (Z46944) non-photosynthetic
                   ferredoxin [Citrus sinensis]
```

Seq. No.

Seq. ID Method



```
BLASTX
Method
NCBI GI
                  q3264769
                  618
BLAST score
                  1.0e-64
E value
Match length
                  140
                  57
% identity
                  (AF071894) late embryogenesis-like protein [Prunus
NCBI Description
                  armeniaca]
                  233119
Seq. No.
                  LIB3272-008-P1-K1-C9
Seq. ID
                  BLASTX
Method
                  g2132474
NCBI GI
                  177
BLAST score
                  7.0e-13
E value
                  63
Match length
                  52
% identity
                  probable membrane protein YDR091c - yeast (Saccharomyces
NCBI Description
                  cerevisiae) >gi 914875 emb CAA90450 (Z50111) unknown
                  [Saccharomyces cerevisiae]
                  233120
Seq. No.
                  LIB3272-008-P1-K1-D1
Seq. ID
                  BLASTX
Method
                  g3122785
NCBI GI
                  503
BLAST score
E value
                  5.0e-51
Match length
                  125
                  82
% identity
                  40S RIBOSOMAL PROTEIN S14 >gi 2565340 (AF026079) ribosomal
NCBI Description
                  protein S14 [Lupinus luteus]
                  233121
Seq. No.
                  LIB3272-008-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g441457
BLAST score
                   648
                   4.0e-68
E value
                   122
Match length
% identity
                  (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                   esculentum]
                   233122
Seq. No.
                   LIB3272-008-P1-K1-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4193388
BLAST score
                  253
E value
                   8.0e-22
Match length
                   76
% identity
                   (AF091455) translationally controlled tumor protein [Hevea
NCBI Description
                  brasiliensis]
```

LIB3272-008-P1-K1-D4

233123

BLASTX



```
q4336436
NCBI GI
                  493
BLAST score
E value
                  6.0e-50
Match length
                  139
% identity
                 (AF092432) protein phosphatase type 2C [Lotus japonicus]
NCBI Description
                  233124
Seq. No.
Seq. ID
                  LIB3272-008-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q2146797
BLAST score
                  549
E value
                  2.0e-56
Match length
                  141
% identity
                  74
                  protein disulfide-isomerase (EC 5.3.4.1) - Castor bean
NCBI Description
                  >qi 1134968 (U41385) protein disulphide isomerase PDI
                   [Ricinus communis] >gi_1587210_prf__2206331A protein
                  disulfide isomerase [Ricinus communis]
Seq. No.
                  233125
                  LIB3272-008-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g508304
BLAST score
                  218
E value
                  1.0e-17
                  76
Match length
% identity
                   58
NCBI Description (L22305) corC [Medicago sativa]
Seq. No.
                   233126
                  LIB3272-008-P1-K1-E1
Seq. ID
Method
                  BLASTX
                  g3894171
NCBI GI
BLAST score
                  496
                   3.0e-50
E value
                  131
Match length
                   69
% identity
                  (AC005312) putative glutathione s-transferase [Arabidopsis
NCBI Description
                   thaliana]
                   233127
Seq. No.
Seq. ID
                  LIB3272-008-P1-K1-E10
Method
                  BLASTX
NCBI GI
                   g2435604
BLAST score
                  172
                   9.0e-27
E value
                  139
Match length
                   52
% identity
NCBI Description (AF026213) strong similarity to Saccharomyces cerevisiae
                   endosomal P24A protein (SP:P32802) [Caenorhabditis elegans]
Seq. No.
                   233128
```

Seq. ID LIB3272-008-P1-K1-E12

Method BLASTX NCBI GI g2895870 BLAST score 336



```
2.0e-31
E value
Match length
                  83
                  67
% identity
                  (AF046001) zinc finger transcription factor [Homo sapiens]
NCBI Description
                  >gi 4508017 ref NP 003448.1_pZNF207_ zinc finger protein
                  233129
Seq. No.
                  LIB3272-008-P1-K1-E3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4220481
                  332
BLAST score
                  5.0e-31
E value
                  106
Match length
                  59
% identity
                  (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                  233130
Seq. No.
                  LIB3272-008-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024500
BLAST score
                  469
                  4.0e-47
E value
                  99
Match length
                  93
% identity
                  RAS-RELATED PROTEIN RAB11A >gi 1370142 emb CAA98177
NCBI Description
                  (Z73949) RAB11A [Lotus japonicus]
Seq. No.
                  233131
                  LIB3272-008-P1-K1-E5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g119150
                  716
BLAST score
                  5.0e-76
E value
Match length
                  136
                  100
% identity
NCBI Description
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                  >gi_82081_pir__S10507 translation elongation factor eEF-1
                  alpha chain - tomato >gi_19273_emb_CAA32618_ (X14449) EF
                  1-alpha (AA 1-448) [Lycopersicon esculentum]
                  >gi_295810_emb_CAA37212_ (X53043) elongation factor 1-alpha
                   [Lycopersicon esculentum]
Seq. No.
                  233132
Seq. ID
                  LIB3272-008-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g2414158
BLAST score
                  368
E value
                   3.0e-35
Match length
                  140
% identity
NCBI Description (Z72436) major allergen Bet v 1 [Betula pendula]
                  233133
```

Seq. No.

Seq. ID LIB3272-008-P1-K1-E7

BLASTX Method NCBI GI g3885334 BLAST score 264



```
5.0e-23
E value
                   70
Match length
% identity
                   64
NCBI Description
                   (AC005623) putative argonaute protein [Arabidopsis
                   thaliana]
                   233134
Seq. No.
                  LIB3272-008-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3820531
BLAST score
                   383
E value
                   5.0e - 37
Match length
                  102
                   65
% identity
NCBI Description
                  (AF072736) beta-glucosidase [Pinus contorta]
                   233135
Seq. No.
                  LIB3272-008-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g629597
BLAST score
                   359
                   3.0e - 34
E value
Match length
                   83
                   78
% identity
NCBI Description
                  proline-rich protein - rape >gi 545029 bbs 142669 (S68113)
                   proline-rich SAC51 [Brassica napus=oilseed rape, pods,
                   Peptide, 147 aa] [Brassica napus]
                   233136
Seq. No.
                   LIB3272-008-P1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3702962
BLAST score
                   577
                   9.0e-60
E value
Match length
                   126
% identity
                   88
NCBI Description
                   (AF079484) rac GTP binding protein Arac7 [Arabidopsis
                   thalianal
                   233137
Seq. No.
Seq. ID
                   LIB3272-008-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   g643469
BLAST score
                   298
E value
                   3.0e-27
Match length
                   113
% identity
                   57
NCBI Description (U19886) unknown [Lycopersicon esculentum]
Seq. No.
                   233138
Seq. ID
                   LIB3272-008-P1-K1-F2
Method
                  BLASTX
```

Method BLASTX
NCBI GI g464981
BLAST score 378
E value 2.0e-36
Match length 70
% identity 99



NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi\_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 233139

Seq. ID LIB3272-008-P1-K1-F5

Method BLASTX
NCBI GI g100277
BLAST score 104
E value 1.0e-09
Match length 73
% identity 56

NCBI Description translation initiation factor eIF-5A.1 - curled-leaved

tobacco (fragment) >gi\_829282\_emb\_CAA45103\_ (X63541)

eukaryotic initiation factor 5A (1) [Nicotiana

plumbaginifolia]

Seq. No. 233140

Seq. ID LIB3272-008-P1-K1-G4

Method BLASTX
NCBI GI g3122785
BLAST score 538
E value 4.0e-55
Match length 130
% identity 85

NCBI Description 40S RIBOSOMAL PROTEIN S14 >gi 2565340 (AF026079) ribosomal

protein S14 [Lupinus luteus]

Seq. No. 233141

Seq. ID LIB3272-008-P1-K1-G7

Method BLASTX
NCBI GI g81661
BLAST score 331
E value 7.0e-31
Match length 89
% identity 75

NCBI Description tryptophan synthase (EC 4.2.1.20) beta-2 chain -

Arabidopsis thaliana

Seq. No. 233142

Seq. ID LIB3272-008-P1-K1-H1

Method BLASTX
NCBI GI g2130459
BLAST score 232
E value 3.0e-19
Match length 109
% identity 44

NCBI Description LCB2 protein - fission yeast (Schizosaccharomyces pombe)

(fragment)

Seq. No. 233143

Seq. ID LIB3272-008-P1-K1-H10

Method BLASTX
NCBI GI g1350680
BLAST score 539
E value 2.0e-55
Match length 125



% identity 79

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No.

233144

Seq. ID

LIB3272-008-P1-K1-H11

BLASTX Method q730463 NCBI GI 322 BLAST score 8.0e-30 E value 105 Match length 59

% identity NCBI Description

60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)

>gi\_630323\_pir\_\_S44069 ribosomal protein L35a.e.c15 - yeast

(Saccharomyces cerevisiae) >gi 484241 (L23923) ribosomal

protein L37 [Saccharomyces cerevisiae]

>gi 1420537 emb CAA99454 (Z75142) ORF YOR234c

[Saccharomyces cerevisiae]

Seq. No.

Seq. ID

233145

LIB3272-008-P1-K1-H12

BLASTX Method NCBI GI g2499946 585 BLAST score 1.0e-60 E value 136

Match length 85 % identity

NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE

PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE

DECARBOXYLASE >gi 747980 (U22260) UMP synthase [Nicotiana

tabacum]

233146 Seq. No.

LIB3272-008-P1-K1-H2 Seq. ID

Method BLASTX NCBI GI q729470 BLAST score 666 E value 4.0e-70 Match length 141 90 % identity

NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)

 $>gi_542089_pir_JQ2272$  formate dehydrogenase (EC 1.2.1.2) precursor, mitochondrial - potato >gi 297798 emb CAA79702\_ (Z21493) mitochondrial formate dehydrogenase precursor

[Solanum tuberosum]

Seq. No. 233147

Seq. ID LIB3272-008-P1-K1-H3

Method BLASTX NCBI GI q1170747 BLAST score 353 E value 2.0e-33 Match length 84 82 % identity

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345

(M88324) late embryogenesis-abundant protein [Gossypium

hirsutum] >gi 167347 (M37697) Lea5-A late



## embryogenesis-abundant protein [Gossypium hirsutum]

```
Seq. No.
                  233148
                  LIB3272-008-P1-K1-H6
Seq. ID
                  BLASTX
Method
                  g1361983
NCBI GI
                  208
BLAST score
                  1.0e-16
E value
                  92
Match length
                  47
% identity
                  ARP protein - Arabidopsis thaliana >gi 886434_emb_CAA89858_
NCBI Description
                  (Z49776) ARP protein [Arabidopsis thaliana]
                  233149
Seq. No.
                  LIB3272-008-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2660676
BLAST score
                  177
                  6.0e-13
E value
                  38
Match length
                  87
% identity
                  (AC002342) Dreg-2 like protein [Arabidopsis thaliana]
NCBI Description
                  233150
Seq. No.
                  LIB3272-008-P1-K1-H9
Seq. ID
                  BLASTX
Method
                  g4572676
NCBI GI
                  276
BLAST score
                  2.0e-24
E value
                  90
Match length
                  60
% identity
NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]
                  233151
Seq. No.
                  LIB3272-009-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3319354
BLAST score
                  441
                  8.0e-44
E value
Match length
                  106
                  85
% identity
NCBI Description
                  (AF077407) contains similarity to sugar transporters (Pfam:
                  sugar tr.hmm, score: 395.39) [Arabidopsis thaliana]
                  233152
Seq. No.
                  LIB3272-009-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2499946
BLAST score
                   460
E value
                   5.0e-46
Match length
                  119
                   74
% identity
                  URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
NCBI Description
                   PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
```

tabacum]

DECARBOXYLASE >gi 747980 (U22260) UMP synthase [Nicotiana



```
Seq. No. 233153
Seq. ID LIB327
```

LIB3272-009-P1-K1-A5

Method BLASTX
NCBI GI g541943
BLAST score 163
E value 3.0e-11
Match length 57
% identity 53

NCBI Description metallothionein - soybean >gi 228682 prf 1808316A

metallothionein-like protein [Glycine max]

Seq. No. 233154

Seq. ID LIB3272-009-P1-K1-A7

Method BLASTX
NCBI GI g2347199
BLAST score 399
E value 7.0e-39
Match length 120
% identity 68

NCBI Description (AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No. 233155

Seq. ID LIB3272-009-P1-K1-A9

Method BLASTX
NCBI GI g2499710
BLAST score 606
E value 3.0e-63
Match length 129
% identity 89

NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)

(PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)

>gi\_1438075 (L33686) phospholipase D [Ricinus communis]

Seq. No. 233156

Seq. ID LIB3272-009-P1-K1-B1

Method BLASTX
NCBI GI g2440042
BLAST score 266
E value 2.0e-23
Match length 66
% identity 77

NCBI Description (AJ001292) major intrinsic protein PIPa2 [Craterostigma

plantagineum]

Seq. No. 233157

Seq. ID LIB3272-009-P1-K1-B11

Method BLASTX
NCBI GI g3123274
BLAST score 272
E value 5.0e-24
Match length 73
% identity 73

NCBI Description 60S RIBOSOMAL PROTEIN L32 (RP49) >gi\_1928968 (U92431)

ribosomal protein 49 [Drosophila melanogaster]

>gi\_2739301\_emb\_CAA74278\_ (Y13939) ribosomal protein 49

[Drosophila melanogaster]

Seq. ID Method

NCBI GI



```
233158
Seq. No.
                  LIB3272-009-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3924597
BLAST score
                  207
E value
                  2.0e-16
                  113
Match length
                  37
% identity
                 (AF069442) putative oxidoreductase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  233159
                  LIB3272-009-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3413473
BLAST score
                  281
                  4.0e-25
E value
Match length
                  116
                  50
% identity
                  (AJ006308) tyrosine phosphatase 1 [Glycine max]
NCBI Description
Seq. No.
                  233160
Seq. ID
                  LIB3272-009-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g4512653
BLAST score
                  163
E value
                  2.0e-22
                  88
Match length
                  70
% identity
NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]
                  233161
Seq. No.
                  LIB3272-009-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                  471
E value
                  2.0e-47
Match length
                  106
% identity
                  87
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                  233162
Seq. No.
Seq. ID
                  LIB3272-009-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  q134792
BLAST score
                  226
E value
                  1.0e-18
Match length
                  89
% identity
                  52
NCBI Description
                  MICROSOMAL SIGNAL PEPTIDASE 21 KD SUBUNIT (SPC21)
                  >gi_89064_pir__A34229 signal peptidase (EC 3.4.99.-) 21K
                  chain - dog >gi_164084 (J05069) signal peptidase 21 kDa
                  subunit [Canis familiaris]
Seq. No.
                  233163
```

33630

LIB3272-009-P1-K1-C10

BLASTX

g445613

E value

Match length

% identity

3.0e-25

97

55

```
BLAST score
                    461
                    3.0e-46
.... E value
                    120
 Match length
                    76
  % identity
 NCBI Description ribosomal protein L7 [Solanum tuberosum] .
                    233164
 Seq. No.
                    LIB3272-009-P1-K1-C11
 Seq. ID
                    BLASTX
 Method
                    g4468979
 NCBI GI
                    304
 BLAST score
                    7.0e-28
 E value
 Match length
                    68
  % identity
                    84
 NCBI Description
                   (AL035605) putative protein [Arabidopsis thaliana]
 Seq. No.
                    233165
                    LIB3272-009-P1-K1-C2
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2791834
 BLAST score
                    411
 E value
                    1.0e-46
                    109
 Match length
  % identity
                    82
                   (AF041463) elongation factor 1-alpha [Manihot esculenta]
 NCBI Description
 Seq. No.
                    233166
                    LIB3272-009-P1-K1-C6
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1304227
 BLAST score
                    532
 E value
                    2.0e-54
 Match length
                    133
                    73
  % identity
                    (D63781) Epoxide hydrolase [Glycine max]
  NCBI Description
                    >gi_2764804_emb_CAA55293_ (X78547) epoxide hydrolase
                     [Glycine max]
  Seq. No.
                    233167
                    LIB3272-009-P1-K1-C7
  Seq. ID
 Method
                    BLASTX
  NCBI GI
                    q67529
                    223
  BLAST score
                     3.0e-18
  E value
 Match length
                    124
  % identity
 NCBI Description
                    membrane alanyl aminopeptidase (EC 3.4.11.2) - Escherichia
                    coli
                    233168
  Seq. No.
  Seq. ID
                    LIB3272-009-P1-K1-C8
 Method
                    BLASTX
  NCBI GI
                    q529353
  BLAST score
                    283
```





```
NCBI Description (U12757) diphenol oxidase [Acer pseudoplatanus]
Seq. No.
                  233169
Seq. ID
                  LIB3272-009-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q3063396
BLAST score
                  533
E value
                  1.0e-54
Match length
                  118
                  85
% identity
NCBI Description (AB012947) vcCyP [Vicia faba]
Seq. No.
                  233170
Seq. ID
                  LIB3272-009-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g543905
BLAST score
                  694
E value
                  2.0e-73
Match length
                  133
                  95
% identity
NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162)
                  brassinosteroid-regulated protein [Glycine max]
Seq. No.
                  233171
                  LIB3272-009-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1703446
BLAST score
                  410
E value
                  3.0e-40
Match length
                  122
% identity
                  69
NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
                  >gi_1076292_pir__S53127 asparaginase - Arabidopsis thaliana
                  >gi_735918 emb CAA84367 (Z34884) asparaginase [Arabidopsis
                  thaliana]
Seq. No.
                  233172
Seq. ID
                  LIB3272-009-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g484656
BLAST score
                  488
E value
                  2.0e-49
Match length
                  131
% identity
NCBI Description
                  monodehydroascorbate reductase (NADH) (EC 1.6.5.4) -
                  cucumber >gi 452165 dbj BAA05408 (D26392)
                  monodehydroascorbate reductase [Cucumis sativus]
Seq. No.
                  233173
Seq. ID
                  LIB3272-009-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g543905
BLAST score
                  515
E value
                  2.0e-52
Match length
                  106
% identity
                  88
```

NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi 347459 (L22162)



## brassinosteroid-regulated protein [Glycine max]

```
Seq. No.
                  233174
Seq. ID
                  LIB3272-009-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g3063396
BLAST score
                  516
E value
                  1.0e-52
Match length
                  116
% identity
                  84
NCBI Description (AB012947) vcCyP [Vicia faba]
Seq. No.
                  233175
Seq. ID
                  LIB3272-009-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g3184082
BLAST score
                  245
E value
                  8.0e-21
Match length
                  131
% identity
                  37
NCBI Description
                  (AL023781) N-terminal acetyltransferase 1
                  [Schizosaccharomyces pombe]
Seq. No.
                  233176
Seq. ID
                  LIB3272-009-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  q1076414
BLAST score
                  366
E value
                  5.0e-35
Match length
                  129
                  57
% identity
                  subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis
NCBI Description
                  thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974)
                  subtilisin-like protease [Arabidopsis thaliana]
Seq. No.
                  233177
Seq. ID
                  LIB3272-009-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g549063
BLAST score
                  388
E value
                  1.0e-37
Match length
                  117
% identity
                  66
NCBI Description
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                  >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
                  factor homolog - rice >gi 303835 dbj BAA02151 (D12626)
                  21kd polypeptide [Oryza sativa]
Seq. No.
                  233178
                  LIB3272-009-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2564237
BLAST score
                  558
                  2.0e-57
E value
Match length
                  103
% identity
                  100
```

NCBI Description (Y10112) omega-6 desaturase [Gossypium hirsutum]

NCBI Description

233184

Seq. No.



```
233179
Seq. No.
                  LIB3272-009-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2160166
                  460
BLAST score
                  5.0e-46
E value
                  133
Match length
                   64
% identity
                  (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  233180
                  LIB3272-009-P1-K1-E12
Seq. ID
Method
                  BLASTX
                  g2500399
NCBI GI
BLAST score
                  503
E value
                  4.0e-51
Match length
                  114
                  91
% identity
                  40S RIBOSOMAL PROTEIN S3 >gi 1836060 bbs 179561 (S83098)
NCBI Description
                  ribosomal protein S3 [Ambystoma mexicanum=Mexican axolotls,
                  embryos, Peptide, 253 aa] [Ambystoma mexicanum]
Seq. No.
                  233181
                  LIB3272-009-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1657621
BLAST score
                   395
                  2.0e-38
E value
                  117
Match length
                   67
% identity
NCBI Description
                  (U72505) G6p [Arabidopsis thaliana] >gi 3068711 (AF049236)
                  putative acyl-coA dehydrogenase [Arabidopsis thaliana]
                  233182
Seq. No.
Seq. ID
                  LIB3272-009-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g2146774
                  342
BLAST score
E value
                  1.0e-45
Match length
                  115
% identity
NCBI Description
                  serine acetyltransferase (EC 2.3.1.30) Sat-52 - Arabidopsis
                   thaliana >gi_905391 (U30298) serine acetyltransferase
                   [Arabidopsis thaliana]
Seq. No.
                  233183
Seq. ID
                  LIB3272-009-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  q1332579
BLAST score
                  550
E value
                  1.0e-56
Match length
                  112
% identity
```

(X98063) polyubiquitin [Pinus sylvestris]



Seq. ID LIB3272-009-P1-K1-E9

Method BLASTX
NCBI GI g2739044
BLAST score 575
E value 2.0e-59
Match length 134
% identity 80

NCBI Description (AF024651) polyphosphoinositide binding protein Sshlp

[Glycine max]

Seq. No. 233185

Seq. ID LIB3272-009-P1-K1-F10

Method BLASTX
NCBI GI g2739279
BLAST score 341
E value 4.0e-32
Match length 118
% identity 59

NCBI Description (AJ223177) short chain alcohol dehydrogenase [Nicotiana

tabacum] >gi 2791348 emb CAA11154 (AJ223178) short chain

alcohol dehydrogenase [Nicotiana tabacum]

Seq. No. 233186

Seq. ID LIB3272-009-P1-K1-F5

Method BLASTX
NCBI GI g3046695
BLAST score 196
E value 4.0e-15
Match length 60
% identity 62

NCBI Description (AL022224) putative protein [Arabidopsis thaliana]

Seq. No. 233187

Seq. ID LIB3272-009-P1-K1-F7

Method BLASTX
NCBI GI g131385
BLAST score 555
E value 3.0e-57
Match length 134
% identity 84

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN)

Seq. No. 233188

Seq. ID LIB3272-009-P1-K1-F8

Method BLASTX
NCBI GI g1173218
BLAST score 489
E value 2.0e-49
Match length 110
% identity 89

NCBI Description 40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal

protein S15 [Arabidopsis thaliana] >gi\_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No. 233189

```
Seq. ID
                  LIB3272-009-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g82734
BLAST score
                  617
                  2.0e-64
E value
Match length
                  124
                  30
% identity
                  ubiquitin precursor - maize (fragment)
NCBI Description
                  >gi_226763_prf__1604470A poly-ubiquitin [Zea mays]
Seq. No.
                  233190
Seq. ID
                  LIB3272-009-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g3986695
BLAST score
                  570
                  5.0e-59
E value
Match length
                  122
                  93
% identity
                  (AF101423) ribosomal protein L12 [Cichorium intybus]
NCBI Description
                  233191
Seq. No.
                  LIB3272-009-P1-K1-G12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2160166
BLAST score
                  328
                  1.0e-30
E value
Match length
                  130
                  57
% identity
NCBI Description
                  (AC000132) No definition line found [Arabidopsis thaliana]
                  233192
Seq. No.
                  LIB3272-009-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4193388
BLAST score
                  462
                  3.0e-46
E value
                  113
Match length
                  81
% identity
NCBI Description
                  (AF091455) translationally controlled tumor protein [Hevea
                  brasiliensis]
                  233193
Seq. No.
                  LIB3272-009-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2911039
                  397
BLAST score
                  1.0e-38
E value
Match length
                  115
% identity
                   65
NCBI Description
                  (AL021961) cinnamyl alcohol dehydrogenase - like protein
                   [Arabidopsis thaliana]
```

Seq. No. 233194

Seq. ID LIB3272-009-P1-K1-G9

Method BLASTX NCBI GI g4539417 BLAST score 288

Match length

% identity

104



```
E value
                  7.0e-26
Match length
                  69
                  75
% identity
NCBI Description (AL049171) putative protein [Arabidopsis thaliana]
                  233195
Seq. No.
Seq. ID
                  LIB3272-009-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g3928760
BLAST score
                  306
E value
                  5.0e-28
Match length
                  124
                  54
% identity
NCBI Description (AB011797) homolog to plastid-lipid-associated protein
                  [Citrus unshiu]
                  233196
Seq. No.
Seq. ID
                  LIB3272-009-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g2944417
BLAST score
                  197
E value
                  1.0e-22
Match length
                  112
                  56 ′
% identity
NCBI Description (AF049881) peroxidase FLXPER4 [Linum usitatissimum]
                  233197
Seq. No.
Seq. ID
                  LIB3272-009-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g2440042
BLAST score
                  176
E value
                  2.0e-13
Match length
                  37
                  89
% identity
NCBI Description (AJ001292) major intrinsic protein PIPa2 [Craterostigma
                  plantagineum]
Seq. No.
                  233198
                  LIB3272-009-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131773
BLAST score
                  571
E value
                  5.0e-59
Match length
                  134
                  87
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
                  >gi 82724 pir B30097 ribosomal protein S14 (clone MCH2) -
                  maize
Seq. No.
                  233199
Seq. ID
                  LIB3272-009-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g3702368
BLAST score
                  403
E value
                  2.0e-39
```

Seq. No.

Seq. ID

233205

LIB3272-010-P1-K1-A6



```
(AJ001855) alpha subunit of F-actin capping protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  233200
                  LIB3272-009-P1-K1-H9
Seq. ID
Method
                  BLASTX
                  q4510413
NCBI GI
BLAST score
                  143
E value
                  7.0e-09
                  113
Match length
                  36
% identity
                 (AC006929) putative chloroplast nucleoid DNA binding
NCBI Description
                  protein [Arabidopsis thaliana]
                  233201
Seq. No.
                  LIB3272-010-P1-K1-A10
Seq. ID
Method
                  BLASTX
                  q4191788
NCBI GI
BLAST score
                  462
E value
                  3.0e-46
                  129
Match length
                  66
% identity
NCBI Description (AC005917) putative 1-aminocyclopropane-1-carboxylate
                  oxidase [Arabidopsis thaliana]
                  233202
Seq. No.
                  LIB3272-010-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3617770
BLAST score
                  422
E value
                  8.0e-42
Match length
                  98
% identity
                  81
NCBI Description (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]
Seq. No.
                  233203
                  LIB3272-010-P1-K1-A3
Seq. ID
                  BLASTX
Method
                  q2970051
NCBI GI
BLAST score
                  372
E value
                  9.0e-36
Match length
                  95
                  73
% identity
NCBI Description (AB012110) ARG10 [Vigna radiata]
Seq. No.
                  233204
Seq. ID
                  LIB3272-010-P1-K1-A5
                  BLASTX
Method
NCBI GI
                  q285741
BLAST score
                  338
E value
                  9.0e-32
                  109
Match length
                   59
% identity
NCBI Description (D14550) EDGP precursor [Daucus carota]
```

Match length

% identity

116

69



```
Method
                  \mathtt{BLASTX}
NCBI GI
                  g3158476
BLAST score
                  413
E value
                  1.0e-40
                  97
Match length
% identity
                  81
NCBI Description (AF067185) aquaporin 2 [Samanea saman]
Seq. No.
                  233206
Seq. ID
                  LIB3272-010-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q4102582
BLAST score
                  248
E value
                  3.0e-21
                  115
Match length
% identity
                  26
NCBI Description (AF013115) CAO [Arabidopsis thaliana]
Seq. No.
                  233207
Seq. ID
                  LIB3272-010-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  q2462929
BLAST score
                  441
E value
                  7.0e-44
Match length
                  121
% identity
                  67
NCBI Description (Y12295) glutathione transferase [Arabidopsis thaliana]
Seq. No.
                  233208
Seq. ID
                  LIB3272-010-P1-K1-B12
                  BLASTX
Method
NCBI GI
                  g1351014
BLAST score
                  459
E value
                  7.0e-46
Match length
                  112
% identity
                  83
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj BAA07207 (D38010)
                  ribosomal protein S8 [Oryza sativa]
Seq. No.
                  233209
Seq. ID
                  LIB3272-010-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g1619300
BLAST score
                  275
                  3.0e-24
E value
Match length
                  63
                  79
% identity
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]
                  233210
Seq. No.
Seq. ID
                  LIB3272-010-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q3320379
BLAST score
                  314
E value
                  3.0e-31
```



```
NCBI Description (AF014375) putative JUN kinase activation domain binding
                   protein [Medicago sativa]
 Seq. No.
                   233211
Seq. ID
                   LIB3272-010-P1-K1-B4
 Method
                   BLASTX
                   g3157936
 NCBI GI
 BLAST score
                   193
 E value
                   9.0e-15
                  91
Match length
                   45
 % identity
 NCBI Description (AC002131) Contains similarity to NFATc3 gb U28807 from Mus
                  musculus. [Arabidopsis thaliana]
 Seq. No.
                  233212
 Seq. ID
                  LIB3272-010-P1-K1-B5
 Method
                  BLASTX
NCBI GI
                  g1351014
BLAST score
                  489
E value
                   2.0e-49
Match length
                  130
                   76
 % identity
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi 968902_dbj_BAA07207 (D38010)
                  ribosomal protein S8 [Oryza sativa]
 Seq. No.
                  233213
 Seq. ID
                  LIB3272-010-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g4469003
BLAST score
                  248
E value
                   3.0e-21
Match length
                  86
 % identity
                   51
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
 Seq. No.
                   233214
 Seq. ID
                  LIB3272-010-P1-K1-B8
Method
                  BLASTX
                  q1666234
NCBI GI
BLAST score
                  296
E value
                   5.0e-27
Match length
                  56
 % identity
                  100
NCBI Description (U76193) actin [Pisum sativum] >gi_1724143 (U81049) actin
                  [Pisum sativum]
Seq. No.
                   233215
Seq. ID
                  LIB3272-010-P1-K1-B9
Method
                  BLASTX
```

NCBI GI g2160166 BLAST score 256 E value 3.0e-22 . Match length 118 % identity 54

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 233216



```
LIB3272-010-P1-K1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2119278
BLAST score
                  563
                   4.0e-58
E value
Match length
                  105
                  96
% identity
NCBI Description
                 tubulin beta-1 chain - rice
                  233217
Seq. No.
Seq. ID
                  LIB3272-010-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  q1170747
BLAST score
                  302
E value
                  1.0e-27
Match length
                  73
                  82
% identity
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
NCBI Description
                   (M88324) late embryogenesis-abundant protein [Gossypium
                  hirsutum] >gi_167347 (M37697) Lea5-A late
                  embryogenesis-abundant protein [Gossypium hirsutum]
Seq. No.
                  233218
Seq. ID
                  LIB3272-010-P1-K1-C4
Method
                  BLASTX
NCBI GI
                   q4490705
BLAST score
                  505
                  2.0e-51
E value
Match length
                  116
                   87
% identity
NCBI Description
                  (AL035680) ribosomal protein L14-like protein [Arabidopsis
                  thaliana]
Seq. No.
                   233219
Seq. ID
                  LIB3272-010-P1-K1-C5
Method
                  BLASTX
NCBI GI
                   q100490
BLAST score
                   625
E value
                   2.0e-65
Match length
                   128
% identity
                   28
                  polyubiquitin - garden snapdragon (fragment)
NCBI Description
                   >gi 16071 emb CAA48140 (X67957) ubiquitin [Antirrhinum
                  majus]
Seq. No.
                   233220
                  LIB3272-010-P1-K1-C6
Seq. ID
                  {\tt BLASTX}
Method
NCBI GI
                   g4538967
BLAST score
                   548
E value
                   2.0e-56
Match length
                  131
% identity
                  (AL049488) major intrinsic protein (MIP)-like [Arabidopsis
NCBI Description
```

Seq. No. 233221

thaliana]



Seq. ID LIB3272-010-P1-K1-C7 Method BLASTX NCBI GI q2129758 BLAST score 316 E value 2.0e-29 Match length 75

NCBI Description ubiquitin conjugating enzyme E2 protein - Arabidopsis thaliana >gi 992704 (U33757) UBC7 [Arabidopsis thaliana]

Seq. No. 233222

% identity

Seq. ID LIB3272-010-P1-K1-D1

79

Method BLASTX NCBI GI q4490321 BLAST score 431 E value 1.0e-42 Match length 132 % identity 64

NCBI Description (AJ011604) nitrate transporter [Arabidopsis thaliana]

233223 Seq. No.

Seq. ID LIB3272-010-P1-K1-D10

Method BLASTX NCBI GI q2792297 BLAST score 261 E value 9.0e-23 Match length 77 58 % identity

NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa]

Seq. No. 233224

Seq. ID LIB3272-010-P1-K1-D11

Method BLASTX NCBI GI g2497953 BLAST score 293 E value 1.0e-26 Match length 95

% identity 65

NCBI Description MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM

> COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi 1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] >gi\_4469123 emb CAB38312 (AJ236870) molybdenum

cofactor biosynthesis enzyme [Arabidopsis thaliana]

Seq. No. 233225

Seq. ID LIB3272-010-P1-K1-D2

Method BLASTX NCBI GI q4033467 BLAST score 416 E value 6.0e-41Match length 130 51 % identity

ARGININE/SERINE-RICH SPLICING FACTOR RSP31 NCBI Description

>gi\_1707366\_emb\_CAA67798\_ (X99435) splicing factor

[Arabidopsis thaliana]

Seq. No. 233226

E value

Match length

2.0e-12

38



```
Seq. ID
                  LIB3272-010-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g4454097
BLAST score
                  158
E value
                  9.0e-11
Match length
                  51
% identity
                  63
NCBI Description (X85206) hybrid proline-rich protein [Catharanthus roseus]
Seq. No.
                  233227
Seq. ID
                  LIB3272-010-P1-K1-D5
                  BLASTX
Method
NCBI GI
                  q2662343
BLAST score
                  577
E value
                  8.0e-60
Match length
                  110
% identity
                  100
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                  233228
Seq. ID
                  LIB3272-010-P1-K1-D7
Method
                  BLASTX
                  g3559805
NCBI GI
BLAST score
                  515
E value
                  1.0e-52
Match length
                  119
                  76
% identity
NCBI Description (AJ006787) putative phytochelatin synthetase [Arabidopsis
                  thaliana]
Seq. No.
                  233229
Seq. ID
                  LIB3272-010-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g693933
BLAST score
                  180
E value
                  6.0e-28
                  123
Match length
                  50
% identity
NCBI Description (X84907) carbonate dehydratase [Homo sapiens]
Seq. No.
                  233230
Seq. ID
                  LIB3272-010-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g3928150
BLAST score
                  559
E value
                  9.0e-58
Match length
                  128
% identity
                  87
NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]
Seq. No.
                  233231
Seq. ID
                  LIB3272-010-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  q4455223
BLAST score
                  173
```

% identity

81



```
% identity
NCBI Description
                  (AL035440) putative DNA binding protein [Arabidopsis
                  thaliana]
                   233232
Seq. No.
Seq. ID
                  LIB3272-010-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g4193388
BLAST score
                  298
E value
                   3.0e-27
                  70
Match length
% identity
                  81
NCBI Description
                  (AF091455) translationally controlled tumor protein [Hevea
                  brasiliensis]
Seq. No.
                  233233
Seq. ID
                  LIB3272-010-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g3641868
BLAST score
                  197
E value
                  3.0e-15
Match length
                  50
                  76
% identity
NCBI Description (AJ011012) hypothetical protein [Cicer arietinum]
Seq. No.
                  233234
Seq. ID
                  LIB3272-010-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g4218121
BLAST score
                  167
E value
                  1.0e-11
Match length
                  39
% identity
                  74
NCBI Description (AL035353) putative protein [Arabidopsis thaliana]
Seq. No.
                  233235
Seq. ID.
                  LIB3272-010-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g730449
BLAST score
                  484
E value
                  7.0e-49
Match length
                  113
% identity
                  78
NCBI Description
                  60S RIBOSOMAL PROTEIN L13-1 (COLD INDUCED PROTEIN C24A)
                  >gi_480647_pir__S37132 ribosomal protein L13.A - rape
                  >gi 398918_emb_CAA80341_ (Z22618) cold induced protein
                  (BnC24A) [Brassica napus]
Seq. No.
                  233236
Seq. ID
                  LIB3272-010-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g1172977
BLAST score
                  427
E value
                  3.0e-42
Match length
                  100
```

NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi\_606970 (U15741) cytoplasmic

E value

Match length

1.0e-27

73





## ribosomal protein L18 [Arabidopsis thaliana]

```
Seq. No.
                   233237
Seq. ID
                  LIB3272-010-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g2129630
BLAST score
                  208
E value
                   2.0e-16
Match length
                  76
% identity
                   46
NCBI Description lamin - Arabidopsis thaliana >gi 1262754 emb CAA65750
                   (X97023) lamin [Arabidopsis thaliana] >gi 3395760 (U77721)
                  unknown [Arabidopsis thaliana]
Seq. No.
                   233238
Seq. ID
                  LIB3272-010-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g3360289
BLAST score
                  238
E value
                   5.0e-20
                  74
Match length
% identity
                   58
NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase
                   1 [Zea mays]
Seq. No.
                  233239
Seq. ID
                  LIB3272-010-P1-K1-F5
Method
                  BLASTX
NCBI GI
                   g729470
BLAST score
                  234
E value
                   7.0e-20
                  70
Match length
% identity
                   66
NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
                   (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
                  >gi 542089 pir JQ2272 formate dehydrogenase (EC 1.2.1.2)
                  precursor, mitochondrial - potato >gi 297798 emb CAA79702
                   (Z21493) mitochondrial formate dehydrogenase precursor
                   [Solanum tuberosum]
Seq. No.
                  233240
Seq. ID
                  LIB3272-010-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g1694621
BLAST score
                  366
E value
                   5.0e-35
                  109
Match length
% identity
                   69
NCBI Description (D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]
Seq. No.
                  233241
Seq. ID
                  LIB3272-010-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g1170747
BLAST score
                  302
```



```
% identity
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
NCBI Description
                   (M88324) late embryogenesis-abundant protein [Gossypium
                  hirsutum] >gi 167347 (M37697) Lea5-A late
                  embryogenesis-abundant protein [Gossypium hirsutum]
Seq. No.
                  233242
                  LIB3272-010-P1-K1-F8
Seq. ID
Method
                  BLASTX
                  g3868758
NCBI GI
BLAST score
                  230
E value
                  4.0e-19
Match length
                  100
                  63
% identity
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
                  233243
Seq. No.
                  LIB3272-010-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3668089
BLAST score
                  212
E value
                  5.0e-17
Match length
                  78
                  47
% identity
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.
                  233244
                  LIB3272-010-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1107526
BLAST score
                  511
E value
                  5.0e-52
Match length
                  128
                  75
% identity
NCBI Description (X87931) SIEP1L protein [Beta vulgaris]
Seq. No.
                  233245
                  LIB3272-010-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q431144
BLAST score
                  201
E value
                  9.0e-16
Match length
                  116
% identity
                  47
NCBI Description (D21824) HSP70 [Lilium longiflorum]
Seq. No.
                  233246
Seq. ID
                  LIB3272-010-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q462195
```

Method BLASTX
NCBI GI g462195
BLAST score 385
E value 3.0e-37
Match length 81
% identity 91

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)

>gi\_100682\_pir\_\_S21636 GOS2 protein - rice

>gi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]



>qi 3789950 (AF094774) translation initiation factor [Oryza sativa]

233247 Seq. No.

LIB3272-010-P1-K1-G8 Seq. ID

87

Method BLASTX NCBI GI g133940 BLAST score 451 E value 6.0e-45Match length 109

% identity 40S RIBOSOMAL PROTEIN S3A (S1A) >qi 70851 pir R3XL3A NCBI Description

ribosomal protein S3a - African clawed frog

>gi\_65091\_emb\_CAA40592\_ (X57322) ribosomal protein S1a
[Xenopus laevis]

Seq. No. 233248

LIB3272-010-P1-K1-H10 Seq. ID

Method BLASTX NCBI GI g549620 BLAST score 169 E value 6.0e-12 Match length 101 % identity 39

NCBI Description HYPOTHETICAL 46.5 KD PROTEIN IN MRS4-DYN1 INTERGENIC REGION

>gi\_539263\_pir\_\_S38127 hypothetical protein YKR053c - yeast

(Saccharomyces cerevisiae) >gi 486509 emb CAA82131 (Z28278) ORF YKR053c [Saccharomyces cerevisiae]

Seq. No. 233249

Seq. ID LIB3272-010-P1-K1-H4

Method BLASTX NCBI GI g2129583 BLAST score 316 E value 3.0e-29 83 Match length 77 % identity

NCBI Description ferritin - Arabidopsis thaliana >qi 1246401 emb CAA63932

(X94248) ferritin [Arabidopsis thaliana].

Seq. No. 233250

LIB3272-010-P1-K1-H5 Seq. ID

 ${\tt BLASTX}$ Method NCBI GI g3868758 BLAST score 430 E value 1.0e-42 105 Match length 75 % identity

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 233251

Seq. ID LIB3272-010-P1-K1-H8

Method BLASTX NCBI GI g508304 BLAST score 212 E value 5.0e-17 Match length 51.



% identity NCBI Description (L22305) corC [Medicago sativa] 233252 Seq. No. Seq. ID LIB3272-011-P1-K1-A12 Method BLASTX NCBI GI g2662343 BLAST score 606 E value 4.0e-63 Match length 116 100 % identity NCBI Description (D63581) EF-1 alpha [Oryza sativa] 233253 Seq. No. Seq. ID LIB3272-011-P1-K1-A3 BLASTX Method NCBI GI g2662343 BLAST score 653 E value 1.0e-68 Match length 125 100 % identity NCBI Description (D63581) EF-1 alpha [Oryza sativa] Seq. No. 233254 Seq. ID LIB3272-011-P1-K1-A5 BLASTX Method NCBI GI g1279588 BLAST score 405 E value 1.0e-39 Match length 114 % identity 68 NCBI Description (Z71749) glutathione S-transferase [Nicotiana plumbaginifolia] Seq. No. 233255 Seq. ID LIB3272-011-P1-K1-A6 BLASTX Method NCBI GI g1263291 BLAST score 565 E value 2.0e-58 117 Match length % identity 88 NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum] 233256 Seq. No. Seq. ID LIB3272-011-P1-K1-A8 Method BLASTX g120669

NCBI GI BLAST score 229 E value 3.0e-19 Match length 54 % identity

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate

dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi 19566 emb CAA42905 (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

```
233257
Seq. No.
Seq. ID
                  LIB3272-011-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g1170747
BLAST score
                  338
E value
                  1.0e-31
Match length
                  79
% identity
                  84
NCBI Description
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
                   (M88324) late embryogenesis-abundant protein [Gossypium
                  hirsutum] >gi_167347 (M37697) Lea5-A late
                  embryogenesis-abundant protein [Gossypium hirsutum]
Seq. No.
                  233258
Seq. ID
                  LIB3272-011-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g3033391
BLAST score
                  538
E value
                  3.0e-55
Match length
                  132
% identity
                  78
NCBI Description (AC004238) putative amino acid transporter [Arabidopsis
                  thaliana]
                  233259
Seq. No.
                  LIB3272-011-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3953463
BLAST score
                  254
E value
                  7.0e-22
Match length
                  93
% identity
                  52
NCBI Description (AC002328) F20N2.8 [Arabidopsis thaliana]
Seq. No.
                  233260
Seq. ID
                  LIB3272-011-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q3914605
BLAST score
                  348
```

E value 7.0e-33 Match length 117 % identity 61

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE PRECURSOR (RUBISCO ACTIVASE) >gi\_541930\_pir\_\_S39551 ribulose-1,5-bisphosphate carboxylase/oxygenase activase -

apple tree >gi\_415852 emb CAA79857 (Z21794)

ribulose-1,5-bisphosphate carboxylase/oxygenase activase

[Malus domestica]

Seq. No. 233261

Seq. ID LIB3272-011-P1-K1-B8

Method BLASTX NCBI GI g1632822 BLAST score 184 E value 6.0e-14 Match length 69

% identity NCBI Description (Y08962) transmembrane protein [Oryza sativa] >gi 1667594 (U77297) transmembrane protein [Oryza sativa] Seq. No. 233262 Seq. ID LIB3272-011-P1-K1-B9 Method BLASTX NCBI GI g2160166 BLAST score 328 E value 1.0e-30 Match length 130 % identity 57 NCBI Description (AC000132) No definition line found [Arabidopsis thaliana] Seq. No. 233263 Seq. ID LIB3272-011-P1-K1-C1 Method BLASTX NCBI GI g1928981 BLAST score 261 E value 3.0e-2355 Match length % identity 93 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica oleracea var. botrytis] Seq. No. 233264 Seq. ID LIB3272-011-P1-K1-C11 Method BLASTX NCBI GI g2642154 BLAST score 204 E value 5.0e-16Match length 124 % identity 44 (AC003000) unknown protein [Arabidopsis thaliana] NCBI Description >gi 3790595 (AF079186) RING-H2 finger protein RHC2a [Arabidopsis thaliana] Seq. No. 233265

Seq. ID LIB3272-011-P1-K1-C12

Method BLASTX NCBI GI g3094012 BLAST score 367 E value 4.0e-35 Match length 75 % identity 87

NCBI Description (AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]

Seq. No. 233266

Seq. ID LIB3272-011-P1-K1-C3

Method BLASTX NCBI GI g4185819 BLAST score 192 E value 1.0e-14 Match length 47 % identity

NCBI Description (AF116845) metallothionein-like type 1 protein [Ipomoea

batatas]

```
Seq. No.
                    233267
 Seq. ID
                    LIB3272-011-P1-K1-C4
                    BLASTX
 Method
                    g3790569
 NCBI GI
 BLAST score
                    171
                    4.0e-12
 E value
 Match length
                    51
 % identity
 NCBI Description
                   (AF078822) RING-H2 finger protein RHA2a [Arabidopsis
                    thaliana]
                    233268
 Seq. No.
 Seq. ID
                    LIB3272-011-P1-K1-C6
 Method
                    BLASTX
 NCBI GI
                    g2961372
 BLAST score
                    647
 E value
                    6.0e-68
 Match length
                    126
 % identity
                    94
 NCBI Description
                   (AL022141) putative ribosomal protein L8 [Arabidopsis
                    thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal
                    protein L2 [Arabidopsis thaliana]
 Seq. No.
                    233269
 Seq. ID
                    LIB3272-011-P1-K1-D1
 Method
                    BLASTX
 NCBI GI
                    g2583134
 BLAST score
                    198
 E value
                    2.0e-15
 Match length
                    62
 % identity
 NCBI Description (AC002387) putative proline-rich protein [Arabidopsis
                    thalianal
                    233270
 Seq. No.
 Seq. ID
                    LIB3272-011-P1-K1-D11
Method
                    BLASTX
 NCBI GI
                    q3643609
 BLAST score
                    434
 E value
                    5.0e-43
 Match length
                    134
                    65
 % identity
 NCBI Description
                  (AC005395) putative Cys3His zinc finger protein
                    [Arabidopsis thaliana]
 Seq. No.
                    233271
 Seq. ID
                    LIB3272-011-P1-K1-D12
 Method
                    BLASTX
 NCBI GI
                    g4426565
```

Method BLASTX
NCBI GI 94426565
BLAST score 165
E value 2.0e-11
Match length 87
% identity 40

NCBI Description (AF031483) unknown [Rattus norvegicus]

Seq. No. 233272



```
LIB3272-011-P1-K1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1743354
BLAST score
                   416
E value
                   7.0e-41
Match length
                   96
% identity
                   79
NCBI Description (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
                   233273
Seq. No.
Seq. ID
                   LIB3272-011-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   q2499945
BLAST score
                   416
E value
                   7.0e-41
Match length
                   131
% identity
                   64
                   URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
NCBI Description
                   PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                   DECARBOXYLASE >gi_1076363_pir__S46440 orotate
phosphoribosyltransferase (EC 2.4.2.10) /
                   orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) -
                   Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842)
                   pyrE-F [Arabidopsis thaliana]
Seq. No.
                   233274
                   LIB3272-011-P1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1076510
BLAST score
                   555
E value
                   3.0e-57
Match length
                   122
% identity
                   84
                   peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean
NCBI Description
                   >gi 829119 emb CAA52414 (X74403) cyclophilin [Phaseolus
                   vulgaris]
                   233275
Seq. No.
Seq. ID
                   LIB3272-011-P1-K1-E10
                   BLASTX
Method
NCBI GI
                   g3158376
BLAST score
                   431
E value
                   1.0e-42
                   118
Match length
                   75
% identity
NCBI Description (AF035385) unknown [Arabidopsis thaliana]
                   233276
Seq. No.
Seq. ID
                   LIB3272-011-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   g401322
BLAST score
                   273
```

4.0e-24 E value 67 Match length % identity 82

NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi 167313 (L03186) vacuolar H+-ATPase catalytic



#### subunit [Gossypium hirsutum]

```
Seq. No.
                  233277
                  LIB3272-011-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455171
                  527
BLAST score
E value
                  6.0e-54
Match length
                  131
% identity
                  74
NCBI Description (AL035521) hypothetical protein [Arabidopsis thaliana]
                  233278
Seq. No.
Seq. ID
                  LIB3272-011-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  q2662343
BLAST score
                  534
E value
                  8.0e-55
Match length
                  104
% identity
                   99
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                   233279
                 LIB3272-011-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2811025
BLAST score
                  233
E value
                   2.0e-19
                   77
Match length
% identity
                   61
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607_
                   (AB002695) aspartic endopeptidase [Cucurbita pepo]
Seq. No.
                   233280
Seq. ID
                  LIB3272-011-P1-K1-E9
Method
                  BLASTX
NCBI GI
                   q3063396
BLAST score
                  363
E value
                   6.0e-35
                  76
Match length
                  88
% identity
NCBI Description (AB012947) vcCyP [Vicia faba]
                   233281
Seq. No.
Seq. ID
                  LIB3272-011-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g3522943
BLAST score
                  415
                   9.0e-41
E value
Match length
                  135
% identity
                   31
NCBI Description (AC004411) putative p-glycoprotein [Arabidopsis thaliana]
                  233282
Seq. No.
Seq. ID
                  LIB3272-011-P1-K1-F10
Method
                  BLASTX
NCBI GI
                   g3094012
```



233283

BLAST score E value 3.0e-36 Match length 96 % identity 82

NCBI Description (AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]

Seq. No. Seq. ID

LIB3272-011-P1-K1-F12

Method BLASTX NCBI GI g1076621 BLAST score 560 E value 9.0e-58 Match length 119 % identity 85

NCBI Description cytochrome b5 - common tobacco >qi 296386 emb CAA50575

(X71441) cytochrome b5 [Nicotiana tabacum]

Seq. No.

233284 Seq. ID LIB3272-011-P1-K1-F3

Method BLASTX NCBI GI q464986 BLAST score 256 E value 2.0e-22 Match length 54 % identity

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN

LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi\_421857\_pir\_\_S32674 ubiquitin--protein ligase (EC
6.3.2.19) UBC9 - Arabidopsis thaliana

>gi\_297884\_emb\_CAA78714\_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi\_349211 (L00639)

ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi\_600391\_emb\_CAA51201\_ (X72626) ubiquitin conjugating

enzyme E2 [Arabidopsis Thaliana]

>gi\_4455355\_emb\_CAB36765.1\_ (AL035524) ubiquitin-protein

ligase UBC9 [Arabidopsis thaliana]

Seq. No. 233285

Seq. ID LIB3272-011-P1-K1-F5

Method BLASTX NCBI GI g1703446 BLAST score 386 E value 2.0e-37 Match length 122 % identity 65

NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)

>gi 1076292 pir\_\_S53127 asparaginase - Arabidopsis thaliana >gi 735918 emb CAA84367 (Z34884) asparaginase [Arabidopsis

thaliana]

Seq. No. 233286

Seq. ID LIB3272-011-P1-K1-F6

Method BLASTX NCBI GI g133940 BLAST score 140 E value 1.0e-08 Match length 39



```
% identity
NCBI Description
                    40S RIBOSOMAL PROTEIN S3A (S1A) >gi 70851 pir R3XL3A
                    ribosomal protein S3a - African clawed frog >gi_65091_emb_CAA40592_(X57322) ribosomal protein S1a
                    [Xenopus laevis]
Seq. No.
                    233287
Seq. ID
                    LIB3272-011-P1-K1-G1
Method
                    BLASTX
NCBI GI
                    g231587
BLAST score
                    331
E value
                    4.0e-31
Match length
                    80
% identity
                    85
NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
                    >gi_283001_pir__S25304 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor, mitochondrial - rice
                    >gi_218147_dbj_BAA01372_ (D10491) mitochondrial F1-ATPase
                    [Oryza sativa]
Seq. No.
                    233288
Seq. ID
                    LIB3272-011-P1-K1-G10
Method
                    BLASTX
NCBI GI
                    g3643609
BLAST score
                    434
E value
                    5.0e-43
Match length
                    133
% identity
                    65
NCBI Description (AC005395) putative Cys3His zinc finger protein
                    [Arabidopsis thaliana]
Seq. No.
                    233289
Seq. ID
                    LIB3272-011-P1-K1-G11
Method
                    BLASTX
NCBI GI
                    q3334261
BLAST score
                    141
E value
                    1.0e-08
Match length
                    48
% identity
                    56
NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi 1655851 (U61973)
                    metallothionein-like protein [Malus domestica]
Seq. No.
                    233290
Seq. ID
                    LIB3272-011-P1-K1-G12
Method
                    BLASTX
NCBI GI
                    q629597
```

BLAST score 362 E value 1.0e-34Match length 83 % identity 80

NCBI Description proline-rich protein - rape >gi 545029 bbs 142669 (S68113)

proline-rich SAC51 [Brassica napus=oilseed rape, pods,

Peptide, 147 aa] [Brassica napus]

Seq. No. 233291

Seq. ID LIB3272-011-P1-K1-G5

Method BLASTX



NCBI GI q122085 BLAST score 493 E value 6.0e-50 Match length 115 87 % identity

NCBI Description HISTONE H3 >gi 81641 pir S06250 histone H3 - Arabidopsis thaliana >gi 82482 pir S04099 histone H3 (variant H3R-21) - rice >gi\_1362194\_pir\_\_S57626 histone H3 - maize >gi\_20251\_emb\_CAA31969\_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi 20253 emb CAA31970 (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi\_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi 168495 (M13378) histone H3 [Zea mays] >qi 168497 (M13379) histone H3 [Zea mays] >qi 168506  $(M3\overline{5}388)$  histone H3 [Zea mays]  $>gi_169\overline{6}55$   $(M7\overline{7}493)$  histone H3 [Petroselinum crispum] >gi 169657 (M77494) histone H3 [Petroselinum crispum] >gi 169659 (M77495) histone H3 [Petroselinum crispum] >gi\_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi\_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi\_886738\_emb\_CAA59111\_ (X84377) histone 3 [Zea mays] >gi 1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi 1314779 (U54827) histone H3 homolog [Brassica napus] >gi 1531754 emb CAA57811 (X82414) Histone H3 [Asparagus officinalis] >gi 1667592 (U77296) histone 3 [Oryza sativa] >gi 3249101 (AC003114) Match to histone H3 gene gb M17131 and gb M35387 from A. thaliana. ESTs gb H76511 gb H76255, gb  $AA7\overline{1}2452$ , gb N65260 and gb T42306 come from this gene. [Arabidopsis thaliana] >gi\_225459\_prf 1303352A histone H3 [Helicoverpa zea] >gi 225839 prf 1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 233292 Seq. ID LIB3272-011-P1-K1-H1 Method BLASTX NCBI GI q120669 BLAST score 576 1.0e-59 E value

Match length 114 % identity 95

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi 66014 pir DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi 19566 emb CAA42905 (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 233293

Seq. ID LIB3272-011-P1-K1-H2

Method BLASTX NCBI GI g3759184 BLAST score 283 E value 3.0e-25Match length 135 % identity 50

NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

233294 Seq. No.

LIB3272-011-P1-K1-H3 Seq. ID

Method BLASTX



```
NCBI GI
                    g2347098
 BLAST score
                    340
 E value
                    6.0e-32
 Match length
                    69
                    90
  % identity
                    (U76845) ubiquitin-specific protease [Arabidopsis thaliana]
 NCBI Description
                    >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific
                    protease (AtUBP3) [Arabidopsis thaliana]
                    233295
 Seq. No.
  Seq. ID
                    LIB3272-011-P1-K1-H6
 Method
                    BLASTX
 NCBI GI
                    q3894178
  BLAST score
                    269
 E value
                    1.0e-23
 Match length
                    57
                    86
  % identity
                    (AC005312) putative nucleic acid binding protein
 NCBI Description
                    [Arabidopsis thaliana]
                    233296
  Seq. No.
  Seq. ID
                    LIB3272-011-P1-K1-H7
 Method
                    BLASTX
 NCBI GI
                    q1170748
  BLAST score
                    337
。 E value
                    1.0e-31
                    79
 Match length
                    84
  % identity
                   LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-D >gi_167349
  NCBI Description
                     (M88323) late embryogenesis-abundant protein [Gossypium
                    hirsutum] >gi 167351 (L01102) late embryogenesis-abundant
                    protein [Gossypium hirsutum]
  Seq. No.
                    233297
  Seq. ID
                    LIB3272-012-P1-K1-A10
  Method
                    BLASTX
  NCBI GI
                    q508304
  BLAST score
                    261
  E value
                    9.0e-23
  Match length
                    61
                    80
  % identity
  NCBI Description (L22305) corC [Medicago sativa]
                    233298
  Seq. No.
  Seq. ID
                    LIB3272-012-P1-K1-A11
  Method
                    BLASTX
  NCBI GI
                    g4510373
  BLAST score
                    291
  E value
                    3.0e-26
  Match length
                    109
                    56
  % identity
  NCBI Description (AC007017) putative harpin-induced protein [Arabidopsis
                    thaliana]
```

Seq. No. 233299

Seq. ID LIB3272-012-P1-K1-A12

Method BLASTX



```
g113621
NCBI GI
BLAST score
                     486
E value
                     4.0e-49
Match length
                    110
% identity
                    87
                    FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
NCBI Description
                    >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
                    4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850 emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A
                    cytoplasmic aldolase [Zea mays]
Seq. No.
                    233300
Seq. ID
                    LIB3272-012-P1-K1-A6
Method
                    BLASTX
NCBI GI
                    g1332579
BLAST score
                     456
E value
                     5.0e-56
Match length
                    120
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
Seq. No.
                    233301
                    LIB3272-012-P1-K1-B12
Seq. ID
Method
                    BLASTX
NCBI GI
                    q1732511
BLAST score
                    447
E value
                    1.0e-44
Match length
                    99
% identity
                     85
NCBI Description (U62742) Ran binding protein 1 homolog [Arabidopsis
                     thaliana]
                    233302
Seq. No.
Seq. ID
                    LIB3272-012-P1-K1-B2
Method
                    BLASTX
NCBI GI
                     q2895866
BLAST score
                     472
E value
                     2.0e-47
Match length
                    138
% identity
                     64
NCBI Description (AF045770) methylmalonate semi-aldehyde dehydrogenase
                     [Oryza sativa]
Seq. No.
                     233303
Seq. ID
                    LIB3272-012-P1-K1-C1
Method
                    BLASTX
NCBI GI
                     q1928981
BLAST score
                     583
E value
                     2.0e-60
                    122
Match length
```

% identity 63

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

233304 Seq. No.

LIB3272-012-P1-K1-C10 Seq. ID

NCBI GI

E value

BLAST score

g3290020

8.0e-53

518

```
Method
                  BLASTX
NCBI GI
                  g1769903
BLAST score
                  376
E value
                  3.0e-36
Match length
                  118
                  59
% identity
NCBI Description (X95738) proline transporter 2 [Arabidopsis thaliana]
Seq. No.
                  233305
Seq. ID
                  LIB3272-012-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  q1666234
BLAST score
                  276
E value
                  5.0e-32
Match length
                  87
% identity
                  79
NCBI Description (U76193) actin [Pisum sativum] >gi 1724143 (U81049) actin
                  [Pisum sativum]
Seq. No.
                  233306
Seq. ID
                  LIB3272-012-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g2388575
BLAST score
                  261
E value
                  1.0e-22
Match length
                  130
% identity
                  40
NCBI Description (AC000098) YUP8H12.18 [Arabidopsis thaliana]
Seq. No.
                  233307
Seq. ID
                  LIB3272-012-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g4335763
BLAST score
                  251
E value
                  2.0e-21
                  90
Match length
                  50
% identity
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]
Seq. No.
                  233308
Seq. ID
                  LIB3272-012-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g3941543
BLAST score
                  193
E value
                  1.0e-14
Match length
                  54
% identity
                  70
NCBI Description
                  (AF069497) pelota [Arabidopsis thaliana]
                  >gi_4469016_emb_CAB38277 (AL035602) pelota (PEL1)
                  [Arabidopsis thaliana]
Seq. No.
                  233309
Seq. ID
                  LIB3272-012-P1-K1-C7
Method
                  BLASTX
```



```
Match length
                  116
% identity
                  88
NCBI Description
                  (AF044172) cysteine synthase; CS-A; O-acetylserine (thiol)
                  lyase; cytosolic isoform [Solanum tuberosum]
                  233310
Seq. No.
Seq. ID
                  LIB3272-012-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q2244754
BLAST score
                  505
E value
                  2.0e-51
Match length
                  111
```

Seq. No. 233311 Seq. ID LIB3272-012-P1-K1-D11

Method BLASTX
NCBI GI g2980793
BLAST score 547
E value 3.0e-56
Match length 135
% identity 73

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 233312

Seq. ID LIB3272-012-P1-K1-D12

Method BLASTX
NCBI GI g3242783
BLAST score 352
E value 1.0e-36
Match length 120
% identity 72

NCBI Description (AF055354) respiratory burst oxidase protein B [Arabidopsis

thaliana]

Seq. No. 233313

Seq. ID LIB3272-012-P1-K1-D2

Method BLASTX
NCBI GI g2995949
BLAST score 382
E value 7.0e-37
Match length 79
% identity 67

NCBI Description (AF053563) ubiquitin [Mesembryanthemum crystallinum]

Seq. No. 233314

Seq. ID LIB3272-012-P1-K1-D3

Method BLASTX
NCBI GI g3834309
BLAST score 325
E value 3.0e-30
Match length 110
% identity 52

NCBI Description (AC005679) Strong similarity to glycoprotein EP1 gb\_L16983

Daucus carota and a member of S locus glycoprotein family



PF\_00954. ESTs gb\_F13813, gb\_T21052, gb\_R30218 and gb\_W43262 come from this gene. [Arabidopsis thaliana]

Seq. No. 233315 Seq. ID LIB3272-012-P1-K1-D6 BLASTX Method NCBI GI g4056494 BLAST score 255 E value 5.0e-22 Match length 130 50 % identity NCBI Description (AC005896) putative protein translocase [Arabidopsis thaliana] 233316 Seq. No. Seq. ID LIB3272-012-P1-K1-D7

Method BLASTX
NCBI GI g1483218
BLAST score 236

NCBI GI G148321 BLAST score 236 E value 9.0e-20 Match length 64 % identity 67

NCBI Description (X99793) induced upon wounding stress [Arabidopsis

thaliana]

Seq. No. 233317

Seq. ID LIB3272-012-P1-K1-D8

Method BLASTX
NCBI GI g2911060
BLAST score 291
E value 3.0e-26
Match length 113
% identity 38

NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

>gi\_3297826 emb CAA19884.1 (AL031032) putative protein

[Arabidopsis thaliana]

Seq. No. 233318

Seq. ID LIB3272-012-P1-K1-D9

Method BLASTX
NCBI GI g1706918
BLAST score 250
E value 2.0e-21
Match length 107
% identity 49

NCBI Description FLAVONOL SULFOTRANSFERASE-LIKE >gi\_498647 (U10277) sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No. 233319

Seq. ID LIB3272-012-P1-K1-E12

Method BLASTX
NCBI GI g3955021
BLAST score 591
E value 2.0e-61
Match length 129
% identity 88

NCBI Description (AJ010811) HB2 homeodomain protein [Populus tremula x

Match length

% identity

77



### Populus tremuloides]

```
Seq. No.
                  233320
Seq. ID
                  LIB3272-012-P1-K1-E2
Method
                  BLASTX
                  g1279206
NCBI GI
BLAST score
                  565
E value
                  2.0e-58
Match length
                  124
% identity
                  89
NCBI Description (X97446) alpha-tubulin [Avena sativa]
Seq. No.
                  233321
Seq. ID
                  LIB3272-012-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g399392
BLAST score
                  323
E value
                  6.0e-30
Match length
                  107
% identity
                   65
NCBI Description
                  DIHYDROLIPOAMIDE DEHYDROGENASE PRECURSOR (GLYCINE CLEAVAGE
                  SYSTEM L PROTEIN) >gi_100037_pir__S22384 dihydrolipoamide
                  dehydrogenase (EC 1.8.1.4) - garden pea
                   >gi_20806_emb_CAA45066_ (X63464) dihydrolipoamide
                  dehydrogenase [Pisum sativum]
Seq. No.
                  233322
Seq. ID
                  LIB3272-012-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g2267567
BLAST score
                  398
E value
                  9.0e-39
Match length
                  86
% identity
                  87
NCBI Description
                  (AF009003) glycine-rich RNA binding protein 1 [Pelargonium
                  x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding
                  protein 2 [Pelargonium x hortorum]
Seq. No.
                  233323
Seq. ID
                  LIB3272-012-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g3292817
BLAST score
                  249
E value
                   3.0e-21
Match length
                  80
% identity
NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana]
                  233324
Seq. No.
Seq. ID
                  LIB3272-012-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g2558655
BLAST score
                  157
E value
                   4.0e-18
```

33662

NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]

Match length

% identity

115

57



```
Seq. No.
                  233325
Seq. ID
                  LIB3272-012-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g1170747
BLAST score
                  331
E value
                  6.0e-31
Match length
                  78
% identity
                  83
NCBI Description
                 LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
                  (M88324) late embryogenesis-abundant protein [Gossypium
                  hirsutum] >gi_167347 (M37697) Lea5-A late
                  embryogenesis-abundant protein [Gossypium hirsutum]
Seq. No.
                  233326
                  LIB3272-012-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170747
BLAST score
                  172
E value
                  2.0e-12
Match length
                  40
                  93
% identity
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
                  (M88324) late embryogenesis-abundant protein [Gossypium
                  hirsutum] >gi_167347 (M37697) Lea5-A late
                  embryogenesis-abundant protein [Gossypium hirsutum]
Seq. No.
                  233327
                  LIB3272-012-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2160166
BLAST score
                  319
E value
                  2.0e-29
Match length
                  129
% identity
                  57
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
                  233328
Seq. No.
Seq. ID
                  LIB3272-012-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g1621268
BLAST score
                  375
E value
                  3.0e-36
Match length
                  112
% identity
                  70
NCBI Description (Z81012) unknown [Ricinus communis]
                  233329
Seq. No.
Seq. ID
                  LIB3272-012-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q629483
BLAST score
                  325
E value
                  3.0e-30
```

33663

>gi\_534898\_emb\_CAA54696\_ (X77601) 1 Sc-3 [Betula pendula]

NCBI Description gene 1-Sc3 protein - European white birch

Seq. ID



pendula]



>gi 1584322 prf 2122374C allergen Bet v 1-Sc3 [Betula

```
233330
Seq. No.
Seq. ID
                  LIB3272-012-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g3851636
                  582
BLAST score
E value
                  2.0e-60
Match length
                  133
                  83
% identity
NCBI Description (AF098519) unknown [Avicennia marina] >gi 4128206
                  (AF056316) 40S ribosome protein S7 [Avicennia marina]
                  233331
Seq. No.
Seq. ID
                  LIB3272-012-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g1703375
BLAST score
                  606
E value
                  4.0e-63
Match length
                  119
% identity
                  99
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 965483 dbj BAA08259 (D45420)
                  DcARF1 [Daucus carota]
Seq. No.
                  233332
Seq. ID
                  LIB3272-012-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g2443757
BLAST score
                  243
E value
                  7.0e-21
Match length
                  69
% identity
                  68
NCBI Description (AF020434) cyclophilin [Arabidopsis thaliana]
Seq. No.
                  233333
Seq. ID
                  LIB3272-012-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g3641312
BLAST score
                  552
E value
                  7.0e-57
Match length
                  121
% identity
                  85
NCBI Description (AF087412) AJH2 [Arabidopsis thaliana]
Seq. No.
                  233334
Seq. ID
                  LIB3272-012-P1-K1-G4
                  BLASTX
Method
NCBI GI
                  q2970051
BLAST score
                  649
                  3.0e-68
E value
Match length
                  137
% identity
                  91
NCBI Description (AB012110) ARG10 [Vigna radiata]
Seq. No.
                  233335
```

LIB3272-012-P1-K1-G7

Method

NCBI GI

BLASTX

q2462762



```
BLASTX
Method
NCBI GI
                  g122770 .
BLAST score
                  491
                  1.0e-49
E value
Match length
                  126
% identity
                  81
                  HEMOGLOBIN II >gi 99509 pir S13378 hemoglobin II - swamp
NCBI Description
                  oak >gi 18015 emb CAA37898 (X53950) hemoglobin [Casuarina
                  glauca]
                  233336
Seq. No.
Seq. ID
                  LIB3272-012-P1-K1-H11
                  BLASTX
Method
NCBI GI
                  q2463569
BLAST score
                  466
E value
                  7.0e-48
Match length
                  111
                  82
% identity
NCBI Description (AB007503) squalene synthase [Glycine max]
Seq. No.
                  233337
Seq. ID
                  LIB3272-012-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g132853
BLAST score
                  279
E value
                  3.0e-37
Match length
                  122
% identity
                  63
                  60S RIBOSOMAL PROTEIN L2 >gi_71076_pir__R5D02 ribosomal
NCBI Description
                  protein L8.e - slime mold (Dictyostelium discoideum)
                  >gi_7355_emb_CAA33741_ (X15710) ribosomal protein L2 (AA
                  1-237) [Dictyostelium discoideum]
Seq. No.
                  233338
Seq. ID
                  LIB3272-012-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q3337367
BLAST score
                  202
E value
                  9.0e-16
                  95
Match length
% identity
                  45
NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana]
                  233339
Seq. No.
Seq. ID
                  LIB3272-012-P1-K1-H9
                  BLASTX
Method
NCBI GI
                  q224293
BLAST score
                  410
E value
                  3.0e-40
Match length
                  82
% identity
                  100
NCBI Description histone H4 [Triticum aestivum]
Seq. No.
                  233340
Seq. ID
                  LIB3272-013-P1-K1-A1
```



BLAST score 193 E value 8.0e-15 Match length 100 % identity 47

NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 233341

Seq. ID LIB3272-013-P1-K1-A12

Method BLASTX
NCBI GI g2129759
BLAST score 493
E value 6.0e-50
Match length 128
% identity 78

NCBI Description UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana

>gi 1143392 emb CAA90941 (Z54214) uridine diphosphate

glucose epimerase [Arabidopsis thaliana]

Seq. No. 233342

Seq. ID LIB3272-013-P1-K1-A2

Method BLASTX
NCBI GI g3204106
BLAST score 123
E value 9.0e-11
Match length 66
% identity 58

NCBI Description (AJ006763) putative beta-amilase [Cicer arietinum]

Seq. No. 233343

Seq. ID LIB3272-013-P1-K1-A3

Method BLASTX
NCBI GI g2924509
BLAST score 274
E value 3.0e-24
Match length 95
% identity 55

NCBI Description (AL022023) subtilisin proteinase - like [Arabidopsis

thalianal

Seq. No. 233344

Seq. ID LIB3272-013-P1-K1-A6

Method BLASTX
NCBI GI g481236
BLAST score 246
E value 5.0e-21
Match length 60
% identity 80

NCBI Description hypothetical protein - Madagascar periwinkle

>gi 407410\_emb\_CAA81526\_ (Z26880) 14 kDa polypeptide

[Catharanthus roseus]

Seq. No. 233345

Seq. ID LIB3272-013-P1-K1-A7

Method BLASTX NCBI GI g2462753 BLAST score 172

% identity

70



```
E value
                  2.0e-12
Match length
                   43
                  72
% identity
                  (AC002292) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
                  233346
Seq. No.
                  LIB3272-013-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3492806
BLAST score
                  204
                  1.0e-17
E value
                  107
Match length
                   55
% identity
NCBI Description
                  (AJ225045) adventitious rooting related oxygenase [Malus
                  domestica]
                  233347
Seq. No.
                  LIB3272-013-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2462753
BLAST score
                   168
                  7.0e-12
E value
Match length
                   43
% identity
                   72
NCBI Description
                  (AC002292) putative polygalacturonase [Arabidopsis
                  thaliana]
                   233348
Seq. No.
                  LIB3272-013-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3252868
BLAST score
                   224
E value
                   2.0e-18
Match length
                   77
% identity
                   53
NCBI Description (AF033536) putative zinc transporter [Arabidopsis thaliana]
Seq. No.
                   233349
                   LIB3272-013-P1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4567301
BLAST score
                   179
E value
                   3.0e-13
                   54
Match length
% identity
NCBI Description (AC005956) putative protein kinase [Arabidopsis thaliana]
                   233350
Seq. No.
                  LIB3272-013-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1172873
BLAST score
                  536
E value
                   5.0e-55
Match length
                  128
```

NCBI Description CYSTEINE PROTEINASE RD21A PRECURSOR >gi 541857 pir JN0719



drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi\_435619\_dbj\_BAA02374\_ (D13043) thiol protease [Arabidopsis thaliana]

233351 Seq. No. LIB3272-013-P1-K1-B12 Seq. ID Method BLASTX NCBI GI g2213852 BLAST score 200 E value 1.0e-15 Match length 87 % identity 52 NCBI Description (AF003007) VVTL1 [Vitis vinifera] 233352 Seq. No. LIB3272-013-P1-K1-B3 Seq. ID Method BLASTX NCBI GI g3868758 BLAST score 417 E value 5.0e-41100 Match length 76 % identity NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa] Seq. No. 233353 LIB3272-013-P1-K1-B4 Seq. ID Method BLASTX NCBI GI a2739365 BLAST score 540 2.0e-55 E value Match length 119 % identity NCBI Description (AC002505) unknown protein [Arabidopsis thaliana] Seq. No. 233354 Seq. ID LIB3272-013-P1-K1-B6 Method BLASTX NCBI GI q4006854 379 BLAST score E value 1.0e-36 Match length 118 % identity 65 NCBI Description (Z99707) putative protein [Arabidopsis thaliana] 233355 Seq. No. Seq. ID LIB3272-013-P1-K1-B9 Method BLASTX NCBI GI g113621 BLAST score 483 E value 9.0e-49 Match length 108 88 % identity NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi\_68196\_pir\_\_ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi\_168420 (M16220) aldolase
[Zea mays] >gi\_295850\_emb\_CAA31366\_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi\_225624\_prf\_\_1307278A

NCBI Description

thaliana]



#### cytoplasmic aldolase [Zea mays]

```
Seq. No.
                   233356
Seq. ID
                  LIB3272-013-P1-K1-C10
Method
                  BLASTX
NCBI GI
                   g2924520
BLAST score
                   501
E value
                   7.0e-51
Match length
                  106
% identity
                   92
                   (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   233357
                  LIB3272-013-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2576361.
BLAST score
                   514
E value
                   2.0e-52
Match length
                   100
% identity
                   91
NCBI Description
                  (U39782) lysine and histidine specific transporter
                   [Arabidopsis thaliana]
Seq. No.
                   233358
                  LIB3272-013-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g951427
BLAST score
                   436
E value
                   3.0e-43
Match length
                  100
                   83
% identity
                  (M59857) stearoyl-acyl-carrier protein desaturase [Ricinus
NCBI Description
                  communis]
                   233359
Seq. No.
Seq. ID
                  LIB3272-013-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g167367
BLAST score
                   498
E value
                   2.0e-50
Match length
                  123
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                   233360
Seq. No.
Seq. ID
                  LIB3272-013-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g3281869
BLAST score
                  264
E value
                   4.0e-23
Match length
                  71
                   72
% identity
```

(AL031004) RSZp22 splicing factor [Arabidopsis thaliana] >gi 3435094 (AF033586) 9G8-like SR protein [Arabidopsis

% identity

NCBI Description



```
Seq. No.
                     233361
  Seq. ID
                     LIB3272-013-P1-K1-C8
  Method
                     BLASTX
  NCBI GI
                     g400650
  BLAST score
                     183
  E value
                     1.0e-13
  Match length
                     93
  % identity
                     42
  NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (COMPLEX
                     I-13KD-B) (CI-13KD-B) (B13) >gi_346535_pir_S28244 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B13 -
                     bovine >gi_238_emb_CAA44903 (X63218) NADH dehydrogenase
                     [Bos taurus]
  Seq. No.
                     233362
  Seq. ID
                     LIB3272-013-P1-K1-C9
  Method
                     BLASTX
  NCBI GI
                     g1658197
  BLAST score
                     584
  E value
                     1.0e-60
  Match length
                     122
  % identity
                     87
  NCBI Description (U74630) calreticulin [Ricinus communis] >gi 1763297
                     (U74631) calreticulin [Ricinus communis]
  Seq. No.
                     233363
  Seq. ID
                     LIB3272-013-P1-K1-D1
  Method
                     BLASTX
  NCBI GI
                     g3094012
  BLAST score
                     360
  E value
                     2.0e-34
  Match length
                     75
  % identity
                     85
  NCBI Description (AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]
  Seq. No.
                     233364
  Seq. ID
                     LIB3272-013-P1-K1-D10
  Method
                     BLASTX
  NCBI GI
                     g2493130
  BLAST score
                     625
  E value
                     2.0e-65
  Match length
                     121
  % identity
                     100
  NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B
                     SUBUNIT) >gi 459200 (U07053) vacuolar H+-ATPase subunit B
                     [Gossypium hirsutum]
  Seq. No.
                     233365
  Seq. ID
                     LIB3272-013-P1-K1-D11
  Method
                     BLASTX
  NCBI GI
                     g4323298
  BLAST score
                     228
  E value
                     7.0e-19
Match length
                     107
```

33670

potassium SPOCK1 [Samanea saman]

(AF099096) pulvinus outward-rectifying channel for

```
Seq. No.
                  233366
Seq. ID
                  LIB3272-013-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g4567251
BLAST score
                  514
E value
                  2.0e-52
Match length
                  123
% identity
                  80
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
Seq. No.
                  233367
Seq. ID
                  LIB3272-013-P1-K1-D6
Method
                  BLASTX
                  q3080428
NCBI GI
BLAST score
                  321
E value
                  9.0e-30
Match length
                  98
% identity
                  56
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
Seq. No.
                  233368
Seq. ID
                  LIB3272-013-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  q3851636
BLAST score
                  474
E value
                  9.0e-48
Match length
                  108
% identity
                  82
NCBI Description (AF098519) unknown [Avicennia marina] >gi 4128206
                  (AF056316) 40S ribosome protein S7 [Avicennia marina]
Seq. No.
                  233369
Seq. ID
                  LIB3272-013-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q4510363
BLAST score
                  348
E value
                  6.0e-33
Match length
                  81
% identity
NCBI Description (AC007017) putative DNA-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  233370
Seq. ID
                  LIB3272-013-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q231536
BLAST score
                  553
E value
                  5.0e-57
Match length
                  130
% identity
                  81
NCBI Description CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP)
                  (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL
                  AMINOPEPTIDASE) >gi_99683 pir S22399 leucyl aminopeptidase
                  (EC 3.4.11.1) - Arabidopsis thaliana
```

33671

>gi\_16394\_emb\_CAA45040\_ (X63444) leucine aminopeptidase
[Arabidopsis thaliana] >gi\_4115380 (AC005967) putative



# leucine aminopeptidase [Arabidopsis thaliana]

```
233371
Seq. No.
Seq. ID
                  LIB3272-013-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g2708484
BLAST score
                  148
E value
                  2.0e-09
                  115
Match length
                  38
% identity
NCBI Description (U79557) IAA24 [Arabidopsis thaliana]
                  233372
Seq. No.
Seq. ID
                  LIB3272-013-P1-K1-E12
                  BLASTX
Method
NCBI GI
                  g122770
BLAST score
                  341
                  2.0e-37
E value
Match length
                  112
                  75
% identity
NCBI Description HEMOGLOBIN II >gi_99509_pir__S13378 hemoglobin II - swamp
                  oak >gi 18015 emb CAA37898 (X53950) hemoglobin [Casuarina
                  glauca]
                  233373
Seq. No.
Seq. ID
                  LIB3272-013-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g1166450
BLAST score
                  321
E value
                  9.0e-30
                  71
Match length
% identity
                  82
NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]
Seq. No.
                  233374
Seq. ID
                  LIB3272-013-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g2497538
BLAST score
                  396
E value
                  1.0e-38
Match length
                  122
% identity
                  71
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632)
                  pyruvate kinase [Glycine max]
                  233375
Seq. No.
                  LIB3272-013-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g416639
BLAST score
                  154
E value
                  3.0e-10
Match length
                  76
% identity
                  46
NCBI Description INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG2
                  >gi_287564_dbj_BAA03307_ (D14411) ORF [Vigna radiata]
```

33672

233376

Seq. No.



```
Seq. ID
                   LIB3272-013-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   q132745
BLAST score
                   160
E value
                   5.0e-22
Match length
                   93
% identity
                   60
NCBI Description 60S RIBOSOMAL PROTEIN L1B >gi_71067_pir__R5XL1B ribosomal
                   protein XL1b - African clawed frog (fragment)
                   >gi_899428_emb_CAA28844_ (X05217) ribosomal protein L1b
                   (396 AA) [Xenopus laevis] >gi_224829_prf__1202260B
                   ribosomal protein L1b [Xenopus laevis]
Seq. No.
                   233377
                   LIB3272-013-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g585204
BLAST score
                  413
E value
                   1.0e-40
Match length
                   79
% identity
                   96
NCBI Description GLUTAMINE SYNTHETASE ROOT ISOZYME 4 (GLUTAMATE--AMMONIA
                  LIGASE) (GS107) >gi_481809_pir__S39480 glutamate--ammonia ligase (EC 6.3.1.2) 1-4, cytosolic - maize
                   >gi 434330 emb CAA46722 (X65929) glutamine synthetase [Zea
                   mays]
                   233378
Seq. No.
Seq. ID
                   LIB3272-013-P1-K1-F3
Method
                  BLASTX
NCBI GI
                   q3643602
BLAST score
                   301
E value
                   2.0e-27
Match length
                   110
% identity
NCBI Description (AC005395) putative tonoplast intrinsic protein
                   [Arabidopsis thaliana]
Seq. No.
                   233379
Seq. ID
                   LIB3272-013-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   g2306917
BLAST score
                   258
E value
                   2.0e-22
Match length
                   98
                   57
% identity
NCBI Description (AF003728) plasma membrane intrinsic protein [Arabidopsis
                   thaliana]
                   233380
Seq. No.
                   LIB3272-013-P1-K1-F8
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI 9729470
BLAST score 471
E value 2.0e-47
Match length 116
% identity 78



NCBI Description

MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR

(NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)

>gi\_542089\_pir\_\_JQ2272 formate dehydrogenase (EC 1.2.1.2)

precursor, mitochondrial - potato >gi\_297798\_emb\_CAA79702\_

(Z21493) mitochondrial formate dehydrogenase precursor

[Solanum tuberosum]

Seq. No. 233381

Seq. ID LIB3272-013-P1-K1-G10 Method BLASTX NCBI GI g2980793 BLAST score 515 E value 2.0e-52 Match length % identity 74

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 233382

Seq. ID LIB3272-013-P1-K1-G12

Method BLASTX
NCBI GI g1361979
BLAST score 241
E value 2.0e-20
Match length 75
% identity 68

NCBI Description serine O-acetyltransferase (EC 2.3.1.30) - watermelon

>gi\_1350550\_dbj\_BAA12843\_ (D85624) serine acetyltransferase

[Citrullus lanatus] >gi\_1841312 dbj BAA08479 (D49535)

serine acetyltransferase. [Citrullus lanatus] >gi\_2337772\_dbj\_BAA21827\_ (AB006530) serine

acetyltransferase [Citrullus lanatus]

Seq. No. 233383

Seq. ID LIB3272-013-P1-K1-G3

Method BLASTX
NCBI GI g1130684
BLAST score 151
E value 5.0e-10
Match length 100
% identity 38

NCBI Description (Z46960) acetohydroxyacid synthase [Gossypium hirsutum]

Seq. No. 233384

Seq. ID LIB3272-013-P1-K1-G5

Method BLASTX
NCBI GI g2980793
BLAST score 513
E value 3.0e-52
Match length 129
% identity 74

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 233385

Seq. ID LIB3272-013-P1-K1-G6

Method BLASTX
NCBI GI g1063415
BLAST score 612

E value

Match length

% identity

2.0e-20

50



```
E value
                    7.0e-64
 Match length
                   122
 % identity
                    92
 NCBI Description (L40948) K+ channel protein [Arabidopsis thaliana]
 Seq. No.
                   233386
 Seq. ID
                   LIB3272-013-P1-K1-G8
 Method
                   BLASTX
 NCBI GI
                   g2564066
 BLAST score
                   246
 E value
                   4.0e-21
 Match length
                   83
 % identity
                   63
 NCBI Description (D45900) LEDI-3 protein [Lithospermum erythrorhizon]
 Seq. No.
                   233387
 Seq. ID
                   LIB3272-013-P1-K1-H12
 Method
                   BLASTX
 NCBI GI
                   g1709498
 BLAST score
                   377
 E value
                   2.0e-36
                   97
 Match length
 % identity
                   73
                   OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
 NCBI Description
                   >gi_1362001 pir__S57524 osmotin precursor - Arabidopsis
                   thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
                   [Arabidopsis thaliana]
 Seq. No.
                   233388
 Seq. ID
                   LIB3272-013-P1-K1-H2
 Method
                   BLASTX
 NCBI GI
                   g2160166
 BLAST score
                   264
 E value
                   4.0e-23
 Match length
                   107
 % identity
                   57
 NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
 Seq. No.
                   233389
 Seq. ID
                   LIB3272-013-P1-K1-H3
 Method
                   BLASTX
NCBI GI
                   q585550
BLAST score
                   146
E value
                   2.0e-09
Match length
                   49
 % identity
                   NADPH-CYTOCHROME P450 REDUCTASE (CPR) >gi 295448 (L07843)
NCBI Description
                   NADPH cytochrome P450 [Vigna radiata]
Seq. No.
                   233390
Seq. ID
                   LIB3272-013-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   g2244810
BLAST score
                   241
```



NCBI Description (Z97336) CCAAT-binding transcription factor subunit A(CBF-A) [Arabidopsis thaliana]

Seq. No. 233391

Seq. ID LIB3272-014-P1-K1-A1

Method BLASTX
NCBI GI g3334405
BLAST score 513
E value 2.0e-52
Match length 108
% identity 97

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)

>gi\_2267583 (AF009338) vacuolar H+-ATPase subunit E

[Gossypium hirsutum]

Seq. No. 233392

Seq. ID LIB3272-014-P1-K1-A10

Method BLASTX
NCBI GI g2347199
BLAST score 642
E value 2.0e-67
Match length 137
% identity 82

NCBI Description (AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No. 233393

Seq. ID LIB3272-014-P1-K1-A11

Method BLASTX
NCBI GI g508304
BLAST score 241
E value 2.0e-20
Match length 82
% identity 57

NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 233394

Seq. ID LIB3272-014-P1-K1-A2

Method BLASTX
NGBI GI g3643594
BLAST score 458
E value 8.0e-46
Match length 125
% identity 74

NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 233395

Seq. ID LIB3272-014-P1-K1-A4

Method BLASTX
NCBI GI g1709970
BLAST score 446
E value 2.0e-44

Match length 121 % identity 74

NCBI Description 60S RIBOSOMAL PROTEIN L10A

Seq. No. 233396

Seq. ID LIB3272-014-P1-K1-A5



```
Method
                   BLASTX
NCBI GI
                   g2970051
BLAST score
                   397
E value
                   1.0e-38
Match length
                   99
% identity
                   75
NCBI Description (AB012110) ARG10 [Vigna radiata]
Seq. No.
                   233397
Seq. ID
                   LIB3272-014-P1-K1-A6
Method
                  BLASTX
NCBI GI
                   g3608412
BLAST score
                   615
E value
                   3.0e-64
Match length
                   137
% identity
                   85
NCBI Description
                  (AF079355) protein phosphatase-2c [Mesembryanthemum
                   crystallinum]
Seq. No.
                   233398
Seq. ID
                  LIB3272-014-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g120669
BLAST score
                   547
E value
                   3.0e-56
Match length
                  108
% identity
                   94
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                  233399
Seq. ID
                  LIB3272-014-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g549063
BLAST score
                  351
E value
                   3.0e-33
Match length
                  108
% identity
                   65
NCBI Description
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                  >gi 1072464_pir__A38958 IgE-dependent histamine-releasing
                   factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                  21kd polypeptide [Oryza sativa]
Seq. No.
                  233400
Seq. ID
                  LIB3272-014-P1-K1-B2
Method
                  BLASTX
                  q4490308
                  493
                  6.0e-50
                  109
```

NCBI GI BLAST score E value Match length % identity 87

(AL035678) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 233401



```
LIB3272-014-P1-K1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1743354
BLAST score
                   625
E value
                   2.0e-65
Match length
                   137
% identity
NCBI Description
                  (Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
Seq. No.
                   233402
Seq. ID
                   LIB3272-014-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   q584892
BLAST score
                   471
E value
                   2.0e-47
Match length
                   111
% identity
                   71
                   SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)
NCBI Description
                   >gi_629805_pir__S43516 serine carboxypeptidase I - rice
                   >gi_409580_dbj_BAA04510 (D17586) serine carboxypeptidase I
                   [Oryza satīva]
Seq. No.
                   233403
Seq. ID
                   LIB3272-014-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   g2146731
BLAST score
                   388
E value
                   1.0e-37
Match length
                   137
% identity
                   20
NCBI Description FK506-binding protein - Arabidopsis thaliana >gi 1354207
                   (U49453) rof1 [Arabidopsis thaliana]
Seq. No.
                   233404
Seq. ID
                   LIB3272-014-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   g3158376
BLAST score
                   488
E value
                   3.0e-49
Match length
                   131
                   75
% identity
NCBI Description (AF035385) unknown [Arabidopsis thaliana]
Seq. No.
                   233405
                   LIB3272-014-P1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4115379
BLAST score
                   265
E value
                   3.0e-23
Match length
                   83
% identity
NCBI Description
                  (AC005967) putative carbonyl reductase [Arabidopsis
                   thaliana]
```

od BLASTX

233406

LIB3272-014-P1-K1-B8

Seq. No.

Seq. ID

Method



```
NCBI GI
                   g2252836
BLAST score
                  398
E value
                  9.0e-39
                  135
Match length
                  63
% identity
NCBI Description (AF013293) contains weak similarity to S. cerevisiae BOB1
                  protein (PIR:S45444) [Arabidopsis thaliana]
                  233407
Seq. No.
Seq. ID
                  LIB3272-014-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g3492806
BLAST score
                  351
E value
                  2.0e-33
Match length
                  102
% identity
                  68
NCBI Description (AJ225045) adventitious rooting related oxygenase [Malus
                  domestica]
Seq. No.
                  233408
Seq. ID
                  LIB3272-014-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g2911060
BLAST score
                  144
E value
                  1.0e-11
Match length
                  94
% identity
                  42
NCBI Description
                  (AL021961) putative protein [Arabidopsis thaliana]
                  >gi 3297826 emb CAA19884.1 (AL031032) putative protein
                  [Arabidopsis thaliana]
Seq. No.
                  233409
Seq. ID
                  LIB3272-014-P1-K1-C3
Method
                  {\tt BLASTX}
NCBI GI
                  g510876
BLAST score
                  472
                  2.0e-47
E value
Match length
                  132
% identity
                  67
NCBI Description (X80051) NADP dependent malic enzyme [Phaseolus vulgaris]
                  233410
Seq. No.
Seq. ID
                  LIB3272-014-P1-K1-C5
Method
                  {\tt BLASTX}
NCBI GI
                  g2213592
BLAST score
                  207
E value
                  1.0e-16
Match length
                  80
% identity
                  27
NCBI Description (AC000348) T7N9.12 [Arabidopsis thaliana]
Seq. No.
                  233411
Seq. ID
                  LIB3272-014-P1-K1-C7
```

Method BLASTX q1706918 NCBI GI BLAST score 264 E value 5.0e-23



Match length 95
% identity 48
NCBI Description FLAVONOL SULFOTRANSFERASE-LIKE >gi\_498647 (U10277)
sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No. 233412
Seq. ID LIB3272-014-P1-K1-C8

Method BLASTX
NCBI GI g2352492
BLAST score 428
E value 3.0e-42
Match length 133
% identity 65

NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi\_2352494 (AF005048) transport inhibitor

response 1 [Arabidopsis thaliana]

Seq. No. 233413

Seq. ID LIB3272-014-P1-K1-C9

Method BLASTX
NCBI GI g285741
BLAST score 437
E value 2.0e-43
Match length 126
% identity 67

NCBI Description (D14550) EDGP precursor [Daucus carota]

Seq. No. 233414

Seq. ID LIB3272-014-P1-K1-D10

Method BLASTX
NCBI GI g136057
BLAST score 385
E value 2.0e-37
Match length 102
% identity 73

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

>gi\_99499\_pir\_\_A32187 (S)-tetrahydroberberine oxidase Coptis japonica >gi 556171 (J04121) triosephosphate

isomerase [Coptis japonica]

Seq. No. 233415

Seq. ID LIB3272-014-P1-K1-D11

Method BLASTX
NCBI GI g3819164
BLAST score 381
E value 7.0e-37
Match length 93
% identity 84

NCBI Description (AJ012318) cytosolic chaperonin, delta-subunit [Glycine

max]

Seq. No. 233416

Seq. ID LIB3272-014-P1-K1-D12

Method BLASTX
NCBI GI g1928981
BLAST score 318
E value 2.0e-29



```
Match length
% identity
                  46
                 (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                  oleracea var. botrytis]
                  233417
Seq. No.
Seq. ID
                  LIB3272-014-P1-K1-D2
                  BLASTX
Method
NCBI GI
                  g549063
                  497
BLAST score
E value
                  2.0e-50
Match length
                  114
% identity
                  82
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                  >gi 1072464 pir A38958 IgE-dependent histamine-releasing
                  factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                  21kd polypeptide [Oryza sativa]
                  233418
Seq. No.
Seq. ID
                  LIB3272-014-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g1684857
BLAST score
                  648
E value
                  4.0e-68
Match length
                  130
                  40
% identity
NCBI Description (U77940) polyubiquitin [Phaseolus vulgaris]
Seq. No.
                  233419
Seq. ID
                  LIB3272-014-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g4103324
BLAST score
                  467
E value
                  7.0e-47
                  101
Match length
% identity
                  92
NCBI Description (AF022716) GDP-mannose pyrophosphorylase [Solanum
                  tuberosum]
Seq. No.
                  233420
                  LIB3272-014-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4008159
BLAST score
                  680
E value
                  8.0e-72
Match length
                  136
% identity
NCBI Description (AB015601) DnaJ homolog [Salix gilgiana]
```

Seq. No. 233421

Seq. ID LIB3272-014-P1-K1-D7

Method BLASTX NCBI GI q464981 BLAST score 478 E value 3.0e-48Match length 89 % identity 98



NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi\_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 233422

Seq. ID LIB3272-014-P1-K1-D8

Method BLASTX
NCBI GI g2499946
BLAST score 461
E value 4.0e-46
Match length 137
% identity 67

NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE

PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi\_747980 (U22260) UMP synthase [Nicotiana

tabacum]

Seq. No. 233423

Seq. ID LIB3272-014-P1-K1-E1

Method BLASTX
NCBI GI g4455329
BLAST score 297
E value 6.0e-27
Match length 107
% identity 57

NCBI Description (AL035525) lysine-ketoglutarate reductase/saccharopine

[Arabidopsis thaliana]

Seq. No. 233424

Seq. ID LIB3272-014-P1-K1-E10

Method BLASTX
NCBI GI g3123745
BLAST score 204
E value 5.0e-16
Match length 102
% identity 42

NCBI Description (AB013447) aluminum-induced [Brassica napus]

Seq. No. 233425

Seq. ID LIB3272-014-P1-K1-E3

Method BLASTX
NCBI GI g4457221
BLAST score 153
E value 5.0e-10
Match length 45
% identity 67

NCBI Description (AF127797) putative bZIP DNA-binding protein [Capsicum

chinense]

Seq. No. 233426

Seq. ID LIB3272-014-P1-K1-E4

Method BLASTX
NCBI GI g2463569
BLAST score 466
E value 9.0e-47
Match length 103
% identity 83

Method

BLASTX





```
NCBI Description (AB007503) squalene synthase [Glycine max]
Seq. No.
                  233427
Seq. ID
                  LIB3272-014-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g553107
BLAST score
                  399
E value
                  7.0e-39
Match length
                  114
% identity
                  68
NCBI Description (L04967) triosephosphate isomerase [Oryza sativa]
Seq. No.
                  233428
Seq. ID
                  LIB3272-014-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g2160166
BLAST score
                  304
E value
                  1.0e-27
Match length
                  128
% identity
                  55
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.
                  233429
Seq. ID
                  LIB3272-014-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g4056494
BLAST score
                  306
E value
                  5.0e-28
Match length
                  100
% identity
                  61
NCBI Description (AC005896) putative protein translocase [Arabidopsis
                  thaliana]
                  233430
Seq. No.
Seq. ID
                  LIB3272-014-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g4467159
BLAST score
                  443
E value
                  5.0e-44
Match length
                  132
% identity
                  67
NCBI Description (AL035540) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  233431
Seq. ID
                  LIB3272-014-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g3334147
BLAST score
                  439
E value
                  1.0e-43
Match length
                  122
                  70
% identity
NCBI Description ENDOCHITINASE 1 PRECURSOR >gi 1469788 (U60197) class I
                  chitinase [Gossypium hirsutum]
Seq. No.
                  233432
Seq. ID
                  LIB3272-014-P1-K1-F10
```

Match length

% identity

124

62



```
NCBI GI
                   q2738949
BLAST score
                   540
E value
                   2.0e-55
Match length
                   113
% identity
                   88
NCBI Description
                  (AF022213) cytosolic ascorbate peroxidase [Fragaria x
                   ananassa]
Seq. No.
                   233433
Seq. ID
                   LIB3272-014-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   g3759184
BLAST score
                   233
E value
                   9.0e-26
Match length
                   128
% identity
                   55
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
                   233434
Seq. ID
                   LIB3272-014-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   g4406815
BLAST score
                   434
E value
                   5.0e-43
Match length
                   131
% identity
                   65
NCBI Description
                  (AC006201) putative peptide methionine sulfoxide reductase
                   [Arabidopsis thaliana]
Seq. No.
                   233435
Seq. ID
                  LIB3272-014-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g1402912
BLAST score
                  479
E value
                   3.0e-48
Match length
                  134
% identity
                   69
NCBI Description (X98317) peroxidase [Arabidopsis thaliana]
Seq. No.
                  233436
Seq. ID
                  LIB3272-014-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g3986110
BLAST score
                  218
                  1.0e-17
E value
Match length
                  57
% identity
                  75
NCBI Description (AB012716) heat shock protein 70 cognate [Salix gilgiana]
Seq. No.
                  233437
Seq. ID
                  LIB3272-014-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  q4406815
BLAST score
                  388
E value
                  1.0e-37
```



```
NCBI Description (AC006201) putative peptide methionine sulfoxide reductase
                  [Arabidopsis thaliana]
Seq. No.
                  233438
Seq. ID
                  LIB3272-014-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g2500378
BLAST score
                  434
E value
                  5.0e-43
Match length
                  95
% identity
                  83
NCBI Description 60S RIBOSOMAL PROTEIN L37
Seq. No.
                  233439
Seq. ID
                  LIB3272-014-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g1928981
BLAST score
                  583
E value
                  2.0e-60
Match length
                  122
% identity
                  63
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                  oleracea var. botrytis]
Seq. No.
                  233440
Seq. ID
                  LIB3272-014-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g3980415
BLAST score
                  396
E value
                  2.0e-38
Match length
                  120
% identity
                  62
NCBI Description (AC004561) putative tropinone reductase [Arabidopsis
                  thaliana]
Seq. No.
                  233441
Seq. ID
                  LIB3272-014-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g629483
BLAST score
                  338
E value
                  1.0e-31
Match length
                  122
% identity
                  56
NCBI Description gene 1-Sc3 protein - European white birch
                  >gi 534898 emb_CAA54696 (X77601) 1 Sc-3 [Betula pendula]
                  >gi 1584322 prf 2122374C allergen Bet v 1-Sc3 [Betula
                  pendula]
Seq. No.
                  233442
Seq. ID
                  LIB3272-014-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g2244847
```

NCBI GI g2244847 BLAST score 311 E value 1.0e-28

Match length 119 % identity 55

NCBI Description (Z97337) hydroxyproline-rich glycoprotein homolog



## [Arabidopsis thaliana]

```
Seq. No.
                   233443
Seq. ID
                   LIB3272-014-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g2995384
BLAST score
                   258
E value
                   2.0e-22
Match length
                  105
% identity
                   56
NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]
Seq. No.
                  233444
Seq. ID
                  LIB3272-014-P1-K1-G7
Method
                  BLASTX
NCBI GI
                   g4567251
BLAST score
                  309
E value
                   2.0e-28
Match length
                  80
% identity
                   66
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
Seq. No.
                  233445
Seq. ID
                  LIB3272-014-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g3880506
BLAST score
                  176
E value
                  9.0e-27
Match length
                  103
% identity
                  53
NCBI Description
                  (Z93391) predicted using Genefinder; Similarity to Human
                  RAS-related protein RAB11 (SW:P24410) [Caenorhabditis
                  elegans]
Seq. No.
                  233446
Seq. ID
                  LIB3272-014-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g117765
BLAST score
                  230
                  5.0e-19
E value
Match length
                  67
% identity
                  64
NCBI Description
                  CYTOCHROME C1, HEME PROTEIN PRECURSOR (CLONE PC13III)
                  >gi_21439_emb_CAA44055_ (X62124) cytochrome c1 [Solanum
                  tuberosum]
Seq. No.
                  233447
Seq. ID
                  LIB3272-014-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g2668744
BLAST score
                  273
E value
                  2.0e-30
Match length
                  81
% identity
                  72
```

Seq. No. 233448

NCBI Description

(AF034946) ubiquitin conjugating enzyme [Zea mays]



```
LIB3272-014-P1-K1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1928981
BLAST score
                   522
E value
                   2.0e-53
Match length
                   108
% identity
                   94
NCBI Description
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                   oleracea var. botrytis]
Seq. No.
                   233449
Seq. ID
                   LIB3272-015-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   q2970051
BLAST score
                   424
E value
                   8.0e-42
Match length
                   105
                   76
% identity
NCBI Description (AB012110) ARG10 [Vigna radiata]
Seq. No.
                   233450
Seq. ID
                   LIB3272-015-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   g2833379
BLAST score
                   234
E value
                   2.0e-19
Match length
                   62
% identity
                   68
NCBI Description RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 1 (PHOSPHORIBOSYL
                   PYROPHOSPHATE SYNTHETASE 1) (PRS I) >gi_1076397_pir__S51270
                   ribose-phosphate pyrophosphokinase (\stackrel{.}{\text{EC}} \overline{2}.7.6.1)
                   Arabidopsis thaliana >gi_633140_emb_CAA58717_ (X83764)
                   phosphoribosyl diphosphate synthetase [Arabidopsis
                   thaliana] >gi_3608149 (AC005314) phosphoribosyl diphosphate
                   synthetase [Arabidopsis thaliana]
Seq. No.
                   233451
Seq. ID
                   LIB3272-015-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   g3915826
BLAST score
                   562
E value
                   5.0e-58
Match length
                   127
% identity
                   82
NCBI Description 60S RIBOSOMAL PROTEIN L5
Seq. No.
                   233452
Seq. ID
                   LIB3272-015-P1-K1-A3
                   BLASTX
Method
NCBI GI
                   q3158376
BLAST score
                   478
E value
                   3.0e-48
Match length
                   126
```

% identity 76

NCBI Description (AF035385) unknown [Arabidopsis thaliana]

Seq. No. 233453



```
LIB3272-015-P1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4097915
BLAST score
                   168
E value
                   9.0e-12
Match length
                   103
                   37
% identity
NCBI Description
                  (U72147) unknown [Anabaena sp. CA]
                   233454
Seq. No.
Seq. ID
                   LIB3272-015-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   q4468813
BLAST score
                   377
E value
                   3.0e - 36
Match length
                   132
% identity
NCBI Description (AL035601) putative protein [Arabidopsis thaliana]
Seq. No.
                   233455
Seq. ID
                   LIB3272-015-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   g549063
BLAST score
                   404
È value
                   2.0e-39
Match length
                   108
% identity
                   71
NCBI Description
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
Seq. No.
                   233456
Seq. ID
                   LIB3272-015-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   g2618689
BLAST score
                   634
E value
                   2.0e-66
Match length
                   138
% identity
                   88
NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]
Seq. No.
                   233457
Seq. ID
                   LIB3272-015-P1-K1-B12
Method
                   BLASTX
NCBI GI .
                   g2191136
                   162
BLAST score
                   2.0e-11
E value
                   66
Match length
% identity
NCBI Description
                   (AF007269) Similar to UTP-Glucose Glucosyltransferase;
                   coded for by A. thaliana cDNA T46230; coded for by A.
                   thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                   [Arabidopsis thaliana]
```

Seq. No. 233458

Seq. ID LIB3272-015-P1-K1-B5

% identity



```
Method
                  BLASTX
NCBI GI
                  g2262173
BLAST score
                  376
                  3.0e-36
E value
Match length
                  137
                  57
% identity
NCBI Description
                  (AC002329) NADPH thioredoxin reductase [Arabidopsis
                  thaliana]
                  233459
Seq. No.
Seq. ID
                  LIB3272-015-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q2961372
BLAST score
                  355
E value
                  9.0e-47
Match length
                  114
% identity
                  85
NCBI Description
                  (AL022141) putative ribosomal protein L8 [Arabidopsis
                  thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal
                  protein L2 [Arabidopsis thaliana]
Seq. No.
                  233460
Seq. ID
                  LIB3272-015-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q267069
BLAST score
                  382
E value
                  4.0e-37
Match length
                  72
% identity
                  96
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                  233461
Seq. ID
                  LIB3272-015-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  q1703108
BLAST score
                  490
E value
                  1.0e-49
Match length
                  90
% identity
                  100
NCBI Description ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis
                  thaliana >gi 2129528 pir S68107 actin 7 - Arabidopsis
                  thaliana >gi 1049307 (U37281) actin-2 [Arabidopsis
                  thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis
                  thaliana]
Seq. No.
                  233462
Seq. ID
                  LIB3272-015-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  q3193298
BLAST score
                  364
E value
                  9.0e-35
Match length
                  110
```

33689

NCBI Description (AF069298) T14P8.17 gene product [Arabidopsis thaliana]



```
Seq. No.
                    233463
 Seq. ID
                    LIB3272-015-P1-K1-C2
 Method
                    BLASTX
 NCBI GI
                    g3158376
 BLAST score
                    165
 E value
                    6.0e-21
 Match length
                    106
 % identity
                    55
 NCBI Description
                   (AF035385) unknown [Arabidopsis thaliana]
                    233464
 Seq. No.
                    LIB3272-015-P1-K1-C6
 Seq. ID
Method
                    BLASTX
 NCBI GI
                    q629483
 BLAST score
                    334
 E value
                    3.0e-31
 Match length
                    122
 % identity
                    55
 NCBI Description
                    gene 1-Sc3 protein - European white birch
                    >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula]
                    >gi_1584322_prf__2122374C allergen Bet v 1-Sc3 [Betula
                    pendula]
 Seq. No.
                    233465
 Seq. ID
                    LIB3272-015-P1-K1-C7
 Method
                    BLASTX
 NCBI GI
                    q2231034
 BLAST score
                    576
 E value
                    1.0e-59
 Match length
                    125
 % identity
                    87
 NCBI Description (Y12785) MAP kinase I [Petroselinum crispum]
 Seq. No.
                    233466
 Seq. ID
                    LIB3272-015-P1-K1-C9
 Method
                    BLASTX
 NCBI GI
                    q3482918
 BLAST score
                    589
 E value
                    4.0e-61
 Match length
                    130
                    89
 % identity
                   (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
 NCBI Description
                    thaliana]
 Seq. No.
                    233467
 Seq. ID
                    LIB3272-015-P1-K1-D1
 Method
                    BLASTX
 NCBI GI
                    q2129605
 BLAST score
                    290
 E value
                    2.0e-26
 Match length
                    65
 % identity
                    85
 NCBI Description
                    GTP-binding protein 2 - Arabidopsis thaliana
                    >gi_2129702_pir__S71585 Rab2 homolog GTP-binding protein
```

33690

ATGB2 - Arabidopsis thaliana >gi\_1184983 (U46925) ATGB2 [Arabidopsis thaliana] >gi\_3805852 emb\_CAA21472 (AL031986)

Seq. ID



## GTP-binding protein GB2 [Arabidopsis thaliana]

```
Seq, No.
                  233468
                  LIB3272-015-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1703375
BLAST score
                  610
                  1.0e-63
E value
Match length
                  120
                  99
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 965483_dbj BAA08259 (D45420)
                  DcARF1 [Daucus carota]
                  233469
Seq. No.
Seq. ID
                  LIB3272-015-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q2911039
                  498
BLAST score
                  2.0e-50
E value
Match length
                  125
% identity
                  70
                  (AL021961) cinnamyl alcohol dehydrogenase - like protein
NCBI Description
                  [Arabidopsis thaliana]
                  233470
Seq. No.
Seq. ID
                  LIB3272-015-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q2662343
BLAST score
                  546
                  4.0e-56
E value
Match length
                  105
                  99
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                  233471
Seq. ID
                  LIB3272-015-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g2191150
BLAST score
                  286
E value
                  1.0e-25
Match length
                  90
% identity
                  69
                 (AF007269) similar to mitochondrial carrier family
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  233472
                  LIB3272-015-P1-K1-D5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1843527
BLAST score
                  694
E value
                  2.0e-73
                  137
Match length
                  56
% identity
NCBI Description (U73747) annexin [Gossypium hirsutum]
Seq. No.
                  233473
```

33691

LIB3272-015-P1-K1-D6



```
BLASTX
Method
NCBI GI
                    g416649
BLAST score
                    367
                    4.0e-35
E value-
Match length
                    111
% identity
                    63
                    PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN
NCBI Description
                    PGNT1/PCNT110) >gi_100303_pir__S16267 auxin-induced protein (clone pGNT1) - common tobacco >gi_19789_emb_CAA39709_
                    (X56268) auxin-induced protein [Nicotiana tabacum]
                    >gi_19795_emb_CAA39705_ (X56264) auxin-induced protein
                    [Nicotiana tabacum]
Seq. No.
                    233474
Seq. ID
                    LIB3272-015-P1-K1-D9
Method
                    BLASTX
NCBI GI
                    g464986
BLAST score
                    577
E value
                    9.0e-60
Match length
                    108
% identity
                    99
NCBI Description
                    UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
                    LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi 421857_pir S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana
                    >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                    enzyme homolog [Arabidopsis thaliana] >gi 349211 (L00639)
                    ubiquitin conjugating enzyme [Arabidopsis thaliana]
                    >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating
                    enzyme E2 [Arabidopsis thaliana]
                    >gi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein
                    ligase UBC9 [Arabidopsis thaliana]
                    233475
Seq. No.
Seq. ID
                    LIB3272-015-P1-K1-E1
Method
                    BLASTX
NCBI GI
                    g2129889
BLAST score
                    524
E value
                    1.0e-53
                    102
Match length
                    97
% identity
NCBI Description methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea
Seq. No.
                    233476
Seq. ID
                    LIB3272-015-P1-K1-E11
Method
                    BLASTX
NCBI GI
                    q2970654
BLAST score
                    321
```

Method BLASTX
NCBI GI g297065
BLAST score 321
E value 1.0e-29
Match length 111
% identity 66

NCBI Description (AF052058) ferritin subunit cowpea2 precursor [Vigna

unguiculata]

Seq. No. 233477

Seq. ID LIB3272-015-P1-K1-E4

Method BLASTX

BLAST score

E value

560 9.0e-58

```
g4164159
NCBI GI
BLAST score
                   512
E value
                   4.0e-52
Match length
                   104
                   92
% identity
                  (AB015496) ethylene receptor [Passiflora edulis]
NCBI Description
                   233478
Seq. No.
Seq. ID
                   LIB3272-015-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   g1166450
BLAST score
                   310
E value
                   2.0e-28
Match length
                   68
% identity
                   82
NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]
                   233479
Seq. No.
                   LIB3272-015-P1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q629483
BLAST score
                   336
E value
                   2.0e-31
Match length
                   119
% identity
                   60
                   gene 1-Sc3 protein - European white birch
NCBI Description
                   >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula] >gi_1584322_prf__2122374C allergen Bet v 1-Sc3 [Betula
                   pendula]
                   233480
Seq. No.
Seq. ID
                   LIB3272-015-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   g508304
BLAST score
                   235
E value
                   1.0e-19
Match length
                   81
                   57
% identity
NCBI Description (L22305) corC [Medicago sativa]
                    233481
Seq. No.
Seq. ID
                   LIB3272-015-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   g1928981
BLAST score
                   585
E value
                   1.0e-60
                   125
Match length
                    63
% identity
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                   oleracea var. botrytis]
                    233482
Seq. No.
Seq. ID
                   LIB3272-015-P1-K1-F10
                   BLASTX
Method
NCBI GI
                   q3493172
```

```
Match length
                  120
% identity 92
NCBI Description (U89609) fiber annexin [Gossypium hirsutum]
                  233483
Seq. No.
Seq. ID
                  LIB3272-015-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g2160166
BLAST score
                  316
E value
                  4.0e-29
Match length
                  136
                  54
% identity
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.
                  233484
Seq. ID
                  LIB3272-015-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g1351271
BLAST score
                  436
E value
                  3.0e-43
Match length
                  137
                   69
% identity
NCBI Description
                  TRIOSEPHOSPHATE ISÔMERASE CHLOROPLAST PRECURSOR (TIM)
                  >gi_1084309_pir__S52032 triose-phosphate isomerase (EC
                   5.3.1.1) precursor, chloroplast - spinach >gi_806312
                   (L36387) triosephosphate isomerase, chloroplast isozyme
                   [Spinacia oleracea]
Seq. No.
                   233485
Seq. ID
                  LIB3272-015-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g3334138
BLAST score
                  546
E value
                   4.0e-56
Match length
                  125
% identity
                  82
NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi 669003 (U20502) calnexin
                   [Glycine max]
                   233486
Seq. No.
Seq. ID
                  LIB3272-015-P1-K1-F6
                  BLASTX
Method
NCBI GI
                  g4239845
BLAST score
                  629
E value
                  8.0e-66
Match length
                  141
% identity
                   85
NCBI Description (AB015855) transcription factor TEIL [Nicotiana tabacum]
```

Seq. No. 233487

Seq. ID LIB3272-015-P1-K1-F7

Method BLASTX
NCBI GI g2979555
BLAST score 300
E value 3.0e-27
Match length 129
% identity 52

NCBI Description



```
NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]
                   233488
Seq. No.
                   LIB3272-015-P1-K1-F8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1709651
BLAST score
                   421
E value
                   2.0e-41
Match length
                   132
% identity
                   63
                   PLASTOCYANIN A PRECURSOR >gi_2117431 pir S58209
NCBI Description
                   plastocyanin a precursor - black poplar
                   >gi 929813 emb CAA90564 (Z50185) plastocyanin a [Populus
                   nigra]
Seq. No.
                   233489
                   LIB3272-015-P1-K1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g464986
BLAST score
                   531
E value
                    2.0e-54
Match length
                   98
                    99
% identity
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi 421857 pir S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana
                    >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                    enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                    ubiquitin conjugating enzyme [Arabidopsis thaliana]
                    >gi 600391 emb CAA51201 (X72626) ubiquitin conjugating
                    enzyme E2 [Arabidopsis thaliana]
                    >gi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein
                    ligase UBC9 [Arabidopsis thaliana]
                    233490
Seq. No.
Seq. ID
                   LIB3272-015-P1-K1-G4
                   BLASTX
Method
NCBI GI
                    g2462762
BLAST score
                    354
                    1.0e-33
E value
                   128
Match length
% identity
                    58
NCBI Description
                   (AC002292) Highly similar to auxin-induced protein
                    (aldo/keto reductase family) [Arabidopsis thaliana]
                    233491
Seq. No.
                    LIB3272-015-P1-K1-G7
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1173256
BLAST score
                    616
                    3.0e-64
E value
Match length
                    140
% identity
                    86
```

33695

40S RIBOSOMAL PROTEIN S4 >gi\_629496\_pir\_\_S45026 ribosomal protein S4 - upland cotton >gi\_488739\_emb\_CAA55882\_ (X79300) ribosomal protein, small subunit 4e (RS4e)

NCBI Description

mays]



## [Gossypium hirsutum]

```
Seq. No.
                   233492
Seq. ID
                   LIB3272-015-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g730450
                   360
BLAST score
E value
                   2.0e-34
Match length
                   94
                   72
% identity
                   60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B)
NCBI Description
                   >gi_480649_pir__S37134 cold-induced protein BnC24B - rape
>gi_398922_emb_CAA80343_ (Z22620) cold induced protein
                   (BnC24B) [Brassica napus]
Seq. No.
                   233493
Seq. ID
                   LIB3272-015-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   g1143511
BLAST score
                   760
E value
                   3.0e-81
Match length
                   140
% identity
                   98
                   (Z47076) Ser/Thr protein phosphatase homologous to PPX
NCBI Description
                   [Malus domestica] >gi_1586034_prf__2202340A Ser/Thr protein
                   phosphatase [Malus domestica]
                   233494
Seq. No.
Seq. ID
                   LIB3272-015-P1-K1-H10
Method
                   BLASTX
NCBI GI
                   g2194120
BLAST score
                   144
E value
                   5.0e-09
Match length
                   125
                   37
% identity
NCBI Description (AC002062) No definition line found [Arabidopsis thaliana]
                   233495
Seq. No.
Seq. ID
                   LIB3272-015-P1-K1-H11
                   BLASTX
Method
NCBI GI
                   g3212869
BLAST score
                   531
E value
                   2.0e-54
Match length
                   113
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
                   233496
Seq. No.
Seq. ID
                   LIB3272-015-P1-K1-H12
                   BLASTX
Method
NCBI GI
                   g902584
BLAST score
                   505
E value
                   2.0e-51
Match length
                   113
% identity
```

(U29159) polyubiquitin containing 7 ubiquitin monomers [Zea

Match length

% identity

79

61



```
Seq. No.
                  233497
                  LIB3272-015-P1-K1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4539292
BLAST score
                  521
E value
                  4.0e-53
Match length
                  120
% identity
NCBI Description
                 (AL049480) putative ribosomal protein S10 [Arabidopsis
                  thaliana]
Seq. No.
                  233498
Seq. ID
                  LIB3272-015-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g475048
BLAST score
                  618
E value
                  2.0e-64
Match length
                  132
% identity
                  64
NCBI Description (X72581) tonoplast intrinsic protein gamma (gamma-TIP)
                  [Arabidopsis thaliana]
Seq. No.
                  233499
Seq. ID
                  LIB3272-015-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g3860247
BLAST score
                  556
                  3.0e-57
E value
Match length
                  114
                  89
% identity
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.
                  233500
Seq. ID
                  LIB3272-015-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g2499945
BLAST score
                  490
                  2.0e-49
E value
Match length
                  141
                  67
% identity
NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
                  PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                  DECARBOXYLASE >gi_1076363_pir__S46440 orotate
                  phosphoribosyltransferase (EC 2.4.2.10) /
                  orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) -
                  Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842)
                  pyrE-F [Arabidopsis thaliana]
Seq. No.
                  233501
Seq. ID
                  LIB3272-015-P1-K1-H7
                  BLASTX
Method
NCBI GI
                  g549063
BLAST score
                  236
E value
                  6.0e-20
```



NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 233502

Seq. ID LIB3272-015-P1-K1-H9

Method BLASTX
NCBI GI g1168196
BLAST score 543
E value 9.0e-56
Match length 120
% identity 90

NCBI Description 14-3-3-LIKE PROTEIN >gi\_555974 (U15036) 14-3-3-like protein

[Pisum sativum]

Seq. No. 233503

Seq. ID LIB3272-016-P1-K1-A1

Method BLASTX
NCBI GI g3868758
BLAST score 263
E value 6.0e-23
Match length 76
% identity 79

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 233504

Seq. ID LIB3272-016-P1-K1-A11

Method BLASTX
NCBI GI g167367
BLAST score 380
E value 9.0e-37
Match length 92
% identity 80

NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 233505

Seq. ID LIB3272-016-P1-K1-A2

Method BLASTX
NCBI GI g3128209
BLAST score 282
E value 3.0e-25
Match length 78
% identity 69

NCBI Description (AC004077) unknown protein [Arabidopsis thaliana]

Seq. No. 233506

Seq. ID LIB3272-016-P1-K1-A3

Method BLASTX
NCBI GI g115492
BLAST score 521
E value 3.0e-53
Match length 107
% identity 50

NCBI Description CALMODULIN-RELATED PROTEIN >gi\_169205 (M80831)

calmodulin-related protein [Petunia hybrida]



```
233507
Seq. No.
                  LIB3272-016-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g543905
BLAST score
                  455
                  1.0e-45
E value
Match length
                  107
% identity
                  82
                  BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi 347459 (L22162)
NCBI Description
                  brassinosteroid-regulated protein [Glycine max]
                  233508
Seq. No.
Seq. ID
                  LIB3272-016-P1-K1-A5
                  BLASTX
Method
                  g543905
NCBI GI
                  177
BLAST score
                  6.0e-13
E value
                  73
Match length
                  49
% identity
NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi 347459 (L22162)
                  brassinosteroid-regulated protein [Glycine max]
Seq. No.
                  233509
Seq. ID
                  LIB3272-016-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  ·q464444
                  271
BLAST score
                  5.0e-24
E value
Match length
                  75
                  73
% identity
NCBI Description PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
                  COMPLEX 30 KD SUBUNIT) >gi_541889_pir__S39900 proteasome -
                  Arabidopsis thaliana >gi 166830 (M98495) proteasome
                  [Arabidopsis thaliana]
Seq. No.
                  233510
                  LIB3272-016-P1-K1-A9
Seq. ID
                BLASTX
Method
                  q4580467
NCBI GI
BLAST score
                  170
E value
                  4.0e-12
Match length
                  102
                  52
% identity
NCBI Description (AC006081) putative protein phosphatase; similar to protein
                  phosphatase 2C from Mesembryanthemum [Arabidopsis thaliana]
                  233511
Seq. No.
Seq. ID
                  LIB3272-016-P1-K1-B1
                  BLASTX
Method
NCBI GI
                  q4191785
BLAST score
                  259
                  2.0e-22
E value
```

87 Match length % identity

NCBI Description (AC005917) putative hydrolase [Arabidopsis thaliana]

Seq. No. 233512



```
LIB3272-016-P1-K1-B12
Seq. ID
                  BLASTX
Method
                  g602292
NCBI GI
                  317
BLAST score
                  2.0e-29
E value
                  126
Match length
                  54
% identity
                  (U17987) RCH2 protein [Brassica napus]
NCBI Description
Seq. No.
                  233513
                  LIB3272-016-P1-K1-B3
Seq. ID
                  BLASTX
Method
                  g1170747
NCBI GI
                  278
BLAST score
                   9.0e-25
E value
                  56
Match length
                   100
% identity
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
                   (M88324) late embryogenesis-abundant protein [\overline{G}ossypium]
                  hirsutum] >gi 167347 (M37697) Lea5-A late
                   embryogenesis-abundant protein [Gossypium hirsutum]
                   233514
Seq. No.
                  LIB3272-016-P1-K1-B5
Seq. ID
Method
                   BLASTX
                   q4406780
NCBI GI
                   298
BLAST score
                   4.0e-27
E value
Match length
                   116
                   91
% identity
NCBI Description (AC006532) putative multispanning membrane protein
                   [Arabidopsis thaliana]
Seq. No.
                   233515
Seq. ID
                  LIB3272-016-P1-K1-B7
                  BLASTX
Method
NCBI GI
                   g945039
BLAST score
                   576
E value
                   1.0e-59
                   127
Match length
                   85
% identity
NCBI Description (U25027) phosphatidylinositol-specific phospholipase C
                   [Glycine max]
                   233516
Seq. No.
Seq. ID
                   LIB3272-016-P1-K1-B8
                   BLASTX
Method
                   q3694872
NCBI GI
BLAST score
                   429
                   2.0e-42
E value
                   105
Match length
% identity
                   78
```

NCBI Description (AF092547) profilin [Ricinus communis]

Seq. No. 233517

LIB3272-016-P1-K1-C10 Seq. ID

Method BLASTX



```
NCBI GI
                   q267072
BLAST score
                   161
                                                                wa.
                   3.0e-11
E value
Match length
                   66
                   52
% identity
NCBI Description TUBULIN BETA-1 CHAIN >gi 100072 pir S20868 tubulin beta-1
                   chain - garden pea >gi 20758 emb CAA38613 (X54844)
                   beta-tubulin 1 [Pisum sativum]
                   233518
Seq. No.
Seq. ID
                   LIB3272-016-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   q629483
                   309
BLAST score
                   2.0e-28
E value
Match length
                   115
                   56
% identity
NCBI Description
                  gene 1-Sc3 protein - European white birch
                   >gi 534898 emb CAA54696 (X77601) 1 Sc-3 [Betula pendula]
                   >gi 1584322 prf 2122374C allergen Bet v 1-Sc3 [Betula
                   pendula]
                   233519
Seq. No.
Seq. ID
                   LIB3272-016-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   q266945
BLAST score
                   528
E value
                   5.0e-54
Match length
                   121
% identity
                   88
NCBI Description 60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
                   >gi 100065_pir__S19978 ribosomal protein L9 - garden pea
                   >gi_20727_emb_CAA46273_ (X65155) GA [Pisum sativum]
>gi_1279645_emb_CAA65987_ (X97322) ribosomal protein L9
                   [Pisum sativum]
Seq. No.
                   233520
Seq. ID
                   LIB3272-016-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g3023847
                   523
BLAST score
E value
                   2.0e-53
Match length
                   108
% identity
                   35
NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                   PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta
                   subunit-like [Medicago sativa]
Seq. No.
                   233521
Seq. ID
                   LIB3272-016-P1-K1-C6
                   BLASTX
Method
NCBI GI
                   q2499946
```

Method BLASTX
NCBI GI g2499946
BLAST score 526
E value 8.0e-54
Match length 128
% identity 80

NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE



PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi\_747980 (U22260) UMP synthase [Nicotiana tabacum]

```
233522
Seq. No.
Seq. ID
                  LIB3272-016-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g2209384
BLAST score
                  421
                  2.0e-41
E value
Match length
                  96
% identity
NCBI Description (AF008441) glutathione reductase [Brassica rapa]
Seq. No.
                  233523
                  LIB3272-016-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1709498
BLAST score
                  490
E value
                  1.0e-49
Match length
                  107
                  82
% identity
NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                  >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis
                  thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
                  [Arabidopsis thaliana]
                  233524
Seq. No.
                  LIB3272-016-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g464365
BLAST score
                  492
E value
                  8.0e-50
Match length
                  128
% identity
                  76
NCBI Description PEROXIDASE P7 >gi 66306 pir OPNB7 peroxidase (EC 1.11.1.7)
                  - turnip
                  233525
Seq. No.
Seq. ID
                  LIB3272-016-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g3885884
BLAST score
                  449
E value
                  1.0e-44
Match length
                  101
% identity
                  86
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]
                  233526
Seq. No.
Seq. ID
                  LIB3272-016-P1-K1-D6
Method
                  BLASTX
                  g1170747
NCBI GI
BLAST score
                  285
E value
                  1.0e-25
Match length
                  70
% identity
                  81
```

33702

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEAS-A >qi 167345

Match length

% identity

127

43



(M88324) late embryogenesis-abundant protein [Gossypium hirsutum] >gi\_167347 (M37697) Lea5-A late embryogenesis-abundant protein [Gossypium hirsutum]

```
Seq. No.
Seq. ID
                   233527
                  LIB3272-016-P1-K1-E10
Method
                  BLASTX
NCBI GI
                   q3309243
BLAST score
                  609
                   1.0e-63
E value
                  127
Match length
                   91
% identity
                  (AF073507) aconitase-iron regulated protein 1 [Citrus
NCBI Description
                   limon]
                   233528
Seq. No.
                  LIB3272-016-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1449179
BLAST score
                   591
E value
                   2.0e-61
Match length
                  127
                   93
% identity
                  (D86506) N-ethylmaleimide sensitive fusion protein
NCBI Description
                   [Nicotiana tabacum]
Seq. No.
                   233529
Seq. ID
                   LIB3272-016-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   g1170747
BLAST score
                   184
                   2.0e-22
E value
Match length
                   72
% identity
                   76
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
                   (M88324) late embryogenesis-abundant protein [Gossypium
                   hirsutum] >gi 167347 (M37697) Lea5-A late
                   embryogenesis-abundant protein [Gossypium hirsutum]
Seq. No.
                   233530
Seq. ID
                   LIB3272-016-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   q4519264
BLAST score
                   630
E value
                   5.0e-66
Match length
                   128
% identity
NCBI Description (AB024277) vacuolar H+-ATPase B subunit [Citrus unshiu]
                   233531
Seq. No.
                   LIB3272-016-P1-K1-E4
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1848212
BLAST score
                   591
E value
                   2.0e-61
```



```
NCBI Description
                  (Y11209) protein disulfide-isomerase precursor [Nicotiana
                   tabacum]
Seq. No.
                   233532
Seq. ID
                   LIB3272-016-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   q1777386
BLAST score
                   194
E value
                   7.0e-15
Match length
                   119
% identity
NCBI Description
                  (U39301) caffeic acid O-methyltransferase [Pinus taeda]
                   233533
Seq. No.
Seq. ID
                   LIB3272-016-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   g1709498
BLAST score
                   495
E value
                   3.0e-50
Match length
                   107
                   83
% identity
NCBI Description
                   OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                   >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis
                   thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
                   [Arabidopsis thaliana]
Seq. No.
                   233534
Seq. ID
                   LIB3272-016-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   g1149569
BLAST score
                   598
E value
                   3.0e-62
Match length
                   127
% identity
                   87
NCBI Description (Z50851) HD-zip [Arabidopsis thaliana]
Seq. No.
                   233535
Seq. ID
                   LIB3272-016-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   g3135254
BLAST score
                   443
                   4.0e-44
E value
Match length
                   126
% identity
                   66
NCBI Description (AC003058) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  233536
Seq. ID
                  LIB3272-016-P1-K1-F8
Method
                   BLASTX
                   q232031
                   309
                   2.0e-28
```

NCBI GI BLAST score E value Match length 113 % identity

NCBI Description ELONGATION FACTOR 1 BETA' >gi 322851 pir \$29224

translation elongation factor eEF-1 beta' chain - rice >gi\_218161\_dbj\_BAA02253 (D12821) elongation factor 1 beta'

BLAST score

Match length

E value

239

46

3.0e-20



## [Oryza sativa]

```
Seq. No.
                  233537
                  LIB3272-016-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g730558
BLAST score
                  515
E value
                  2.0e-52
Match length
                  107
                  94
% identity
                  60S RIBOSOMAL PROTEIN L34 >gi_1076636_pir__S48027 ribosomal
NCBI Description
                  protein L34 - common tobacco >gi_2129964_pir_ S48028
                  ribosomal protein L34.e, cytosolic - common tobacco
                  >gi 436030 (L27089) 60S ribosomal protein L34 [Nicotiana
                  tabacum] >gi 436032 (L27107) 60S ribosomal protein L34
                   [Nicotiana tabacum]
Seq. No.
                  233538
Seq. ID
                  LIB3272-016-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q951427
BLAST score
                  479
E value
                  3.0e-48
Match length
                  127
                  70
% identity
NCBI Description
                  (M59857) stearoyl-acyl-carrier protein desaturase [Ricinus
                  communis]
Seq. No.
                  233539
Seq. ID
                  LIB3272-016-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g2829911
BLAST score
                  400
E value
                  5.0e-39
Match length
                  119
% identity
                   39
NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]
                   233540
Seq. No.
Seq. ID
                  LIB3272-016-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g3413717
BLAST score
                  399
                  6.0e-39
E value
Match length
                  87
% identity
                  (AC004747) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3643590 (AC005395) unknown protein [Arabidopsis
                   thaliana]
Seq. No.
                   233541
Seq. ID
                  LIB3272-016-P1-K1-G9
                  BLASTX
Method
NCBI GI
                  g3319340
```



```
% identity
                   (AF077407) contains similarity to E. coli cation transport
NCBI Description
                  protein ChaC (GB:D90756) [Arabidopsis thaliana]
Seq. No.
                  233542
                  LIB3272-016-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q464981
BLAST score
                  371
E value
                   1.0e-35
Match length
                  70
                   96
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 388207 (L23762)
                  ubiquitin carrier protein [Lycopersicon esculentum]
                   233543
Seq. No.
Seq. ID
                  LIB3272-016-P1-K1-H11
Method
                  BLASTX
NCBI GI
                   q1495259
BLAST score
                   242
                   1.0e-20
E value
Match length
                   67
                   69
% identity
NCBI Description (X97826) orf04 [Arabidopsis thaliana]
                   233544
Seq. No.
Seq. ID
                   LIB3272-016-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   g4033467
                   268
BLAST score
                   1.0e-23
E value
Match length
                   76
% identity
                   42
                  ARGININE/SERINE-RICH SPLICING FACTOR RSP31
NCBI Description
                   >gi 1707366 emb CAA67798 (X99435) splicing factor
                   [Arabidopsis thaliana]
                   233545
Seq. No.
                   LIB3272-016-P1-K1-H5
Seq. ID
                   BLAŚTX
Method
NCBI GI
                   g3915031
BLAST score
                   687
                   1.0e-72
E value
Match length
                   129
% identity
                   100
*CBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
                   (STEAROYL-ACP DESATURASE) >gi 1217628 emb CAA65232
                   (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase
                   [Gossypium hirsutum]
                   233546
Seq. No.
Seq. ID
                   LIB3272-016-P1-K1-H6
```

Method BLASTX NCBI GI q2792297 BLAST score 235 E value 1.0e-19



```
Match length
% identity
                  58
                 (AF039183) GAST-like gene product [Fragaria x ananassa]
NCBI Description
                  233547
Seq. No.
Seq. ID
                  LIB3272-016-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g1245182
BLAST score
                  461
                  3.0e-46
E value
Match length
                  110
                  77
% identity
NCBI Description
                 (U49398) sterol delta-7 reductase [Arabidopsis thaliana]
                  233548
Seq. No.
Seq. ID
                  LIB3272-017-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g4263776
BLAST score
                  326
E value
                  3.0e-30
Match length
                  142
% identity
                  55
                  (AC006068) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4510390 gb AAD21478.1 (AC007017) unknown protein
                  [Arabidopsis thaliana]
                  233549
Seq. No.
                  LIB3272-017-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g462195
BLAST score
                  434
E value
                  5.0e-43
                  90
Match length
% identity
                  93
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi 100682 pir S21636 GOS2 protein - rice
                  >gi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                  >gi 3789950 (AF094774) translation initiation factor [Oryza
                  satīva]
Seq. No.
                  233550
Seq. ID
                  LIB3272-017-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q1717949
BLAST score
                  314
                  6.0e-29
E value
                  74
Match length
                  77
% identity
NCBI Description
                  UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 1
                  PRECURSOR (RIESKE IRON-SULFUR PROTEIN 1) (RISP1)
```

>gi 100375 pir B41607 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein precursor - common tobacco (fragment) >gi 170322 (M77225) Rieske Fe-S protein

[Nicotiana tabacum]

Seq. No. 233551

Seq. ID LIB3272-017-P1-K1-A9



```
Method
                    BLASTX
NCBI GI
                    q2739168
BLAST score
                    493
E value
                    7.0e-50
Match length
                   135
                    67
% identity
NCBI Description
                    (AF032386) aldose-1-epimerase-like protein [Nicotiana
                   tabacum]
                   233552
Seq. No.
Seq. ID
                   LIB3272-017-P1-K1-B1
Method
                   BLASTX
NCBI GI
                    q586076
BLAST score
                    654
E value
                    9.0e-69
Match length
                    122
                    98
% identity
                   TUBULIN BETA-1 CHAIN >gi_486734_pir__S35142 tubulin beta chain - white lupine >gi_402636_emb_CAA49736_ (X70184) Beta
NCBI Description
                   tubulin 1 [Lupinus albus]
                    233553
Seq. No.
Seq. ID
                   LIB3272-017-P1-K1-B10
Method
                   BLASTX
NCBI GI
                    g3901014
BLAST score
                    217
E value
                    1.0e-17
Match length
                    56
% identity
                    71
NCBI Description
                   (AJ130886) metallothionein-like protein class II [Fagus
                    sylvatica]
                    233554
Seq. No.
                    LIB3272-017-P1-K1-B11
Seq. ID
Method
                    BLASTX
NCBI GI
                    g729672
BLAST score
                    153
                    2.0e-21
E value
Match length
                    94
                    59
% identity
NCBI Description HISTONE H2A >gi 323111 pir A45564 histone 2A - Plasmodium
                    falciparum >gi 160319 (M86865) H2A [Plasmodium falciparum]
                    233555
Seq. No.
Seq. ID
                    LIB3272-017-P1-K1-B4
                    {\tt BLASTX}
Method
                    q3687243
NCBI GI
BLAST score
                    245
                    8.0e-21
E value
Match length
                    61
                    79
% identity
                   (AC005169) putative ribosomal protein [Arabidopsis
NCBI Description
                    thaliana]
```

Seq. ID LIB3272-017-P1-K1-B6 Method BLASTX

233556

Seq. No.

E value

Match length

2.0e-69

139



```
NCBI GI
                   g121953
BLAST score
                   185
E value
                   9.0e-14
Match length
                   42
                   88
% identity
                   HISTONE H1 >gi_81905_pir__S00033 histone H1.b - garden pea
NCBI Description
                   >gi 20762 emb \overline{\text{CAA29123}} \overline{\text{(X05636)}} H1 histone (AA 1-263)
                   [Pisum sativum]
                   233557
Seq. No.
Seq. ID
                   LIB3272-017-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   q3868758
BLAST score
                   435
E value
                   6.0e-47
Match length
                   138
                   62
% identity
NCBI Description
                   (D89802) elongation factor 1B gamma [Oryza sativa]
Seq. No.
                   233558
                   LIB3272-017-P1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2739168
BLAST score
                   337
E value
                   1.0e-31
Match length
                   123
% identity
                   56
                   (AF032386) aldose-1-epimerase-like protein [Nicotiana
NCBI Description
                   tabacum]
Seq. No.
                   233559
                   LIB3272-017-P1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3395441
BLAST score
                   366
E value
                   5.0e-35
                   84
Match length
% identity
                   81
                  (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   233560
                   LIB3272-017-P1-K1-C2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1841870
BLAST score
                   328
E value
                   1.0e-30
                   81
Match length
                   78
% identity
                  (U87222) elongation factor 1-beta [Pimpinella brachycarpa]
NCBI Description
Seq. No.
                   233561
Seq. ID
                   LIB3272-017-P1-K1-C3
                   BLASTX
Method
NCBI GI
                   g2828296
BLAST score
                   660
```



```
% identity
NCBI Description (AL021687) RNase L inhibitor [Arabidopsis thaliana]
Seq. No.
                  233562
                  LIB3272-017-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q441457
BLAST score
                  634
E value
                  2.0e-66
Match length
                  119
% identity
                  98
                  (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                  esculentum]
Seq. No.
                  233563
                  LIB3272-017-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4105798
BLAST score
                  93
E value
                  5.0e-09
Match length
                  58
                   59
% identity
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]
Seq. No.
                  233564
                  LIB3272-017-P1-K1-C6-
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3901014
                  235
BLAST score
E value
                  1.0e-19
                  55
Match length
                  76
% identity
                  (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                  sylvatica]
                   233565
Seq. No.
Seq. ID
                  LIB3272-017-P1-K1-C7
                  BLASTX
Method
NCBI GI
                  g2909783
BLAST score
                  413
                  1.0e-40
E value
                  138
Match length
% identity
                   63
NCBI Description
                  (AF020289) MgATP-energized glutathione S-conjugate pump
                   [Arabidopsis thaliana]
                   233566
Seq. No.
Seq. ID
                  LIB3272-017-P1-K1-D1
                  BLASTX
Method
NCBI GI
                  g3747050
                   425
BLAST score
                   6.0e-42
E value
                   106
Match length
% identity
                   77
NCBI Description
                 (AF093540) ribosomal protein L26 [Zea mays]
```

Seq. No. 233567



```
LIB3272-017-P1-K1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1684857
BLAST score
                  623
                  4.0e-65
E value
Match length
                  126
% identity
                  40
NCBI Description
                  (U77940) polyubiquitin [Phaseolus vulgaris]
Seq. No.
                  233568
                  LIB3272-017-P1-K1-D11
Seq. ID
                  BLASTX
Method
                  q3080440
NCBI GI
BLAST score
                  151
                  8.0e-10
E value
Match length
                  53
% identity
                  58
                 (AL022605) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  233569
Seq. No.
                  LIB3272-017-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI .
                  q2160166
                  332
BLAST score
E value
                  5.0e-31
                  131
Match length
% identity
                  57
                 (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  233570
                  LIB3272-017-P1-K1-D5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g267131
BLAST score
                  186
E value
                  7.0e-14
                  86
Match length
                  16
% identity
                  NUCLEOLYSIN TIAR (TIA-1 RELATED PROTEIN)
NCBI Description
                  >qi 423120 pir A46174 RNA-binding protein TIAR - human
                  >gi 189310 (M96954) nucleolysin TIAR [Homo sapiens]
                  >gi_4507499_ref_NP_003243.1 pTIAL1 TIA1 cytotoxic
                  granule-associated RNA-binding protein-like
Seq. No.
                  233571
Seq. ID
                  LIB3272-017-P1-K1-D6
                  BLASTX
Method
NCBI GI
                  q4056469
BLAST score
                  581
                  3.0e-60
E value
Match length
                  113
% identity
                  (AC005990) Strong similarity to gb M95166 ADP-ribosylation
NCBI Description
                  factor from Arabidopsis thaliana. ESTs gb Z25826,
```

gb Z25043 come from t

gb R90191, gb N65697, gb AA713150, gb T463 $\overline{3}$ 2, gb AA040967,

gb AA712956, gb T46403, gb T46050, gb AI100391 and



Seq. No. 233572

Seq. ID LIB3272-017-P1-K1-D7

Method BLASTX
NCBI GI g4039014
BLAST score 373
E value 8.0e-36
Match length 134
% identity 52

NCBI Description (AF037338) cleft lip and palate transmembrane protein 1 [Homo sapiens] >gi 4063033 (AF037339) cleft lip and palate

transmembrane protein 1 [Homo sapiens]

 $>gi_4502897\_ref_NP_001285.1\_pCLPTM1\_$  cleft lip and palate

associated transmembrane protein

Seq. No. 233573

Seq. ID LIB3272-017-P1-K1-D8

Method BLASTX
NCBI GI g3687243
BLAST score 245
E value 8.0e-21
Match length 61
% identity 79

NCBI Description (AC005169) putative ribosomal protein [Arabidopsis

thaliana]

Seq. No. 233574

Seq. ID LIB3272-017-P1-K1-D9

Method BLASTX
NCBI GI g119350
BLAST score 369
E value 1.0e-35
Match length 85
% identity 87

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi\_81608\_pir\_\_JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi 16271 emb CAA41114 (X58107) enolase

[Arabidopsis thaliana]

Seq. No. 233575

Seq. ID LIB3272-017-P1-K1-E10

Method BLASTX
NCBI GI g3834321
BLAST score 549
E value 2.0e-56
Match length 133
% identity 84

NCBI Description (AC005679) Strong similarity to F13P17.9 gi 3337356

transport protein SEC61 alpha subunit homolog from Arabidopsis thaliana BAC gb\_AC004481. [Arabidopsis

thaliana]

Seq. No. 233576

Seq. ID LIB3272-017-P1-K1-E4

Method BLASTX NCBI GI g3901014 BLAST score 235

E value

Match length

% identity

1.0e-57

139

79



```
1.0e-19
E value
Match length
                  55
                  76
% identity
                  (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                  sylvatica]
Seq. No.
                  233577
                  LIB3272-017-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2507421
                  492
BLAST score
                  9.0e-50
E value
Match length
                  103
% identity
                  91
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi 1800277
NCBI Description
                  (U81042) translation initiation factor [Arabidopsis
                  thaliana] >gi 4490709 emb CAB38843.1 (AL035680)
                  translation initiation factor [Arabidopsis thaliana]
                  233578
Seq. No.
Seq. ID
                  LIB3272-017-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  q2244734
BLAST score
                  706
                  7.0e-75
E value
Match length
                  138
                  100
% identity
NCBI Description (D88414) actin [Gossypium hirsutum]
                  233579
Seq. No.
                  LIB3272-017-P1-K1-F1
Seq. ID
                  BLASTX
Method
                  q4538911
NCBI GI
BLAST score
                  296
                  8.0e-27
E value
                  136
Match length
% identity
                  48
NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]
                  233580
Seq. No.
                  LIB3272-017-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4150974
BLAST score
                  366
E value
                  5.0e-35
Match length
                  93
% identity
                  70
NCBI Description (AJ224331) cystatin [Castanea sativa]
                  233581
Seq. No.
                  LIB3272-017-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q167367
BLAST score
                  559
```



```
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                    233582
Seq. No.
Seq. ID
                    LIB3272-017-P1-K1-F2
Method
                    BLASTX
NCBI GI
                    g3377843
BLAST score
                    435
E value
                    4.0e-43
Match length
                    122
 % identity
                    73
NCBI Description (AF076274) contains similarity to rat p47 protein
                    (GB:AB002086) [Arabidopsis thaliana]
 Seq. No.
                    233583
                    LIB3272-017-P1-K1-F4
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2088651
BLAST score
                    384
E value
                    3.0e-37
Match length
                    128
 % identity
                    70
NCBI Description (AF002109) hypersensitivity-related gene 201 isolog
                    [Arabidopsis thaliana]
Seq. No.
                    233584
                    LIB3272-017-P1-K1-F5
Seq. ID
Method
                    BLASTX
NCBI GI
                    g120669
BLAST score
                    513
E value
                    3.0e-52
Match length
                    102
 % identity
                    93
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                    >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                    >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
                    3-phosphate dehydrogenase [Magnolia liliiflora]
 Seq. No.
                    233585
 Seq. ID
                    LIB3272-017-P1-K1-F6
 Method
                    BLASTX
 NCBI GI
                    g3759184
 BLAST score
                    339
E value
                    8.0e-32
Match length
                    122
 % identity
                    54
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
                    233586
 Seq. No.
 Seq. ID
                    LIB3272-017-P1-K1-F7
Method
                    BLASTX
NCBI GI
                    g2499945
 BLAST score
                    412
 E value
                    2.0e-40
Match length
                    122
 % identity
                    64
```

NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE



PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi\_1076363\_pir\_\_S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) / orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi\_443818\_emb\_CAA50686\_ (X71842) pyrE-F [Arabidopsis thaliana]

 Seq. No.
 233587

 Seq. ID
 LIB3272-017-P1-K1-F9

 Method
 BLASTX

 NCBI GI
 g3738257

 BLAST score
 474

 E value
 1.0e-47

 Match length
 100

% identity 93
NCBI Description (AB018410) cytosolic phosphoglycerate kinase 1 [Populus

nigra]

Seq. No. 233588

Seq. ID LIB3272-017-P1-K1-G1

Method BLASTX
NCBI GI g68200
BLAST score 404
E value 2.0e-39
Match length 104
% identity 81

NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) precursor,

chloroplast - spinach >gi\_22633\_emb\_CAA47293\_ (X66814)
fructose-bisphosphate aldolase [Spinacia oleracea]

Seq. No. 233589

Seq. ID LIB3272-017-P1-K1-G10

Method BLASTX
NCBI GI g1709498
BLAST score 540
E value 2.0e-55
Match length 129
% identity 78

NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR

>gi\_1362001\_pir\_\_S57524 osmotin precursor - Arabidopsis
thaliana >gi\_887390\_emb\_CAA61411\_ (X89008) osmotin

[Arabidopsis thaliana]

Seq. No. 233590

Seq. ID LIB3272-017-P1-K1-G11

Method BLASTX
NCBI GI g2245060
BLAST score 266
E value 3.0e-23
Match length 80

% identity 64

NCBI Description (Z97342) allergen homolog [Arabidopsis thaliana]

Seq. No. 233591

Seq. ID LIB3272-017-P1-K1-G2

Method BLASTX NCBI GI g508304



```
BLAST score
E value
                   8.0e-17
Match length
                  75
% identity
                   57
NCBI Description (L22305) corC [Medicago sativa]
                  233592
Seq. No.
                  LIB3272-017-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2281631
BLAST score
                  287
E value
                   1.0e-25
Match length
                   132
                   52
% identity
                  (AF003096) AP2 domain containing protein RAP2.3
NCBI Description
                   [Arabidopsis thaliana]
                   233593
Seq. No.
                  LIB3272-017-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4164473
BLAST score
                   165
E value
                   1.0e-11
Match length
                   52
                   63
% identity
                  (AF061157) negatively light-regulated protein [Vernicia
NCBI Description
                   fordii]
Seq. No.
                   233594
Seq. ID
                   LIB3272-017-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g586076
BLAST score
                   649
E value
                   3.0e-68
Match length
                   121
% identity
                   98
                  TUBULIN BETA-1 CHAIN >qi 486734 pir S35142 tubulin beta
NCBI Description
                   chain - white lupine >gi 402636 emb CAA49736 (X70184) Beta
                   tubulin 1 [Lupinus albus]
                   233595
Seq. No.
Seq. ID
                   LIB3272-017-P1-K1-G7
                   \mathtt{BLASTX}
Method
NCBI GI
                   g533084
```

BLAST score 229 7.0e-19 E value 49 Match length 88 % identity

NCBI Description (U07597) delta-9 stearoyl-acyl carrier protein desaturase

precursor [Thunbergia alata]

233596 Seq. No.

LIB3272-017-P1-K1-G8 Seq. ID

Method BLASTX NCBI GI g4572674 BLAST score 267 2.0e-23 E value



```
Match length
                  75
% identity
                  (AC006954) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  233597
                  LIB3272-017-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1724102
BLAST score
                  498
E value
                  2.0e-50
Match length
                  113
% identity
                   (U79766) S-adenosyl-L-homocystein hydrolase; SAH
NCBI Description
                   [Mesembryanthemum crystallinum]
Seq. No.
                  233598
                  LIB3272-017-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3800951
BLAST score
                  180
E value
                   3.0e-13
Match length
                  86
% identity
                   43
                  (AF100657) No definition line found [Caenorhabditis
NCBI Description
                  elegans]
Seq. No.
                   233599
                  LIB3272-017-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g508304
BLAST score
                   215
E value
                   3.0e-17
                   73
Match length
% identity
                   60
NCBI Description (L22305) corC [Medicago sativa]
                   233600
Seq. No.
Seq. ID
                   LIB3272-017-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g3334147
BLAST score
                   484
                   8.0e-49
E value
                   136
Match length
                   71
% identity
                  ENDOCHITINASE 1 PRECURSOR >gi 1469788 (U60197) class I
NCBI Description
                   chitinase [Gossypium hirsutum]
                   233601
Seq. No.
Seq. ID
                   LIB3272-017-P1-K1-H6
                   BLASTX
Method
NCBI GI
                   g3451075
                   370
BLAST score
E value
                   2.0e-35
Match length
                   103
                   64
% identity
```

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

E value

Match length

% identity

8.0e-76

144



```
233602
Seq. No.
Seq. ID
                  LIB3272-017-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q2088652
BLAST score
                  507
                   2.0e-51
E value
Match length
                  122
% identity
                   76
                   (AF002109) 26S proteasome regulatory subunit S12 isolog
NCBI Description
                   [Arabidopsis thaliana] >gi 2351376 (U54561) translation
                   initiation factor eIF2 p47 subunit homolog [Arabidopsis
                   thaliana]
Seq. No.
                   233603
Seq. ID
                  LIB3272-018-P1-K1-A1
Method
                  BLASTX
NCBI GI
                   g114682
BLAST score
                   476
E value
                   7.0e-48
Match length
                  145
% identity
                   67
NCBI Description
                  ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
                   (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)
                   >gi_100471_pir__A35227 H+-transporting ATP synthase (EC
                   3.6.1.34) gamma chain precursor, mitochondrial - sweet
                   potato >qi 168270 (J05397) F-1-ATPase delta subunit
                   precursor (EC 3.6.1.3) [Ipomoea batatas]
Seq. No.
                   233604
                   LIB3272-018-P1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g475048
BLAST score
                   589
E value
                   4.0e-61
Match length
                   132
% identity
                   89
                  (X72581) tonoplast intrinsic protein gamma (gamma-TIP)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   233605
Seq. ID
                   LIB3272-018-P1-K1-A11
                   {\tt BLASTX}
Method
NCBI GI
                   g2564237
BLAST score
                   402
E value
                   8.0e-44
Match length
                   114
                   77
% identity
NCBI Description (Y10112) omega-6 desaturase [Gossypium hirsutum]
Seq. No.
                   233606
                   LIB3272-018-P1-K1-A12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2791834
BLAST score
                   694
```



```
(AF041463) elongation factor 1-alpha [Manihot esculenta]
NCBI Description
Seq. No.
                  233607
                  LIB3272-018-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4056488
BLAST score
                  236
E value
                  9.0e-20
Match length
                  71
                  63
% identity
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]
                  233608
Seq. No.
Seq. ID
                  LIB3272-018-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g285741
BLAST score
                  429
E value
                  2.0e-42
Match length
                  146
% identity
                   59
NCBI Description (D14550) EDGP precursor [Daucus carota]
Seq. No.
                  233609
Seq. ID
                  LIB3272-018-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  q602076
BLAST score
                  345
E value
                   1.0e-32
Match length
                  105
% identity
                   16
NCBI Description (X77456) pentameric polyubiquitin [Nicotiana tabacum]
Seq. No.
                   233610
Seq. ID
                  LIB3272-018-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  q3242075
BLAST score
                  707
E value
                   5.0e-75
                  141
Match length
                   96
% identity
                  (Z97059) S-adenosyl-L-homocysteine hydrolase [Arabidopsis
NCBI Description
                   thaliana]
                   233611
Seq. No.
Seq. ID
                  LIB3272-018-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g2997684
BLAST score
                   327
E value
                   2.0e-30
Match length
                  108
                   63
% identity
                  (AF053302) putative transcriptional co-activator
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   233612
                  LIB3272-018-P1-K1-B11
Seq. ID
```

33719

BLASTX

Method



```
NCBI GI
                   q508304
BLAST score
                   216
                   2.0e-17
E value
Match length
                   75
                   59
% identity
                  (L22305) corC [Medicago sativa]
NCBI Description
                   233613
Seq. No.
Seq. ID
                   LIB3272-018-P1-K1-B12
                   BLASTX
Method
NCBI GI
                   q3901014
                   235
BLAST score
                   1.0e-19
E value
Match length
                   55
% identity
                   76
NCBI Description
                  (AJ130886) metallothionein-like protein class II [Fagus
                   sylvatica]
                   233614
Seq. No.
Seq. ID
                   LIB3272-018-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   q2507442
BLAST score
                   166
E value
                   4.0e-12
Match length
                   42
% identity
                   74
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   >gi 1419685 emb CAA67207 (X98618) TCTP-like protein
                   [Medicago sativa]
Seq. No.
                   233615
                   LIB3272-018-P1-K1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1944403
BLAST score
                   468
E value
                   6.0e-47
Match length
                   127
                   73
% identity
NCBI Description (D86590) cinnamyl alcohol dehydrogenase [Zinnia elegans]
Seq. No.
                   233616
                   LIB3272-018-P1-K1-B4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2695711
BLAST score
                   526
E value
                   1.0e-53
Match length
                   118
                   81
% identity
NCBI Description (AJ001370) cytochome b5 [Olea europaea]
Seq. No.
                   233617
                   LIB3272-018-P1-K1-B5
Seq. ID
```

BLASTX Method NCBI GI g3176691 BLAST score 395 E value 2.0e-38 121 Match length



```
% identity
                  (AC003671) Contains homology to serine/threonine protein
NCBI Description
                  kinase gb X99618 from Mycobacterium tuberculosis. ESTs
                  gb F14403, gb F14404, and gb_N96730 come from this gene.
                  [Arabidopsis thaliana]
                  233618
Seq. No.
                  LIB3272-018-P1-K1-B7
Seq. ID
                  BLASTX
Method
                  g4262174
NCBI GI
                  236
BLAST score
                  2.0e-20
E value
                  50
Match length
                  80
% identity
                  (AC005508) 9058 [Arabidopsis thaliana]
NCBI Description
                  233619
Seq. No.
                  LIB3272-018-P1-K1-B8
Seq. ID
                  BLASTX
Method
                   g3694872
NCBI GI
                   384
BLAST score
                   2.0e - 37
E value
                   80
Match length
                   88
% identity
NCBI Description - (AF092547) profilin [Ricinus communis]
                   233620
Seq. No.
                   LIB3272-018-P1-K1-B9
Seq. ID
                   BLASTX
Method
                   q2677828
NCBI GI
                   456
BLAST score
                   1.0e-45
E value
                   118
Match length
                   70
% identity
NCBI Description (U93166) cysteine protease [Prunus armeniaca]
                   233621
Seq. No.
                   LIB3272-018-P1-K1-C1
Seq. ID
                   BLASTX
Method
                   q2459417
NCBI GI
                   382
BLAST score
E value
                   7.0e-37
                   143
Match length
                   56
 % identity
                  (AC002332) putative pre-mRNA splicing factor PRP19
NCBI Description
                   [Arabidopsis thaliana]
 Seq. No.
                   233622
                   LIB3272-018-P1-K1-C11
 Seq. ID
                   BLASTX
 Method
                   q1665867
 NCBI GI
```

Method BLASTX
NCBI GI g1665867
BLAST score 456
E value 1.0e-45
Match length 117
% identity 70

NCBI Description (Y09123) aspartic proteinase [Centaurea calcitrapa]



```
233623
Seq. No.
                  LIB3272-018-P1-K1-C12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4098321
                  639
BLAST score
                  4.0e-67
E value
                  124
Match length
                  98
% identity
NCBI Description
                  (U76745) beta-tubulin 2 [Triticum aestivum]
                  233624
Seq. No.
                  LIB3272-018-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244750
BLAST score
                  710
                  2.0e-75
E value
Match length
                  139
% identity
                  98
                  (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
NCBI Description
                  >gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                   [Arabidopsis thaliana]
                  233625
Seq. No.
                  LIB3272-018-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1361983
                   405
BLAST score
                   1.0e-39
E value
                   124
Match length
                   62
% identity
                  ARP protein - Arabidopsis thaliana >gi 886434 emb CAA89858
NCBI Description
                   (Z49776) ARP protein [Arabidopsis thaliana]
                   233626
Seq. No.
Seq. ID
                  LIB3272-018-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   q100525
                   599
BLAST score
E value
                   3.0e-62
Match length
                   123
% identity
                   25
                  ubiquitin precursor UbB2 - common sunflower (fragment)
NCBI Description
                   >qi 18803 emb CAA40323 (X57003) polyubiquitin protein
                   [Helianthus annuus]
Seq. No.
                   233627
                   LIB3272-018-P1-K1-C9
Seq. ID
                   BLASTX
Method
                   g119640
NCBI GI
BLAST score
                   165
                   2.0e-11
E value
                   96
Match length
                   40
% identity
                   1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN
NCBI Description
```

33722

esculentum]

E8) >gi\_82109\_pir\_\_S01642 ripening protein E8 - tomato >gi 19199 emb CAA31789 (X13437) E8 protein [Lycopersicon



```
233628
Seq. No.
                  LIB3272-018-P1-K1-D1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2677828
BLAST score
                  197
E value
                  3.0e-15
Match length
                  121
% identity
                  40
                  (U93166) cysteine protease [Prunus armeniaca]
NCBI Description
                  233629
Seq. No.
                  LIB3272-018-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129495
BLAST score
                  269
E value
                  1.0e-23
Match length
                  54
                  89
% identity
                  fiber protein E6 (clone SIE6-2A) - sea-island cotton
NCBI Description
                  >gi 1000088 (U30507) E6 [Gossypium barbadense] >gi_1000090
                   (U30508) E6 [Gossypium barbadense]
Seq. No.
                  233630
                  LIB3272-018-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3068809
BLAST score
                  297
E value
                   4.0e-27
Match length
                  81
                  75
% identity
NCBI Description (AF059295) Skp1 homolog [Arabidopsis thaliana]
Seq. No.
                  233631
                  LIB3272-018-P1-K1-D12
Seq. ID
Method
                  BLASTX
                   q4454097
NCBI GI
BLAST score
                   316
                   4.0e-29
E value
Match length
                   83
                   75
% identity
NCBI Description (X85206) hybrid proline-rich protein [Catharanthus roseus]
                   233632
Seq. No.
Seq. ID
                   LIB3272-018-P1-K1-D2
Method
                  BLASTX
                   g1710585
NCBI GI
BLAST score
                   111
                   5.0e-09
E value
                   65
Match length
                   58
% identity
NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN PO >gi_1143507 emb CAA63786_
                   (X93587) PO ribosomal protein [Lupinus luteus]
```

Seq. ID LIB3272-018-P1-K1-D3

Method BLASTX



```
g1170247
   NCBI GI
                      520
   BLAST score
                      5.0e-53
   E value
                      122
   Match length
                      71
   % identity
   NCBI Description HEVEIN-LIKE PROTEIN PRECURSOR >gi_407248 (U01880)
                      pre-hevein-like protein [Arabidopsis thaliana]
                      233634
   Seq. No.
                      LIB3272-018-P1-K1-D5
   Seq. ID
                      BLASTX
   Method
                      g1107526
   NCBI GI
                      569
   BLAST score
                      8.0e-59
   E value
                      138
   Match length
                      80
   % identity
   NCBI Description (X87931) SIEP1L protein [Beta vulgaris]
                      233635
   Seq. No.
                      LIB3272-018-P1-K1-D7
   Seq. ID
                      BLASTX
   Method
                      g2792297
   NCBI GI
                      261
   BLAST score
                      1.0e-22
   E value
                      77
   Match length
                      58
    % identity
    NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa]
                      233636
    Seq. No.
                      LIB3272-018-P1-K1-D8
    Seq. ID
                      BLASTX
    Method
                      g3309243
    NCBI GI
    BLAST score
                      611
    E value
                      1.0e-63
                      124
    Match length
    % identity
                      (AF073507) aconitase-iron regulated protein 1 [Citrus
    NCBI Description
                      limon]
                       233637
    Seq. No.
                      LIB3272-018-P1-K1-D9
    Seq. ID
    Method
                       BLASTX
                       g1657948
    NCBI GI
                       283
    BLAST score
                       2.0e-25
    E value
                       56
    Match length
% identity
    NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
    Seq. No.
                       233638
                       LIB3272-018-P1-K1-E11
    Seq. ID
    Method
                       BLASTX
                       g4185515
    NCBI GI
                       239
    BLAST score
                       2.0e-20
    E value
                       78
    Match length
```

63

% identity

Seq. ID





```
(AF102824) actin depolymerizing factor 6 [Arabidopsis
NCBI Description
                  thaliana]
                                                        ur : -
Seq. No.
                  233639
                  LIB3272-018-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3892056
BLAST score
                  274
E value
                  2.0e-24
                  72
Match length
                  76
% identity
                  (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]
NCBI Description
                  233640
Seq. No.
Seq. ID
                  LIB3272-018-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  q1839188
BLAST score
                  459
                  7.0e-46
E value
Match length
                  102
% identity
                  84
NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]
                  233641
Seq. No.
                  LIB3272-018-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539545
BLAST score
                  685
                  2.0e-72
E value
                  135
Match length
% identity
                  98
NCBI Description (Y16644) PRCI [Nicotiana tabacum]
                  233642
Seq. No.
Seq. ID
                  LIB3272-018-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g1699024
BLAST score
                  410
E value
                   3.0e-40
Match length
                  116
% identity
                   66
                  (U78866) gene1000 [Arabidopsis thaliana] >gi 1699057
NCBI Description
                   (U78870) unknown [Arabidopsis thaliana]
                   233643
Seq. No.
Seq. ID
                  LIB3272-018-P1-K1-E8
Method
                  BLASTX
NCBI GI
                   g3885328
                  208
BLAST score
E value
                   2.0e-16
Match length
                  126
                   33
% identity
                  (AC005623) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   233644
```

33725

LIB3272-018-P1-K1-E9



BLASTX Method q2462758 NCBI GI 377 BLAST score E value 3.0e - 36126 Match length % identity NCBI Description thaliana]

(AC002292) putative RNA-binding protein [Arabidopsis

233645 Seq. No.

LIB3272-018-P1-K1-F11 Seq. ID

Method BLASTX NCBI GI g3482967 BLAST score 250 8.0e-22 E value 58 Match length 81 % identity

(AL031369) Protein phosphatase 2C-like protein [Arabidopsis NCBI Description

thaliana] >gi 4559345 gb AAD23006.1\_AC006585\_1 (AC006585)

protein phosphatase 2C [Arabidopsis thaliana]

233646 Seq. No.

LIB3272-018-P1-K1-F2 Seq. ID

BLASTX Method g1351411 NCBI GI 502 BLAST score E value 6.0e-51 122 Match length 75 % identity

VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) (PROTEINASE B) NCBI Description

>gi\_1076553\_pir\_\_S49175 cysteine proteinase precursor spring vetch >gi\_2129906\_pir\_\_S68984 cysteine proteinase
precursor - spring vetch >gi\_510358\_emb\_CAA84383\_ (Z34899)

cysteine proteinase [Vicia sativa]

Seq. No. 233647

Seq. ID LIB3272-018-P1-K1-F4

BLASTX Method NCBI GI g2191150 BLAST score 166 1.0e-11 E value Match length 67 63 % identity

(AF007269) similar to mitochondrial carrier family NCBI Description

[Arabidopsis thaliana]

Seq. No. 233648

LIB3272-018-P1-K1-G5 Seq. ID

Method BLASTX q2462748 NCBI GI 591 BLAST score E value 2.0e-61 122 Match length 93 % identity

(AC002292) putative Clathrin Coat Assembly protein NCBI Description

[Arabidopsis thaliana]



```
233649
Seq. No.
                  LIB3272-018-P1-K1-G7
Seq. ID
Method
                  BLASTX
                  g1168727
NCBI GI
BLAST score
                  336
                  4.0e-39
E value
                  113
Match length
                  70
% identity
NCBI Description
                  CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD)
                  >gi_474300_dbj_BAA03099_ (D13991) cinnamyl alcohol
                  dehydrogenase [Aralia cordata] >gi 745086 prf 2015401A
                  cinnamoyl alcohol dehydrogenase [Aralia cordata]
                  233650
Seq. No.
Seq. ID
                  LIB3272-018-P1-K1-H1
                  BLASTX
Method
                  g119350
NCBI GI
BLAST score
                  519
                  6.0e-53
E value
Match length
                  112
                  89
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi 81608 pir JQ1187
                  phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                   thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
                   [Arabidopsis thaliana]
                  233651
Seq. No.
                  LIB3272-018-P1-K1-H11
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3355624
BLAST score
                   410
                   3.0e-42
E value
Match length
                   99
                   86
% identity
                  (AJ000241) partial sequence, homology to protein
NCBI Description
                   phospatases [Hordeum vulgare]
                   233652
Seq. No.
Seq. ID
                  LIB3272-018-P1-K1-H2
Method
                   BLASTX
                   g4490728
NCBI GI
                   298
BLAST score
                   5.0e-27
E value
                   92
Match length
% identity
                   60
                  (AL035709) putative protein [Arabidopsis thaliana]
NCBI Description
                   233653
Seq. No.
Seq. ID
                   LIB3272-018-P1-K1-H5
                   BLASTX
Method
```

Method BLASTX
NCBI GI g2129758
BLAST score 225
E value 1.0e-18
Match length 81
% identity 58

NCBI Description ubiquitin conjugating enzyme E2 protein - Arabidopsis

NCBI Description



```
thaliana >qi 992704 (U33757) UBC7 [Arabidopsis thaliana]
```

```
233654
Seq. No.
Seq. ID
                  LIB3272-018-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g2078350
                  159
BLAST score
                  8.0e-11
E value
Match length
                  77
% identity
                   48
NCBI Description (U95923) transaldolase [Solanum tuberosum]
                  233655
Seq. No.
                  LIB3272-018-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q456568
BLAST score
                  165
E value
                   1.0e-11
                   47
Match length
                   66
% identity
NCBI Description (L29077) ubiquitin conjugating enzyme [Pisum sativum]
                   233656
Seq. No.
Seq. ID
                  LIB3272-018-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   q4056469
BLAST score
                   508
E value
                   6.0e-68
Match length
                   141
                   97
% identity
                   (ACO05990) Strong similarity to gb_M95166 ADP-ribosylation
NCBI Description
                   factor from Arabidopsis thaliana. ESTs gb Z25826,
                   gb R90191, gb N65697, gb AA713150, gb_T46332, gb_AA040967,
                   gb AA712956, gb T46403, gb T46050, gb AI100391 and
                   gb\_Z25043 come \overline{f}rom t
                   233657
Seq. No.
                   LIB3272-019-P1-K1-A1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3641312
BLAST score
                   545
                   5.0e-56
E value
                   121
Match length
                   84
% identity
NCBI Description (AF087412) AJH2 [Arabidopsis thaliana]
                   233658
Seq. No.
                   LIB3272-019-P1-K1-A10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3334147
BLAST score
                   535
                   6.0e-55
E value
Match length
                   121
                   83
% identity
                  ENDOCHITINASE 1 PRECURSOR >gi 1469788 (U60197) class I
```

chitinase [Gossypium hirsutum]



```
233659
Seq. No.
Seq. ID
                  LIB3272-019-P1-K1-A11
                  BLASTX
Method
NCBI GI
                  q231675
BLAST score
                  315
                  2.0e-29
E value
                  66
Match length
                  85
% identity
                  CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi_282955_pir__S23525
NCBI Description
                  cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - common
                  tobacco >gi_19839_emb_CAA44216_ (X62343) cinnamyl-alcohol
                  dehydrogenase [Nicotiana tabacum]
                  233660
Seq. No.
                  LIB3272-019-P1-K1-A2
Seq. ID
Method
                  BLASTX
                  g2811025
NCBI GI
BLAST score
                  262
                  8.0e-23
E value
                  83
Match length
                  63
% identity
                  ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607_
NCBI Description
                  (AB002695) aspartic endopeptidase [Cucurbita pepo]
Seq. No.
                  233661
                  LIB3272-019-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2493131
BLAST score
                  547
E value
                  3.0e-56
Match length
                  114
% identity
                  96
                  VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B
NCBI Description
                  SUBUNIT) >gi_167108 (L11862) vacuolar ATPase B subunit
                   [Hordeum vulgare]
Seq. No.
                  233662
Seq. ID
                  LIB3272-019-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g3320379
BLAST score
                  614
E value
                  4.0e-64
Match length
                  134
% identity
                  90
                  (AF014375) putative JUN kinase activation domain binding
NCBI Description
                  protein [Medicago sativa]
                  233663
Seq. No.
                  LIB3272-019-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q417103
BLAST score
                  466
E value
                  9.0e-47
Match length
                  111
                  89
% identity
```

H3.3-like protein - Arabidopsis thaliana

NCBI Description HISTONE H3.2, MINOR >gi 282871 pir S24346 histone



>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563 (U09458) histone H3.2 [Medicago sativa] >gi 488567 ( $\overline{\text{U}}$ 09460) histone H3.2 [Medicago sativa] >gi 488569 (U09461) histone H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2 [Medicago sativa] >gi\_488577 (U09465) histone H3.2 [Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445\_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi\_3273350\_dbj\_BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AF093633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_ (AL035708) Histon H3 [Arabidopsis thaliana]

```
Seq. No.
                  233664
Seq. ID
                  LIB3272-019-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g119937
BLAST score
                  360
E value
                  2.0e-34
Match length
                  112
                  63
% identity
NCBI Description FERREDOXIN I PRECURSOR >gi 65741 pir FESP1 ferredoxin
```

233665

[2Fe-2S] I precursor - spinach >gi\_170109 (M35660)

ferredoxin I precursor [Spinacia oleracea]

>gi 227453 prf 1704156A ferredoxin I [Spinacia oleracea]

```
LIB3272-019-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1703375
BLAST score
                   558
E value
                   2.0e-57
Match length
                   109
```

99 % identity ADP-RIBOSYLATION FACTOR 1 >gi 965483 dbj BAA08259 (D45420) NCBI Description

DcARF1 [Daucus carota]

Seq. No. 233666

LIB3272-019-P1-K1-B5 Seq. ID

Method BLASTX NCBI GI g232031 BLAST score 183 E value 1.0e-13 Match length 79 49 % identity

NCBI Description ELONGATION FACTOR 1 BETA' >gi 322851 pir S29224

translation elongation factor eEF-1 beta chain - rice >gi 218161 dbj BAA02253 (D12821) elongation factor 1 beta'

[Oryza sativa]

Seq. No. 233667

Seq. ID LIB3272-019-P1-K1-B6



Method BLASTX NCBI GI g3377797 BLAST score 539 E value 3.0e-55 Match length 132 % identity 80 NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

 Seq. No.
 233668

 Seq. ID
 LIB3272-019-P1-K1-C1

 Method
 BLASTX

 NCBI GI
 g4538911

 BLAST score
 562

 E value
 5.0e-58

E value 5.0e-58
Match length 137
% identity 78

NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No. 233669

\*Seq. ID LIB3272-019-P1-K1-C10

Method BLASTX
NCBI GI g114420
BLAST score 223
E value 3.0e-18
Match length 78
% identity 59

NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR

>gi\_100882\_pir\_\_S11491 H+-transporting ATP synthase (EC

3.6.1.34) beta chain, mitochondrial - maize

>gi\_22173\_emb\_CAA38140\_ (X54233) ATPase F1 subunit protein
[Zea mays] >gi\_897618 (M36087) F-1-ATPase subunit 2 [Zea

mays]

Seq. No. 233670

Seq. ID LIB3272-019-P1-K1-C12

Method BLASTX
NCBI GI g3810848
BLAST score 329
E value 1.0e-30
Match length 110
% identity 52

NCBI Description (AL032684) putative autophagy protein [Schizosaccharomyces

pombe]

Seq. No. 233671

Seq. ID LIB3272-019-P1-K1-C6

Method BLASTX
NCBI GI g1213069
BLAST score 458
E value 9.0e-46
Match length 88
% identity 95

NCBI Description (X79675) dihydrodipicolinate synthase [Nicotiana tabacum]



```
233672
Seq. No.
                  LIB3272-019-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3860255
BLAST score
                  164
                  5.0e-22
E value
                  130
Match length
% identity
                  49
NCBI Description (AC005824) hypothetical protein [Arabidopsis thaliana]
                  233673
Seq. No.
                  LIB3272-019-P1-K1-D12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4406775
                  226
BLAST score
                  1.0e-18
E value
Match length
                  98
                   45
% identity
NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]
                  233674
Seq. No.
Seq. ID
                  LIB3272-019-P1-K1-D3
Method
                  BLASTX
                   q3603456
NCBI GI
BLAST score
                   542
                   8.0e-56
E value
Match length
                   108
                   30
% identity
NCBI Description (AF088848) polyubiquitin [Capsicum chinense]
                   233675
Seq. No.
                   LIB3272-019-P1-K1-D4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3810848
BLAST score
                   273
                   3.0e-24
E value
                   92
Match length
% identity
                   51
                  (AL032684) putative autophagy protein [Schizosaccharomyces
NCBI Description
                   pombe]
                   233676
Seq. No.
                   LIB3272-019-P1-K1-D5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g417745
BLAST score
                   684
                   3.0e-72
E value
                   135
Match length
                   97
% identity
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                   HYDROLASE) (ADOHCYASE) >gi 170773 (L11872)
                   S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]
```

33732

233677

BLASTX

LIB3272-019-P1-K1-D7

Seq. No. Seq. ID

Method



```
q2879867
NCBI GI
BLAST score
                  412
                  2.0e-40
E value
Match length
                  115
% identity
                  68
                  (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces
NCBI Description
                  pombe]
Seq. No.
                  233678
                  LIB3272-019-P1-K1-D8
Seq. ID
Method
                  BLASTX
                  q1928981
NCBI GI
                  505
BLAST score
E value
                  2.0e-51
Match length
                  112
% identity
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                  oleracea var. botrytis]
Seq. No.
                  233679
                  LIB3272-019-P1-K1-D9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3901018
BLAST score
                  294
E value
                  2.0e-26
Match length
                  109
% identity
                   56
                  (AJ130889) stress and pathogenesis-related protein [Fagus
NCBI Description
                  sylvatica]
Seq. No.
                   233680
Seq. ID
                  LIB3272-019-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g2618721
BLAST score
                  164
E value
                   2.0e-11
                   77
Match length
                   55
% identity
NCBI Description (U49072) IAA16 [Arabidopsis thaliana]
Seq. No.
                   233681
                   LIB3272-019-P1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2833386
BLAST score
                   347
E value
                   8.0e-33
Match length
                   91
                   79
% identity
                  RIBULOSE-PHOSPHATE 3-EPIMERASE PRECURSOR
NCBI Description
                   (PENTOSE-5-PHOSPHATE 3-EPIMERASE) (PPE) (RPE) (R5P3E)
                   >qi 2129493 pir S62724 ribulose-phosphate 3-epimerase (EC
                   5.1.3.1) precursor - spinach >gi_1162980 (L42328)
                   ribulose-5-phosphate 3-epimerase [Spinacia oleracea]
                   >gi 3264788 (AF070941) ribulose-phosphate 3-epimerase
```

[Spinacia oleracea] >gi\_1587969\_prf\_\_2207382A D-ribulose-5-phosphate 3-epimerase [Sorghum bicolor]

NCBI Description

233687

Seq. No.



```
233682
Seq. No.
Seq. ID
                  LIB3272-019-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g1928981
                  594
BLAST score
                   9.0e-62
E value
Match length
                  125
% identity
                   63
                   (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                  oleracea var. botrytis]
                  233683
Seq. No.
Seq. ID
                  LIB3272-019-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g1408471
BLAST score
                   511
                   6.0e-52
E value
Match length
                  114
% identity
                   81
                   (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                   thaliana] >gi 3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
                   233684
Seq. No.
                  LIB3272-019-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1703446
BLAST score
                   440
E value
                   1.0e-43
                   134
Match length
                   68
% identity
                  L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
NCBI Description
                   >gi 1076292 pir S53127 asparaginase - Arabidopsis thaliana
                   >gi 735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis
                   thaliana]
                   233685
Seq. No.
Seq. ID
                  LIB3272-019-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   g2792297
BLAST score
                   243
E value
                   1.0e-20
Match length
                   77
% identity
                   56
                  (AF039183) GAST-like gene product [Fragaria x ananassa]
NCBI Description
                   233686
Seq. No.
Seq. ID
                   LIB3272-019-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   q4580389
BLAST score
                   200
E value
                   1.0e-15
Match length
                   119
% identity
```

(AC007171) unknown protein [Arabidopsis thaliana]



```
LIB3272-019-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170747
BLAST score
                  324
E value
                  4.0e-30
Match length
                  78
                  82
% identity
NCBI Description
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
                   (M88324) late embryogenesis-abundant protein [Gossypium
                  hirsutum] >gi_167347 (M37697) Lea5-A late
                  embryogenesis-abundant protein [Gossypium hirsutum]
Seq. No.
                  233688
Seq. ID
                  LIB3272-019-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g1170747
BLAST score
                  280
E value
                  6.0e-25
Match length
                  68
% identity
                  84
NCBI Description
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
                   (M88324) late embryogenesis-abundant protein [Gossypium
                  hirsutum] >gi_167347 (M37697) Lea5-A late
                  embryogenesis-abundant protein [Gossypium hirsutum]
Seq. No.
                  233689
Seq. ID
                  LIB3272-019-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g3719211
BLAST score
                  499
E value
                  1.0e-50
Match length
                  120
% identity
                  82
NCBI Description (U97021) UIP2 [Arabidopsis thaliana]
Seq. No.
                  233690
Seq. ID
                  LIB3272-019-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g3021506
BLAST score
                  257
                  2.0e-22
E value
Match length
                  65
                  72
% identity
NCBI Description
                  (X96727) isocitrate dehydrogenase (NAD+) [Nicotiana
                  tabacum]
                  233691
Seq. No.
Seq. ID
                  LIB3272-019-P1-K1-G3
```

Method BLASTX
NCBI GI g1694976
BLAST score 350
E value 4.0e-33
Match length 76
% identity 84

NCBI Description (Y09482) HMG1 [Arabidopsis thaliana]

>gi\_2832361\_emb\_CAA74402\_ (Y14073) HMG protein [Arabidopsis

thaliana]



```
233692
Seq. No.
Seq. ID
                   LIB3272-019-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   g1063415
                   371
BLAST score
                   1.0e-35
E value
                   106
Match length
% identity
                   70
NCBI Description (L40948) K+ channel protein [Arabidopsis thaliana]
Seq. No.
                   233693
                   LIB3272-019-P1-K1-G9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1166450
BLAST score
                   257
                   3.0e-22
E value
                   56
Match length
                   82
% identity
                   (X95262) Tfm5 [Lycopersicon esculentum]
NCBI Description
                   233694
Seq. No.
Seq. ID
                   LIB3272-019-P1-K1-H1
Method
                   BLASTX
NCBI GI
                   g464846
BLAST score
                   404
                   2.0e-39
E value
                   79
Match length
% identity
                   94
                   TUBULIN ALPHA-6 CHAIN >gi_322880_pir__S28983 tubulin alpha-6 chain - maize >gi_22158_emb_CAA44863_ (X63178)
NCBI Description
                   alpha-tubulin #6 [Zea mays]
Seq. No.
                   233695
Seq. ID
                   LIB3272-019-P1-K1-H11
Method
                   BLASTX
                   g3372233
NCBI GI
BLAST score
                   414
                   1.0e-40
E value
                   102
Match length
% identity
                    75
                   (AF019248) RNA polymerase I, II and III 24.3 kDa subunit
NCBI Description
                    [Arabidopsis thaliana]
                   233696
Seq. No.
Seq. ID
                   LIB3272-019-P1-K1-H12
Method
                   BLASTX
                   g3023419
NCBI GI
                   497
BLAST score
E value
                   2.0e-50
Match length
                   102
                   93
% identity
                   CAFFEOYL-COA O-METHYLTRANSFERASE (TRANS-CAFFEOYL-COA
NCBI Description
```

3-O-METHYLTRANSFERASE) (CCOAMT) (CCOAOMT)

O-methyltransferase [Eucalyptus gunnii]

>gi 1934859 emb CAA72911 (Y12228) caffeoyl-CoA



```
233697
Seq. No.
                  LIB3272-019-P1-K1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4539296
                  284
BLAST score
                   2.0e-25
E value
                   107
Match length
                   50
% identity
                   (AL049480) putative pathogenesis-related protein
NCBI Description
                   [Arabidopsis thaliana]
                   233698
Seq. No.
                  LIB3272-019-P1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1657374
BLAST score
                   414
                   1.0e-40
E value
                   89
Match length
                   87
% identity
                   (X96853) endo-beta-1,4-glucanase [Prunus persica]
NCBI Description
                   >gi_1657380_emb_CAA65600_ (X96856) endo-beta-1,4-glucanase
                   [Prunus persica]
                   233699
Seq. No.
                   LIB3272-019-P1-K1-H5
Seq. ID
                   BLASTX
Method
                   q974294
NCBI GI
                   294
BLAST score
                   1.0e-26
E value
                   102
Match length
% identity
                   56
NCBI Description
                  (U31309) LP6 [Pinus taeda]
                   233700
Seq. No.
                   LIB3272-019-P1-K1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q529353
BLAST score
                   122
                   1.0e-10
E value
Match length
                   67
                   57
% identity
                  (U12757) diphenol oxidase [Acer pseudoplatanus]
NCBI Description
                   233701
Seq. No.
                   LIB3272-020-P1-K1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3393062
                   295
BLAST score
                   7.0e-27
E value
                   82
Match length
% identity
                   62
                  (Y17386) putative In2.1 protein [Triticum aestivum]
NCBI Description
                   233702
Seq. No.
                   LIB3272-020-P1-K1-A10
Seq. ID
```

33737

BLASTX

g1657948

Method NCBI GI



```
BLAST score
E value
                       1.0e-42
   Match length
                       98
   % identity
                      (U73466) MipC [Mesembryanthemum crystallinum]
   NCBI Description
                       233703
   Seq. No.
                      LIB3272-020-P1-K1-A11
   Seq. ID
   Method
                      BLASTX
   NCBI GI
                       g1107526
   BLAST score
                       319
   E value
                       1.0e-29
   Match length
                       88
                       68
   % identity
                      (X87931) SIEP1L protein [Beta vulgaris]
   NCBI Description
                       233704
   Seq. No.
                       LIB3272-020-P1-K1-A12
   Seq. ID
   Method
                       BLASTX
                       g4337040
   NCBI GI
   BLAST score
                       383
                       5.0e-37
   E value
   Match length
                       90
                       82
   % identity
                       (AF124159) molybdopterin synthase sulphurylase [Arabidopsis
   NCBI Description
                       thaliana] >gi_4337042_gb_AAD18051_ (AF124160) molybdopterin synthase sulphurylase [Arabidopsis thaliana]
                       233705
   Seq. No.
                       LIB3272-020-P1-K1-A2
   Seq. ID
   Method
                       BLASTX
                       q464987
   NCBI GI
   BLAST score
                       249
                       1.0e-21
   E value
   Match length
                       53
   % identity
                       UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN
   NCBI Description
                       LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10)
                       >gi_421858_pir_S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana
                       >gi 297878 emb CAA78715_ (Z14991) ubiquitin conjugating
                       enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin
                       conjugating enzyme [Arabidopsis thaliana]
   Seq. No.
                       233706
   Seq. ID
                       LIB3272-020-P1-K1-A3
   Method
                       BLASTX
   NCBI GI
                       g2129753
                       222
   BLAST score
                       2.0e-18
   E value
                       83
   Match length
   % identity
                       59
                       threonine synthase (EC 4.2.99.2) precursor - Arabidopsis
   NCBI Description
```

[Arabidopsis thaliana]

thaliana (fragment) >gi 1448917 (L41666) threonine synthase



```
LIB3272-020-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131773
BLAST score
                  252
E value
                  6.0e-22
                  79
Match length
                  65
% identity
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
NCBI Description
                  >qi 82724 pir B30097 ribosomal protein S14 (clone MCH2) -
                  maize
                  233708
Seq. No.
Seq. ID
                  LIB3272-020-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g729273
BLAST score
                  183
                  1.0e-28
E value
                  103
Match length
% identity
                  65
                  CYPRO4 PROTEIN >gi 322804_pir__S28592 cypro4 protein -
NCBI Description
                  cardoon >gi 17959 emb CAA49354 (X69672) cypro4 [Cynara
                  cardunculus]
                  233709
Seq. No.
                  LIB3272-020-P1-K1-A7
Seq. ID
                  BLASTX
Method
                  g3319340
NCBI GI
BLAST score
                  364
E value
                   4.0e-35
                  80
Match length
                  78
% identity
                  (AF077407) contains similarity to E. coli cation transport
NCBI Description
                  protein ChaC (GB:D90756) [Arabidopsis thaliana]
                  233710
Seq. No.
                  LIB3272-020-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g456568
BLAST score
                  158
                   7.0e-11
E value
                   54
Match length
                   65
% identity
NCBI Description (L29077) ubiquitin conjugating enzyme [Pisum sativum]
Seq. No.
                   233711
Seq. ID
                  LIB3272-020-P1-K1-B1
Method
                   BLASTX
                   q4538945
NCBI GI
BLAST score
                   225
                   1.0e-18
E value
                  70
Match length
% identity
NCBI Description (AL049483) putative thioredoxin [Arabidopsis thaliana]
```

Seq. ID LIB3272-020-P1-K1-B10

Method BLASTX

E value

Match length

9.0e-39

118



```
q4249388
NCBI GI
BLAST score
                  440
E value
                  1.0e-43
Match length
                  111
% identity
                  74
                   (AC005966) Similar to gb_AF025438 Opa-interacting protein
NCBI Description
                   (OIP2) from Homo sapiens. [Arabidopsis thaliana]
Seq. No.
                  233713
Seq. ID
                  LIB3272-020-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q167367
BLAST score
                  298
E value
                   4.0e-27
Match length
                  98
                   62
% identity
                  (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
Seq. No.
                  233714
Seq. ID
                  LIB3272-020-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q2129772
BLAST score
                   301
E value
                   2.0e-27
Match length
                  88
% identity
                   65
                  xyloglucan endotransqlycosylase-related protein XTR-7 -
NCBI Description
                  Arabidopsis thaliana >gi 1244760 (U43489) xyloglucan
                   endotransglycosylase-related protein [Arabidopsis thaliana]
Seq. No.
                   233715
                  LIB3272-020-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1332579
BLAST score
                   554
E value
                   4.0e-57
Match length
                  115
                   10
% identity
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
                   233716
Seq. No.
Seq. ID
                  LIB3272-020-P1-K1-B6
Method
                  BLASTX
NCBI GI
                   g2677828
BLAST score
                  194
                   1.0e-16
E value
                  122
Match length
                   42
% identity
                 (U93166) cysteine protease [Prunus armeniaca]
NCBI Description
                   233717
Seq. No.
                  LIB3272-020-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3334147
BLAST score
                   397
```



% identity, ENDOCHITINASE 1 PRECURSOR >gi 1469788 (U60197) class I NCBI Description chitinase [Gossypium hirsutum] Seq. No. 233718 LIB3272-020-P1-K1-C1 Seq. ID Method BLASTX NCBI GI g3033397 BLAST score 336 E value 2.0e-31 Match length 93 % identity 71 (AC004238) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 233719 Seq. ID LIB3272-020-P1-K1-C10 Method BLASTX NCBI GI g416758 BLAST score 162 E value 3.0e-17 Match length 85 55 % identity NCBI Description SERINE CARBOXYPEPTIDASE PRECURSOR >gi\_166674 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi 445120 prf 1908426A carboxypeptidase Y [Arabidopsis thalianal Seq. No. 233720 LIB3272-020-P1-K1-C12 Seq. ID Method BLASTX g1107526 NCBI GI BLAST score 319 E value 2.0e-29 Match length 132 % identity 55 NCBI Description (X87931) SIEP1L protein [Beta vulgaris] 233721 Seq. No. Seq. ID LIB3272-020-P1-K1-C3 Method BLASTX NCBI GI g4220446 BLAST score 486 E value 4.0e-49 Match length 130 % identity 74 NCBI Description (AC006216) Strong similarity to gi 2062155 T02004.2 mitochondrial processing peptidase alpha subunit precusor isolog from Arabidopsis thaliana BAC gb AC001645. ESTs gb Z18504 and gb AA395715 come from this gene. [Arabidopsis

thaliana]

233722 Seq. No.

Seq. ID LIB3272-020-P1-K1-C4

Method BLASTX NCBI GI g120669 BLAST score 472 E value 2.0e-47



```
Match length
% identity
                  93
NCBI Description . GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi 66014 pir DEJMG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                  >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
                  3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                  233723
Seq. ID
                  LIB3272-020-P1-K1-C5
                  BLASTX
Method
NCBI GI
                  q115492
BLAST score
                  525
E value
                  1.0e-53
Match length
                  102
% identity
                  51
NCBI Description CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)
                  calmodulin-related protein [Petunia hybrida]
Seq. No.
                  233724
                  LIB3272-020-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4490321
BLAST score
                  311
E value
                  1.0e-28
Match length
                  78
                  79
% identity
NCBI Description (AJ011604) nitrate transporter [Arabidopsis thaliana]
Seq. No.
                  233725
                  LIB3272-020-P1-K1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4454466
BLAST score
                  192
E value
                  1.0e-14
                  52
Match length
% identity
                  65
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.
                  233726
Seq. ID
                  LIB3272-020-P1-K1-D11
                  BLASTX
Method
NCBI GI
                  g3402703
BLAST score
                  159
E value
                  9.0e-11
Match length
                  116
                  33
% identity
NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  233727
                  LIB3272-020-P1-K1-D12
Seq. ID
                  BLASTX
Method
```

Method BLASTX
NCBI GI 94262154
BLAST score 448
E value 1.0e-44
Match length 129
% identity 73

33742

233733



```
(AC005275) putative protein phosphatase regulatory subunit
NCBI Description
                    [Arabidopsis thaliana]
                    233728
 Seq. No.
                    LIB3272-020-P1-K1-D2
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2257716
 BLAST score
                    454
 E value
                    2.0e-45
 Match length
                    116
 % identity
                    72
                   (U90439) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                    233729
 Seq. No.
 Seq. ID
                    LIB3272-020-P1-K1-D3
 Method
                    BLASTX
 NCBI GI
                    g2144099
 BLAST score
                    184
                    1.0e-13
 E value
 Match length
                    57
                    51
  % identity
                    Set alpha isoform - rat >gi_545263_bbs_143660 (S68589) Set
 NCBI Description
                    alpha isoform=leukemogenesis protein {alternatively
                    spliced} [rats, neonatal kidney, Peptide, 289 aa] [Rattus
                    sp.] >gi 741750 prf 2008109A set gene [Rattus norvegicus]
                    233730
 Seq. No.
                    LIB3272-020-P1-K1-D5
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1220196
 BLAST score
                    589
  E value
                    3.0e-61
 Match length
                    129
  % identity
                    89
  NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
                    233731
  Seq. No.
                    LIB3272-020-P1-K1-D6
  Seq. ID
                    BLASTX
  Method
  NCBI GI
                    g167367
  BLAST score
                    154
                    3.0e-10
  E value
                    95
  Match length
  % identity
  NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                    233732
  Seq. No.
  Seq. ID
                    LIB3272-020-P1-K1-D7
                    BLASTX
  Method
  NCBI GI
                    q3694872
  BLAST score
                    491
                    1.0e-49
  E value
                    115
 Match length
                    80
% identity
                   (AF092547) profilin [Ricinus communis]
  NCBI Description
```

33743



```
LIB3272-020-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132944
BLAST score
                  612
                  7.0e-64
E valuė
Match length
                  121
% identity
                  92
                  60S RIBOSOMAL PROTEIN L3 >gi 81658 pir JQ0772 ribosomal
NCBI Description
                  protein L3 (ARP2) - Arabidopsis thaliana >gi 806279
                  (M32655) ribosomal protein [Arabidopsis thaliana]
                  233734
Seq. No.
Seq. ID
                  LIB3272-020-P1-K1-E11
                  BLASTX
Method
NCBI GI
                  g3789799
BLAST score
                  210
E value
                  9.0e-17
Match length
                  127
% identity
NCBI Description
                  (AF060219) RCC1-like G exchanging factor RLG [Homo sapiens]
                  >gi 4557445 ref NP 001259.1 pCHC1L RCC1-like G exchanging
                  factor RLG
                  233735
Seq. No.
Seq. ID
                  LIB3272-020-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g2129987
BLAST score
                  422
E value
                  1.0e-41
                  92
Match length
                  85
% identity
NCBI Description glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) -
                  potato (fragment) >gi 755187 (U17005) glyceraldehyde
                  3-phosphate dehydrogenase [Solanum tuberosum]
                  233736
Seq. No.
                  LIB3272-020-P1-K1-E2
Seg. ID
Method
                  BLASTX
NCBI GI
                  q4263706
BLAST score
                  343
E value
                  2.0e-32
Match length
                  131
% identity
NCBI Description (AC006223) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  233737
Seq. ID
                  LIB3272-020-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g3789799
BLAST score
                  210
E value
                  9.0e-17
Match length
                  127
```

>gi 4557445 ref NP 001259.1 pCHC1L RCC1-like G exchanging

% identity

NCBI Description

(AF060219) RCC1-like G exchanging factor RLG [Homo sapiens]



Seq. ID LIB3272-020-P1-K1-E7

Method BLASTX
NCBI GI 94337040
BLAST score 344
E value 4.0e-36
Match length 95
% identity 85

NCBI Description (AF124159) molybdopterin synthase sulphurylase [Arabidopsis

 $thaliana] > gi\_4337042\_gb\_AAD18051\_ (AF124160) molybdopterin$ 

synthase sulphurylase [Arabidopsis thaliana]

Seq. No. 233739

Seq. ID LIB3272-020-P1-K1-E9

Method BLASTX
NCBI GI g3123745
BLAST score 169
E value 6.0e-12
Match length 93
% identity 39

NCBI Description (AB013447) aluminum-induced [Brassica napus]

Seq. No. 233740

Seq. ID LIB3272-020-P1-K1-F1

Method BLASTX
NCBI GI g2244979
BLAST score 221
E value 1.0e-29
Match length 126
% identity 58

NCBI Description (Z97340) similarity to enoyl-CoA hydratase [Arabidopsis

thaliana]

Seq. No. 233741

Seq. ID LIB3272-020-P1-K1-F11

Method BLASTX
NCBI GI g3687237
BLAST score 405
E value 1.0e-39
Match length 127
% identity 65

NCBI Description (AC005169) putative Cys3His zinc-finger protein

[Arabidopsis thaliana]

Seq. No. 233742

Seq. ID LIB3272-020-P1-K1-F2

Method BLASTX
NCBI GI 94406787
BLAST score 392
E value 4.0e-38
Match length 102
% identity 78

NCBI Description (AC006532) NADH dehydrogenase [Arabidopsis thaliana]

Seq. No. 233743

Seq. ID LIB3272-020-P1-K1-F4

Method BLASTX



```
NCBI GI
                  g3123745
BLAST score
                  319
E value
                  2.0e-29
Match length
                  97
                  64
% identity
NCBI Description (AB013447) aluminum-induced [Brassica napus]
                  233744
Seq. No.
Seq. ID
                  LIB3272-020-P1-K1-F5
                  BLASTX
Method
NCBI GI
                  g2078350
BLAST score
                  223
E value
                  3.0e-18
                  50
Match length
                  82
% identity
NCBI Description (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                  233745
Seq. ID
                  LIB3272-020-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g730583
BLAST score
                  244
E value
                  9.0e-21
Match length
                  114
                  48
% identity
                  60S ACIDIC RIBOSOMAL PROTEIN P2 >gi 551267.emb CAA55047
NCBI Description
                  (X78213) 60s acidic ribosomal protein P2 [Parthenium
                  argentatum]
Seq. No.
                  233746
Seq. ID
                  LIB3272-020-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g3158474
BLAST score
                  483
                  9.0e-49
E value
                  105
Match length
% identity
                  90
NCBI Description (AF067184) aquaporin 1 [Samanea saman]
                  233747
Seq. No.
                  LIB3272-020-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1174613
BLAST score
                  478
                  3.0e-66
E value
Match length
                  133
% identity
                  99
NCBI Description
                 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
                  PROTEIN HOMOLOG 1) (TBP-1) >gi 556560 dbj BAA04614
                  (D17788) rice homologue of Tat binding protein [Oryza
```

Seq. ID LIB3272-020-P1-K1-G10

sativa]

Method BLASTX NCBI GI g3334147 BLAST score 479

% identity

84



```
E value
                   3.0e-48
Match length
                  130
                  73
% identity
NCBI Description ENDOCHITINASE 1 PRECURSOR >gi 1469788 (U60197) class I
                  chitinase [Gossypium hirsutum]
                  233749
Seq. No.
Seq. ID
                  LIB3272-020-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g3659907
BLAST score
                  448
E value
                  1.0e-44
Match length
                  112
                  79
% identity
NCBI Description (AF091857) protein translation factor SUI1 homolog
                  [Pimpinella brachycarpa]
                  233750
Seq. No.
                  LIB3272-020-P1-K1-G12
Seq. ID
Method
                  BLASTX
                  q1497987
NCBI GI
BLAST score
                  240
E value
                  3.0e-20
Match length
                  129
                  40
% identity
NCBI Description (U62798) SCARECROW [Arabidopsis thaliana]
Seq. No.
                  233751
                  LIB3272-020-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3158376
BLAST score
                  485
E value
                  5.0e-49
Match length
                  129
% identity
                  75
NCBI Description (AF035385) unknown [Arabidopsis thaliana]
Seq. No.
                  233752
Seq. ID
                  LIB3272-020-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g3096931
BLAST score
                  166
E value
                  1.0e-11
Match length
                  62
% identity
                  52
                  (AL023094) putative ribosomal protein S16 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  233753
                  LIB3272-020-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1129145
BLAST score
                  551
E value
                  9.0e-57
Match length
                  134
```

NCBI Description (X75329) acetyl-CoA C-acyltransferase [Mangifera indica]

NCBI Description

233759

Seq. No.



```
Seq. No.
                  233754
Seq. ID
                  LIB3272-020-P1-K1-G6
                  BLASTX
Method
                  g2583134
NCBI GI
                  330
BLAST score
                  8.0e-31
E value
Match length
                  89
% identity
                  70
                  (ACO02387) putative proline-rich protein [Arabidopsis
NCBI Description
                  thaliana]
                  233755
Seq. No.
Seq. ID
                  LIB3272-020-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g629483
BLAST score
                  309
E value
                  2.0e-28
Match length
                  115
                   56
% identity
NCBI Description
                  gene 1-Sc3 protein - European white birch
                  >gi 534898 emb CAA54696 (X77601) 1 Sc-3 [Betula pendula]
                  >gi 158432\overline{2} prf 212237\overline{4}C allergen Bet v 1-Sc3 [Betula
                  pendula]
                  233756
Seq. No.
                  LIB3272-020-P1-K1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4098128
BLAST score
                   549
E value
                   2.0e-56
Match length
                  122
% identity
                   89
NCBI Description
                  (U73588) sucrose synthase [Gossypium hirsutum]
                  233757
Seq. No.
Seq. ID
                  LIB3272-020-P1-K1-H10
Method
                  BLASTX
NCBI GI
                   g3551954
BLAST score
                  191
E value
                   2.0e-14
Match length
                  114
% identity
NCBI Description
                  (AF082030) senescence-associated protein 5 [Hemerocallis
                  hybrid cultivar]
                  . 233758
Seq. No.
                  LIB3272-020-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4454097
BLAST score
                  273
                   4.0e-24
E value
Match length
                   66
% identity
```

33748

(X85206) hybrid proline-rich protein [Catharanthus roseus]



Seq. ID LIB3272-020-P1-K1-H4
Method BLASTX
NCBI GI q4455364

BLAST score 212 E value 4.0e-17 Match length 80 % identity 51

NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis

thaliana]

Seq. No. 233760

Seq. ID LIB3272-020-P1-K1-H8

Method BLASTX
NCBI GI g584872
BLAST score 318
E value 2.0e-29
Match length 114
% identity 49

NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi\_629475\_pir\_\_S39509

cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - Norway spruce >gi\_393443 emb\_CAA51226\_ (X72675) cinnamyl-alcohol dehydrogenase [Picea abies] >gi\_3451286 emb\_CAA05096\_ (AJ001925) cinnamyl alcohol dehydrogenase [Picea abies] >gi\_3451288\_emb\_CAA05097\_ (AJ001926) cinnamyl alcohol

dehydrogenase [Picea abies]

Seq. No. 233761

Seq. ID LIB3272-021-P1-K1-A10

Method BLASTX
NCBI GI g2511574
BLAST score 532 .
E value 2.0e-54
Match length 118
% identity 93

NCBI Description (Y13176) multicatalytic endopeptidase [Arabidopsis

thaliana] >gi\_3421075 (AF043520) 20S proteasome subunit

PAB1 [Arabidopsis thaliana]

Seq. No. 233762

Seq. ID LIB3272-021-P1-K1-A11

Method BLASTX
NCBI GI g2827559
BLAST score 156
E value 2.0e-10
Match length 42
% identity 69

NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]

>gi\_3292808\_emb\_CAA19798\_ (AL031018) putative protein

[Arabidopsis thaliana]

Seq. No. 233763

Seq. ID LIB3272-021-P1-K1-A12

Method BLASTX
NCBI GI g4456760
BLAST score 482
E value 1.0e-48
Match length 110



% identity 73
NCBI Description (AJ000692) osmotin-like protein [Quercus suber]

Seq. No. 233764

Seq. ID LIB3272-021-P1-K1-A4

Method BLASTX
NCBI GI g2829275
BLAST score 508
E value 1.0e-51
Match length 136
% identity 73

NCBI Description (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis

thaliana] >gi\_3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi 4539375 emb CAB40069.1

(AL049525) nucleoside diphosphate kinase 3 (ndpk3)

[Arabidopsis thaliana]

Seq. No. 233765

Seq. ID LIB3272-021-P1-K1-A5

Method BLASTX
NCBI GI g4263791
BLAST score 270
E value 9.0e-24
Match length 133
% identity 40

NCBI Description (AC006068) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 233766

Seq. ID LIB3272-021-P1-K1-A6

Method BLASTX
NCBI GI g729470
BLAST score 487
E value 3.0e-49
Match length 119
% identity 79

NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR

(NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)

>gi\_542089\_pir\_\_JQ2272 formate dehydrogenase (EC 1.2.1.2)
precursor, mitochondrial - potato >gi\_297798\_emb\_CAA79702\_
(Z21493) mitochondrial formate dehydrogenase precursor

[Solanum tuberosum]

Seq. No. 233767

Seq. ID LIB3272-021-P1-K1-A8

Method BLASTX
NCBI GI g3450842
BLAST score 283
E value 2.0e-25
Match length 90
% identity 59

NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza

sativa]

Seq. No. 233768

Seq. ID LIB3272-021-P1-K1-B1



```
Method
                   BLASTX
 NCBI GI
                   q2088654
 BLAST score
                   444
 E value
                   4.0e-44
 Match length
                   102
 % identity
                   84
 NCBI Description (AF002109) 60S acidic ribosomal protein P0 isolog
                   [Arabidopsis thaliana]
 Seq. No.
                   233769
 Seq. ID
                   LIB3272-021-P1-K1-B12
 Method
                   BLASTX
 NCBI GI
                   g3643609
 BLAST score
                   425
 E value
                   6.0e-42
 Match length
                   133
 % identity
                   67
 NCBI Description (AC005395) putative Cys3His zinc finger protein
                   [Arabidopsis thaliana]
                   233770
 Seq. No.
 Seq. ID
                   LIB3272-021-P1-K1-B2
Method
                   BLASTX
                   g3342913
NCBI GI
BLAST score
                   158
E value
                   1.0e-10
                   128
Match length
 % identity
                   31
 NCBI Description (AF078916) oligopeptidase B [Trypanosoma brucei brucei]
 Seq. No.
                   233771
 Seq. ID
                   LIB3272-021-P1-K1-B3
 Method
                   BLASTX
 NCBI GI
                   q3913295
 BLAST score
                   340
 E value
                   3.0e-32
 Match length
                   77
 % identity
                   88
 NCBI Description CAFFEIC ACID 3-0-METHYLTRANSFERASE
                   (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                   3-O-METHYLTRANSFERASE) (COMT) >gi_602588_emb_CAA58218_
                   (X83217) caffeic O-methyltransferase [Prunus dulcis]
 Seq. No.
                   233772
 Seq. ID
                   LIB3272-021-P1-K1-B7
 Method
                   BLASTX
 NCBI GI
                   q4426565
 BLAST score
                   165
 E value
                   2.0e-11
 Match length
                   87
 % identity
                   40
 NCBI Description (AF031483) unknown [Rattus norvegicus]
```

Seq. ID LIB3272-021-P1-K1-B8

Method BLASTX NCBI GI g2687584

33751



```
BLAST score
                  493
                  6.0e-50
E value
Match length
                  135
                  75
% identity
                  (AF033100) S-adenosylmethionine decarboxylase [Nicotiana
NCBI Description
                  tabacum]
Seq. No.
                  233774
                  LIB3272-021-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g121953
BLAST score
                  189
E value
                  3.0e-14
Match length
                  43
% identity
                  88
                  HISTONE H1 >gi 81905_pir__S00033 histone H1.b - garden pea
NCBI Description
                  >gi 20762 emb CAA29123 (X05636) H1 histone (AA 1-263)
                  [Pisum sativum]
Seq. No.
                  233775
                  LIB3272-021-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706547
BLAST score
                  395
E value
                  8.0e-40
Match length
                  127
% identity
                  66
                  GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM
NCBI Description
                  PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE)
                   ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE)
                  >gi_2129912_pir__S65077 beta-1,3-glucanase class I
                  precursor - Para rubber tree >gi 1184668 (U22147)
                  beta-1,3-glucanase [Hevea brasiliensis]
Seq. No.
                  233776
Seq. ID
                  LIB3272-021-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g3868758
BLAST score
                  410
                  3.0e-40
E value
                  77
Match length
                  94
% identity
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
Seq. No.
                  233777
Seq. ID
                  LIB3272-021-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q3694872
BLAST score
                  429
E value
                  2.0e-42
                  108
Match length
                  75
% identity
NCBI Description (AF092547) profilin [Ricinus communis]
```

LIB3272-021-P1-K1-C6 Sea. ID

Method BLASTX

Match length

% identity

134

91



```
NCBI GI
                  q2160166
BLAST score
                  483
                  1.0e-48
E value 👵
                  133
Match length
                  66
% identity
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.
                  233779
Seq. ID
                  LIB3272-021-P1-K1-C8
                  BLASTX
Method
NCBI GI
                  g3242721
BLAST score
                  372
E value
                  1.0e-35
Match length
                  111
% identity
                  60
NCBI Description (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis
                  thaliana]
Seq. No.
                  233780
Seq. ID
                  LIB3272-021-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2078350
BLAST score
                 600
E value
                  2.0e-62
                 134
Match length
                  87
% identity
NCBI Description (U95923) transaldolase [Solanum tuberosum]
                  233781
Seq. No.
Seq. ID
                  LIB3272-021-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g3043432
BLAST score
                  186
E value
                  6.0e-14
Match length
                  34
% identity
                  100
NCBI Description (AJ005348) Ubiquitin conjugating enzyme [Cicer arietinum]
                  233782
Seq. No.
Seq. ID
                  LIB3272-021-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  q543905
BLAST score
                  446
                  2.0e-44
E value
Match length
                 106
% identity
                  82
NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >qi 347459 (L22162)
                  brassinosteroid-regulated protein [Glycine max]
Seq. No.
                  233783
Seq. ID
                  LIB3272-021-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g2500354
BLAST score
                  648
E value
                  3.0e-69 ~
```

33753



NCBI Description 60S RIBOSOMAL PROTEIN L10 (EQM) >gi\_1902894\_dbj\_BAA19462\_ (AB001891) QM family protein [Solanum melongena]

Seq. No. 233784

Seq. ID LIB3272-021-P1-K1-D4

Method BLASTX
NCBI GI g4210948
BLAST score 454
E value 2.0e-45
Match length 96
% identity 91

NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No. 233785

Seq. ID LIB3272-021-P1-K1-D5

Method BLASTX
NCBI GI g3153902
BLAST score 428
E value 3.0e-42
Match length 109
% identity 79

NCBI Description (AF066076) 14-3-3-like protein [Helianthus annuus]

Seq. No. 233786

Seq. ID LIB3272-021-P1-K1-D6

Method BLASTX
NCBI GI g1928981
BLAST score 626
E value 2.0e-65
Match length 133
% identity 64

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

Seq. No. 233787

Seq. ID LIB3272-021-P1-K1-E1

Method BLASTX
NCBI GI g3858935
BLAST score 116
E value 7.0e-09
Match length 92
% identity 48

NCBI Description (AL021636) synaptobrevin-like protein [Arabidopsis

thaliana] >gi\_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis

thaliana]

Seq. No. 233788

Seq. ID LIB3272-021-P1-K1-E3

Method BLASTX
NCBI GI g3024501
BLAST score 516
E value 1.0e-52
Match length 103
% identity 97

NCBI Description RAS-RELATED PROTEIN RAB11C >gi 1370146 emb CAA98179

(Z73951) RAB11C [Lotus japonicus]

E value

Match length

% identity

7.0e-32

112 57



```
233789
Seq. No.
                  LIB3272-021-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3776559
BLAST score
                  325
                  3.0e-30
E value
Match length
                  95
% identity
                  (AC005388) Strong similarity to gene F14J9.26 gi 3482933
NCBI Description
                  cdc2 protein kinase homolog from A. thaliana BAC
                  qb AC003970. ESTs gb Z35332 and gb F19907 come from this
                  gene. [Arabidopsis thaliana]
                  233790
Seq. No.
Seq. ID
                  LIB3272-021-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  q3600058
                  328
BLAST score
E value
                  1.0e-30
Match length
                  90
                  79
% identity
NCBI Description (AF080120) similar to vacuolar ATPases [Arabidopsis
                  thaliana]
                  233791
Seq. No.
Seq. ID
                  LIB3272-021-P1-K1-E8
Method
                  BLASTX
                  g3876865
NCBI GI
BLAST score
                  158
                  1.0e-10
E value
                  122
Match length
% identity
                  36
                  (Z81534) predicted using Genefinder; cDNA EST EMBL: C08177
NCBI Description
                  comes from this gene; cDNA EST EMBL: C09822 comes from this
                  gene; cDNA EST yk359h8.5 comes from this gene; cDNA EST
                  yk374f11.5 comes from this gene; cDNA EST yk359h8.3 co
                  233792
Seq. No.
Seq. ID
                  LIB3272-021-P1-K1-F10
Method
                  BLASTX
                  q3702332
NCBI GI
BLAST score
                  390
E value
                  7.0e-38
Match length
                  108
% identity
                  68
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.
                  233793
                  LIB3272-021-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4454043
BLAST score
                  338
```

33755

NCBI Description (AL035394) putative receptor kinase [Arabidopsis thaliana]

Seq. ID

233799

LIB3272-021-P1-K1-G1



```
233794
Seq. No.
Seq. ID
                  LIB3272-021-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g113220
BLAST score
                  237
E value
                  2.0e-20
                  49
Match length
                  92
% identity
NCBI Description ACTIN 1 >gi_71640_pir__ATZM1 actin - maize
                  233795
Seq. No.
Seq. ID
                  LIB3272-021-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g167367
BLAST score
                  541
E value
                  2.0e-55
Match length
                  135
                  79
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                  233796
Seq. No.
Seq. ID
                  LIB3272-021-P1-K1-F4
                  BLASTX
Method
NCBI GI
                  g2464852
BLAST score
                  207
E value
                  2.0e-16
Match length
                  114
% identity
                  46
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
Seq. No.
                  233797
Seq. ID
                  LIB3272-021-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  q3334245
BLAST score
                  189
                  1.0e-14
E value
Match length
                  45
% identity
                  82
NCBI Description LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)
                  (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE
                  MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE)
                  >gi 2909424 emb CAA12028 (AJ224520) Glyoxalase I [Cicer
                  arietinum]
                  233798
Seq. No.
Seq. ID
                  LIB3272-021-P1-K1-F9
                  BLASTX
Method
NCBI GI
                  q2286153
BLAST score
                  526
E value
                  8.0e-54
Match length
                  106
% identity
                  99
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
```

33756



```
Method
                     BLASTX
   NCBI GI
                     g1850546
   BLAST score
                     403
   E value
                     2.0e-39
   Match length
                     103
                     79
   % identity
   NCBI Description (U88045) syntaxin related protein AtVam3p [Arabidopsis
                     thaliana]
   Seq. No.
                     233800
   Seq. ID
                     LIB3272-021-P1-K1-G10
                     BLASTX
   Method
   NCBI GI
                     g3337366
   BLAST score
                     203
   E value
                     5.0e-16
                     106
   Match length
                     23
   % identity
   NCBI Description (AC004481) unknown protein [Arabidopsis thaliana]
   Seq. No.
                     233801
   Seq. ID
                     LIB3272-021-P1-K1-G11
   Method
                     BLASTX
   NCBI GI
                     q3175990
   BLAST score
                     350
   E value
                     3.0e - 33
  Match length
                     72
                     92
   % identity
   NCBI Description (AJ005836) GDP dissociation inhibitor [Cicer arietinum]
                     233802
   Seq. No.
   Seq. ID
                     LIB3272-021-P1-K1-G12
                     {\tt BLASTX}
  Method
   NCBI GI
                     g419789
   BLAST score
                     296
   E value
                     8.0e-27
  Match length
                     86
% identity
                     67
  NCBI Description hypothetical protein - potato
   Seq. No.
                     233803
   Seq. ID
                     LIB3272-021-P1-K1-G2
   Method
                     BLASTX
   NCBI GI
                     q543867
   BLAST score
                     112
   E value
                     1.0e-11
   Match length
                     95
   % identity
                     56
   NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
                     >gi 1076684 pir A47493 H+-transporting ATP synthase (EC
                     3.6.1.34) gamma chain precursor - sweet potato
                     >gi_303626_dbj_BAA03526_ (D14699) F1-ATPase gammma subunit
                     [Ipomoea batatas]
```

Seq. ID LIB3272-021-P1-K1-G3

Method BLASTX NCBI GI g117549

33757



```
BLAST score
E value
                  1.0e-12
Match length
                  105
% identity
                  39
NCBI Description QUINONE OXIDOREDUCTASE (NADPH:QUINONE REDUCTASE)
                  (ZETA-CRYSTALLIN) >gi_65895_pir__CYGPZ zeta-crystallin /
                  quinone reductase (NADPH) (EC 1.6.-.-) - guinea pig
                  >gi 305333 (M26936) zeta-crystallin [Cavia porcellus]
Seq. No.
                  233805
Seq. ID
                  LIB3272-021-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g3687237
BLAST score
                  255
E value
                  4.0e-22
Match length
                  104
% identity
                  57
NCBI Description (AC005169) putative Cys3His zinc-finger protein
                  [Arabidopsis thaliana]
Seq. No.
                  233806
Seq. ID
                  LIB3272-021-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g3953471
BLAST score
                  328
E value
                  1.0e-30
Match length
                  75
% identity
                  81
NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]
                  233807
Seq. No.
Seq. ID
                  LIB3272-021-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g1350956
BLAST score
                  423
E value
                  1.0e-41
                  97
Match length
                  87
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)
Seq. No.
                  233808
Seq. ID
                  LIB3272-021-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g507275
BLAST score
                  177
                  7.0e-13
E value
Match length
                  103
                  39
% identity
NCBI Description (L34159) NADPH:quinone oxidoreductase/zeta crystallin [Lama
                  guanicoe]
                  233809
Seq. No.
```

Seq. ID LIB3272-021-P1-K1-H12

Method BLASTX NCBI GI q167367 BLAST score 437 2.0e-43 E value



```
Match length 116
% identity 73
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No. 233810
Seq. ID LIB3272-021-P1-K1-H3
```

Method BLASTX
NCBI GI g267082
BLAST score 559
E value 1.0e-57
Match length 106
% identity 94

NCBI Description TUBULIN BETA-8 CHAIN >gi\_320189\_pir\_\_JQ1592 tubulin beta-8 chain - Arabidopsis thaliana >gi\_166908 (M84705) beta-8

tubulin [Arabidopsis thaliana]

Seq. ID LIB3272-021-P1-K1-H4
Method BLASTX
NCBI GI g100203
BLAST score 311
E value 1.0e-28
Match length 107
% identity 60

233811

233812

Seq. No.

Seq. No.

NCBI Description cysteine proteinase (EC 3.4.22.-) precursor - tomato >gi 19195 emb CAA78403 (Z14028) pre-pro-cysteine

proteinase [Lycopersicon esculentum]

NCBI Description (AC005395) putative Cys3His zinc finger protein

[Arabidopsis thaliana]

Seq. No. 233813

Seq. ID LIB3272-021-P1-K1-H6

Method BLASTX
NCBI GI g1279588
BLAST score 411
E value 3.0e-40
Match length 117
% identity 68

NCBI Description (Z71749) glutathione S-transferase [Nicotiana

plumbaginifolia]

Seq. No. 233814

Seq. ID LIB3272-021-P1-K1-H7

Method BLASTX
NCBI GI g1702983
BLAST score 351
E value 3.0e-33
Match length 110

```
% identity
NCBI Description
                   AUXIN-REPRESSED 12.5 KD PROTEIN >qi 99855 pir S11850
                   hypothetical protein - garden strawberry
                   >gi_22573_emb_CAA36676_ (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi_927034 (L44142) auxin-repressed protein
                   [Fragaria ananassa]
Seq. No.
                   233815
                   LIB3272-021-P1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2827528
BLAST score
                   175
E value
                   1.0e-12
Match length
                   70
                   47
% identity
NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]
Seq. No.
                   233816
Seq. ID
                   LIB3272-021-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   g1002800
BLAST score
                   449
E value
                   9.0e-45
Match length
                   104
% identity -
                   76
NCBI Description (U33917) Cpm7 [Craterostigma plantagineum]
Seq. No.
                   233817
Seq. ID
                   LIB3272-022-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   g3668097
BLAST score
                   477
                   5.0e-48
E value
Match length
                   119
                   78
% identity
NCBI Description (AC004667) putative glycine cleavage system protein H
                   precursor [Arabidopsis thaliana]
Seq. No.
                   233818
                   LIB3272-022-P1-K1-A3
Seq. ID
Method
                   BLASTX
                   g992706
                   527
                   7.0e-54
                   100
```

NCBI GI BLAST score E value Match length % identity 92

NCBI Description (U33758) UBC13 [Arabidopsis thaliana]

Seq. No. 233819

Seq. ID LIB3272-022-P1-K1-A4

Method BLASTX NCBI GI g231574 BLAST score 349 E value 5.0e-33 Match length 141 % identity 55

NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)



>gi\_81837\_pir\_\_S22523 asparaginase (EC 3.5.1.1) - tree lupine (fragment) >gi\_19137\_emb\_CAA36824\_ (X52588) asparaginase [Lupinus arboreus]

Seq. No. 233820

Seq. ID LIB3272-022-P1-K1-A6

Method BLASTX NCBI GI q3334147 BLAST score 509 E value 9.0e-52 Match length 138 74 % identity

NCBI Description ENDOCHITINASE 1 PRECURSOR >gi 1469788 (U60197) class I

chitinase [Gossypium hirsutum]

Seq. No. 233821

Seq. ID LIB3272-022-P1-K1-B1

Method BLASTX NCBI GI g445613 BLAST score 386 E value 2.0e-37 Match length 120 % identity 66

NCBI Description ribosomal protein L7 [Solanum tuberosum]

233822 Seq. No.

Seq. ID LIB3272-022-P1-K1-B2

Method BLASTX NCBI GI g3694872 BLAST score 502 E value 5.0e-51118 Match length

% identity 80

NCBI Description (AF092547) profilin [Ricinus communis]

Seq. No. 233823

Seq. ID LIB3272-022-P1-K1-B5

Method BLASTX NCBI GI g1657948 BLAST score 412 E value 2.0e-40 Match length 106 % identity 79

NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]

233824 Seq. No.

Seq. ID LIB3272-022-P1-K1-B8

Method BLASTX NCBI GI q3860255 BLAST score 294 E value 1.0e-26 Match length 143

% identity

NCBI Description (AC005824) hypothetical protein [Arabidopsis thaliana]

Seq. No. 233825

Seq. ID LIB3272-022-P1-K1-B9



```
Method
                   BLASTX
NCBI GI
                   g1173256
BLAST score
                   714
                   8.0e-76
E value
Match length
                   138
                   99
% identity
                  40S RIBOSOMAL PROTEIN S4 >gi_629496_pir S45026 ribosomal
NCBI Description
                   protein S4 - upland cotton >gi 488739 emb CAA55882
                   (X79300) ribosomal protein, small subunit 4e (RS4e)
                   [Gossypium hirsutum]
                   233826
Seq. No.
                   LIB3272-022-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2980770
BLAST score
                   199
                   2.0e-15
E value
Match length
                   48
                   77
% identity
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]
                   233827
Seq. No.
                   LIB3272-022-P1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2708532
BLAST score
                   209
E value
                   4.0e-27
Match length
                   117
% identity
                   56
*NCBI Description (AF029351) putative RNA binding protein [Nicotiana tabacum]
                   233828
Seq. No.
Seq. ID
                   LIB3272-022-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g4115379
BLAST score
                   265
E value
                   4.0e-23
Match length
                   83
% identity
                  (AC005967) putative carbonyl reductase [Arabidopsis
NCBI Description
                   thaliana]
                   233829
Seq. No.
Seq. ID
                   LIB3272-022-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   g122085
                   498
BLAST score
                   2.0e-50
E value
                   119
Match length
                   85
% identity
NCBI Description HISTONE H3 >gi 81641 pir S06250 histone H3 - Arabidopsis
                   thaliana >gi_82482 pir_ S04099 histone H3 (variant H3R-21)
                   - rice >gi 1362194 pir S57626 histone H3 - maize
                   >gi 20251 emb CAA31969 (X13678) histone H3 (AA 1-136)
```

[Oryza sativa] >gi\_20253\_emb\_CAA31970\_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi\_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi\_168495 (M13378) histone H3 [Zea mays]



>gi 168497 (M13379) histone H3 [Zea mays] >gi\_168506
(M35388) histone H3 [Zea mays] >gi\_169655 (M77493) histone
H3 [Petroselinum crispum] >gi\_169657 (M77494) histone H3
[Petroselinum crispum] >gi\_169659 (M77495) histone H3
[Petroselinum crispum] >gi\_387565 (M17130) histone H3
[Arabidopsis thaliana] >gi\_387567 (M17131) histone H3
[Arabidopsis thaliana] >gi\_886738 emb\_CAA59111 (X84377)
histone 3 [Zea mays] >gi\_1040764 (M35387) histone H3
[Arabidopsis thaliana] >gi\_1314779 (U54827) histone H3
homolog [Brassica napus] >gi\_1531754 emb\_CAA57811 (X82414)
Histone H3 [Asparagus officinalis] >gi\_1667592 (U77296)
histone 3 [Oryza sativa] >gi\_3249101 (AC003114) Match to
histone H3 gene gb\_M17131 and gb\_M35387 from A. thaliana.
ESTs gb\_H76511 gb\_H76255, gb\_AA712452, gb\_N65260 and
gb\_T42306 come from this gene. [Arabidopsis thaliana]
>gi\_225459 prf\_1303352A histone H3 [Helicoverpa zea]
>gi\_225839\_prf\_1314298B histone H3 [Arabidopsis thaliana]

 Seq. No.
 233830

 Seq. ID
 LIB3272-022-P1-K1-C5

 Method
 BLASTX

 NCBI GI
 g542200

 BLAST score
 452

 E value
 4.0e-45

 Match length
 125

 % identity
 66

NCBI Description hypothetical protein - garden asparagus

>gi 452714 emb CAA54526\_ (X77320) unknown [Asparagus

officinalis]

Seq. No. 233831

Seq. ID LIB3272-022-P1-K1-C8

Method BLASTX
NCBI GI g1946355
BLAST score 171
E value 4.0e-12
Match length 58
% identity 53

NCBI Description (U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] >gi 2880040 (AC002340) maize

transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq. No. 233832

Seq. ID LIB3272-022-P1-K1-C9

Method BLASTX
NCBI GI g445613
BLAST score 423
E value 1.0e-41
Match length 128
% identity 67

NCBI Description ribosomal protein L7 [Solanum tuberosum]

Seq. No. 233833

Seq. ID LIB3272-022-P1-K1-D11

Method BLASTX
NCBI GI g2499945
BLAST score 355



```
E value
                  9.0e-34
                  112
Match length
                  62
% identity
                  URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
NCBI Description
                  PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                  DECARBOXYLASE >gi_1076363_pir__S46440 orotate
                  phosphoribosyltransferase (EC 2.4.2.10) /
                  orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) -
                  Arabidopsis thaliana >gi 443818 emb CAA50686 (X71842)
                  pyrE-F [Arabidopsis thaliana]
Seq. No.
                  233834
                  LIB3272-022-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1703375
BLAST score
                  490
E value
                  1.0e-49
Match length
                  95
% identity
                  100
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 965483 dbj BAA08259 (D45420)
                  DcARF1 [Daucus carota]
Seq. No.
                  233835
Seq. ID
                  LIB3272-022-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q3386621
BLAST score
                  592
E value
                  2.0e-61
Match length
                  126
                  92
% identity
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
Seq. No.
                  233836
Seq. ID
                  LIB3272-022-P1-K1-D4
                  BLASTX
Method
NCBI GI
                  q3738324
BLAST score
                  260
E value
                  1.0e-22
Match length
                  82
% identity
NCBI Description (AC005170) GMP synthase-like protein [Arabidopsis thaliana]
Seq. No.
                  233837
Seq. ID
                  LIB3272-022-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q1928981
BLAST score
                  474
                  1.0e-47
E value
Match length
                  114
                  77
% identity
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                  oleracea var. botrytis]
Seq. No.
                  233838
Seq. ID
                  LIB3272-022-P1-K1-D6
```

beq. ib biboz/z-ozz-fi-ki-be

Method BLASTX NCBI GI g112863



```
BLAST score
                    256
• E value
                     4.0e-22
                    74
 Match length
                    64
  % identity.
                    STYLE DEVELOPMENT-SPECIFIC PROTEIN 9612 PRECURSOR
  NCBI Description
                    >gi_100227_pir__S12209 hypothetical protein - tomato
                    >gi 19162 emb CAA38979 (X55193) 9612 [Lycopersicon
                    esculentum]
  Seq. No.
                    233839
                    LIB3272-022-P1-K1-D8
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g475048
  BLAST score
                    624
  E value
                    3.0e-65
 Match length
                    133
  % identity
                    64
                    (X72581) tonoplast intrinsic protein gamma (gamma-TIP)
  NCBI Description
                     [Arabidopsis thaliana]
                    233840
  Seq. No.
                    LIB3272-022-P1-K1-E11
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g3551247
  BLAST score
                    486
                    4.0e-49
  E value
  Match length
                    144
  % identity
                    68
  NCBI Description (AB012703) 181 [Daucus carota]
  Seq. No.
                    233841
                    LIB3272-022-P1-K1-E12
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g3329368
                    129
  BLAST score
                    3.0e-11
  E value
                    100
 Match length
                    42
  % identity
 NCBI Description (AF031244) nodulin-like protein [Arabidopsis thaliana]
  Seq. No.
                    233842
  Seq. ID
                    LIB3272-022-P1-K1-E3
  Method
                    BLASTX
  NCBI GI
                    g2791834
  BLAST score
                    333
 E value
                    7.0e-35
 Match length
                    127
                    67
  % identity
  NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta]
  Seq. No.
                    233843
                    LIB3272-022-P1-K1-E4
  Seq. ID
```

Method BLASTX NCBI GI g999542 BLAST score 354 E value 1.0e-33 104 Match length

% identity NCBI Description Spinacia oleracea > gi 999543 pdb 1GYL B Spinacia oleracea 233844 Seq. No. Seq. ID LIB3272-022-P1-K1-E5 Method BLASTX NCBI GI g417719 BLAST score 620 E value 9.0e-65 Match length 140 89 % identity NCBI Description 40S RIBOSOMAL PROTEIN S3 >gi 2144763 pir R3HUS3 ribosomal protein S3 - human >gi 23304 $\overline{2}$  bbs 42 $\overline{65}$ 9 (S42658) S3 ribosomal protein [human, colon, Peptide, 243 aa] [Homo sapiens] >gi\_555941 (U14990) ribosomal protein S3 [Homo sapiens] >gi\_555943 (U14991) ribosomal protein S3 [Homo sapiens] >gi 555945 (U14992) ribosomal protein S3 [Homo sapiens] Seq. No. 233845 Seq. ID LIB3272-022-P1-K1-E7 Method BLASTX NCBI GI g549063 BLAST score 636 E value 1.0e-66 Match length 144 % identity 83 TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) NCBI Description >gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626) 21kd polypeptide [Oryza sativa] Seq. No. 233846 Seq. ID LIB3272-022-P1-K1-E8 BLASTX

Method NCBI GI q3608139 BLAST score 353 E value 9.0e-38 Match length 141 % identity 64

NCBI Description (AC005314) putative fibrillin [Arabidopsis thaliana]

Seq. No. 233847

Seq. ID LIB3272-022-P1-K1-F1

Method BLASTX NCBI GI q441457 BLAST score 562 E value 5.0e-58Match length 109 % identity 97

NCBI Description (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon

esculentum]

Seq. No. 233848

Seq. ID LIB3272-022-P1-K1-F10

Method BLASTX NCBI GI q629483



```
BLAST score
                     2.0e-27
 E value
 Match length
                     125
 % identity
                     50
                    gene 1-Sc3 protein - European white birch
NCBI Description
                     >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula]
>gi_1584322_prf__2122374C allergen Bet v 1-Sc3 [Betula
                     pendula]
                     233849
 Seq. No.
 Seq. ID
                     LIB3272-022-P1-K1-F11
 Method
                     BLASTX
 NCBI GI
                     g2911044
 BLAST score
                     369
 E value
                     2.0e-35
 Match length
                     118
                     60
 % identity
 NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
 Seq. No.
                     233850
                     LIB3272-022-P1-K1-F2
 Seq. ID
 Method
                     BLASTX
                     g1766046
 NCBI GI
 BLAST score
                     341
                     3.0e - 32
 E value
 Match length
                     72
  % identity
 NCBI Description (U81993) NAD+ dependent isocitrate dehydrogenase subunit 1
                     [Arabidopsis thaliana]
 Seq. No.
                     233851
                     LIB3272-022-P1-K1-F3
 Seq. ID
 Method
                     BLASTX
 NCBI GI
                     g1638842
 BLAST score
                     390
                     7.0e-38
 E value
                     93
 Match length
                     78
  % identity
 NCBI Description (Z49697) cysteine proteinase inhibitor [Ricinus communis]
                     233852
  Seq. No.
  Seq. ID
                     LIB3272-022-P1-K1-F4
                     {\tt BLASTX}
 Method
  NCBI GI
                     g629858
                     545
  BLAST score
  E value
                     5.0e-56
                     126
 Match length
                     82
  % identity
  NCBI Description protein kinase C inhibitor - maize
                     233853
  Seq. No.
  Seq. ID
                     LIB3272-022-P1-K1-F5
```

Method BLASTX
NCBI GI g3980393
BLAST score 384
E value 4.0e-37
Match length 110



```
% identity
NCBI Description
                  (AC004561) putative glutathione S-transferase [Arabidopsiş
                  thaliana]
                  233854
Seq. No.
Seq. ID
                  LIB3272-022-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q3980393
BLAST score
                  210
E value
                   6.0e-27
Match length
                  110
% identity
                  53
NCBI Description (AC004561) putative glutathione S-transferase [Arabidopsis
                  thaliana]
                  233855
Seq. No.
Seq. ID
                  LIB3272-022-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g3885515
BLAST score
                   443
E value
                  5.0e-44
Match length
                  101
% identity
                  81
NCBI Description (AF084202) similar to ribosomal protein S26 [Medicago
                  sativa]
                  233856
Séq. No.
Seq. ID
                  LIB3272-022-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g3759184
BLAST score
                  235
                  1.0e-19
E value
Match length
                  82
% identity
                   60
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
                   233857
Seq. ID
                  LIB3272-022-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g1931639
BLAST score
                  237
E value
                   5.0e-20
Match length
                   97
% identity
NCBI Description (U95973) lysophospholipase isolog [Arabidopsis thaliana]
Seq. No.
                   233858
                  LIB3272-022-P1-K1-G5
Seq. ID
Method
                  BLASTX
                  g4406816
NCBI GI
BLAST score
                  624
```

E value 3.0e-65 Match length 123 93 % identity

NCBI Description (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

233859 Seq. No.



```
Seq. ID
                  LIB3272-022-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g2961372
BLAST score
                  341
E value
                  2.0e-32
Match length
                  71
% identity
                  87
NCBI Description
                  (AL022141) putative ribosomal protein L8 [Arabidopsis
                  thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal
                  protein L2 [Arabidopsis thaliana]
Seq. No.
                  233860
Seq. ID
                  LIB3272-022-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g3319355
BLAST score
                  174
E value
                  2.0e-20
Match length
                  103
                  58
% identity
NCBI Description (AF077407) similar to chaperonin containing TCP-1 complex
                  gamma chain [Arabidopsis thaliana]
Seq. No.
                  233861
Seq. ID
                  LIB3272-022-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q2792297
BLAST score
                  261
E value
                  1.0e-22 ~
                  77
Match length
% identity
                  58
NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa]
Seq. No.
                  233862
Seq. ID
                  LIB3272-022-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  q167367
BLAST score
                  401
E value
                  6.0e-40
Match length
                  117
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                  233863
Seq. ID
                  LIB3272-022-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g1709498
BLAST score
                  418
E value
                  3.0e-41
Match length
                  104
% identity
                  75
NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                  >gi 1362001 pir S57524 osmotin precursor - Arabidopsis
                  thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
                  [Arabidopsis thaliana]
```

Seq. No. 233864

Seq. ID LIB3272-022-P1-K1-H11

Seq. No.

Seq. ID

233869

LIB3272-023-P1-K1-A3



```
Method
                   BLASTX
NCBI GI
                   g3935167
BLAST score
                   229
E value
                   3.0e-19
Match length
                   48
% identity
                   92
NCBI Description (AC004557) F17L21.10 [Arabidopsis thaliana]
Seq. No.
                   233865
Seq. ID
                   LIB3272-022-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   q2673912
BLAST score
                   200
E value
                   6.0e-16
Match length
                   67
% identity
                   55
NCBI Description (AC002561) unknown protein [Arabidopsis thaliana]
Seq. No.
                   233866
Seq. ID
                   LIB3272-023-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g1351014
BLAST score
                   439
E value
                   1.0e-43
Match length
                   107
% identity
                   83
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj BAA07207 (D38010)
                   ribosomal protein S8 [Oryza sativa]
Seq. No.
                   233867
Seq. ID
                   LIB3272-023-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   q462147
BLAST score
                   698
E value
                   6.0e-74
Match length
                   138
% identity
                   95
NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI)
                   (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE)
                   (PHI) >gi 541866 pir S41808 glucose-6-phosphate isomerase
                   (EC 5.3.1.9) - Arabidopsis thaliana
                   >gi_415923 emb CAA48940 (X69195) glucose-6-phosphate
                   isomerase [Arabidopsis thaliana]
Seq. No.
                   233868
Seq. ID
                   LIB3272-023-P1-K1-A12
Method
                  BLASTX
NCBI GI
                   q4538929
BLAST score
                   319
E value
                   2.0e-29
Match length
                  118
                   43
% identity
NCBI Description (AL049483) putative nucleic acid binding protein
                   [Arabidopsis thaliana]
```



```
Method
                    BLASTX
NCBI GI
                    g2662343
BLAST score
                    612
E value
                    8.0e-64
Match length
                    121
% identity
                    98
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                    233870
Seq. ID
                    LIB3272-023-P1-K1-A5
Method
                   BLASTX
NCBI GI
                    q3242079
BLAST score
                    218
E value
                    1.0e-17
Match length
                    67
% identity
                    64
NCBI Description (AJ006984) proline-rich protein [Capsicum annuum]
Seq. No.
                    233871
Seq. ID
                    LIB3272-023-P1-K1-A6
Method
                    BLASTX
NCBI GI
                    g2493895
BLAST score
                    677
E value
                    2.0e-71
Match length
                    147
% identity
                    90
NCBI Description CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE)
                    (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                    >gi_1071911_pir__S46438 cysteine synthase (EC 4.2.99.8) - watermelon >gi_540497_dbj_BAA05965_ (D28777) cysteine
                    synthase [Citrullus lanatus]
                    233872
Seq. No.
                    LIB3272-023-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                    q1843527
BLAST score
                    430
E value
                    1.0e-42
Match length
                   113
                    77
% identity
NCBI Description (U73747) annexin [Gossypium hirsutum]
Seq. No.
                    233873
Seq. ID
                    LIB3272-023-P1-K1-B11
Method
                    BLASTX
NCBI GI
                    g3695023
BLAST score
                    265
E value
                    4.0e-23
Match length
                   124
% identity
                    48
NCBI Description (AF055850) unknown [Arabidopsis thaliana]
Seq. No.
                    233874
Seq. ID
                    LIB3272-023-P1-K1-B12
```

33771

BLASTX

528

g4193388

Method NCBI GI

BLAST score



```
6.0e-54
E value
Match length
                   146
% identity
                   73
                   (AF091455) translationally controlled tumor protein [Hevea
NCBI Description
                   brasiliensis]
                   233875
Seq. No.
Seq. ID
                   LIB3272-023-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   g2688830
BLAST score
                   235
E value
                   1.0e-19
Match length
                   61
                   72
% identity
NCBI Description (AF000952) putative sugar transporter [Prunus armeniaca]
                   233876
Seq. No.
Seq. ID
                   LIB3272-023-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   q2760837
BLAST score
                   179
E value
                   5.0e-13
Match length
                   143
% identity
NCBI Description (AC003105) putative cytochrome P450 [Arabidopsis thaliana]
                   233877
Seq. No.
                   LIB3272-023-P1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1169544
BLAST score
                   604
E value
                    6.0e-63
Match length
                   136
% identity
                   85
                   ERD1 PROTEIN PRECURSOR >gi_541859_pir__JN0901 ERD1 protein - Arabidopsis thaliana >gi_497629_dbj_BAA04506_ (D17582)
NCBI Description
                   ERD1 protein [Arabidopsis thaliana]
Seq. No.
                    233878
                   LIB3272-023-P1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2146746
BLAST score
                   349
E value
                    5.0e-33
                   78
Match length
% identity
                   87
NCBI Description protein kinase (EC 2.7.1.-) - Arabidopsis thaliana
                   >gi 166819 (L05562) protein kinase [Arabidopsis thaliana]
                   233879
Seq. No.
Seq. ID
                   LIB3272-023-P1-K1-C12
Method
                   BLASTX
```

Method BLASTX
NCBI GI g3986695
BLAST score 623
E value 4.0e-65
Match length 136
% identity 92



```
NCBI Description (AF101423) ribosomal protein L12 [Cichorium intybus]
Seq. No.
                  233880
                  LIB3272-023-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2911044
BLAST score
                  368
E value
                  3.0e-35
Match length
                  117
                  61
% identity
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
                  233881
Seq. No.
Seq. ID
                  LIB3272-023-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g1928981
BLAST score
                  516
E value
                  1.0e-52
Match length
                  108
% identity
                  94
NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                  oleracea var. botrytis]
Seq. No.
                  233882
Seq. ID
                  LIB3272-023-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g3334115
BLAST score
                  327
E value
                  2.0e-30
Match length
                  100
                  71
% identity
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                  hirsutum]
                  233883
Seq. No.
                  LIB3272-023-P1-K1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1652434
                  177
BLAST score
E value
                  8.0e-13
                  51
Match length
% identity
NCBI Description (D90905) N-acetylglutamate kinase [Synechocystis sp.]
                  233884
Seq. No.
                  LIB3272-023-P1-K1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1709498
BLAST score
                  581
E value
                  3.0e-60
Match length
                  129
% identity
                  81
NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                  >qi 1362001 pir S57524 osmotin precursor - Arabidopsis
```

33773

thaliana >gi\_887390 emb\_CAA61411 (X89008) osmotin

Match length

% identity

116 41



## [Arabidopsis thaliana]

```
233885
Seq. No.
Seq. ID
                  LIB3272-023-P1-K1-C8
Method
                  BLASTX
                  g1619300
NCBI GI
                  315
BLAST score
                   5.0e-29
E value
Match length
                  79
                   73
% identity
                 (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  233886
                  LIB3272-023-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1709498
                   506
BLAST score
                   2.0e-51
E value
                  135
Match length
                   70
% identity
                  OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
NCBI Description
                   >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis
                   thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
                   [Arabidopsis thaliana]
                   233887
Seq. No.
Seq. ID
                  LIB3272-023-P1-K1-D2
Method
                   BLASTX
                   q2865623
NCBI GI
                   300
BLAST score
E value
                   2.0e-41
Match length
                   129
                   71
% identity
                   (AF045286)
NCBI Description
                   GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase
                   [Arabidopsis thaliana]
                   233888
Seq. No.
                   LIB3272-023-P1-K1-D3
Seq. ID
Method
                   BLASTX
                   g1717953
NCBI GI
BLAST score
                   216
E value
                   2.0e-17
Match length
                   114
% identity
                   46
                   UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 5
NCBI Description
                   PRECURSOR (RIESKE IRON-SULFUR PROTEIN 5) (RISP5) >gi_530055
                   (L16813) Rieske iron-sulfur protein [Nicotiana tabacum]
                   233889
Seq. No.
                   LIB3272-023-P1-K1-D5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1234900
BLAST score
                   169
E value
                   7.0e-12
```



```
NCBI Description (X92489) homeobox-leucine zipper protein [Glycine max]
                  233890
Seq. No.
                  LIB3272-023-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914430
BLAST score
                  743
E value
                  3.0e-79
Match length
                  145
                  98
% identity
NCBI Description
                  PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON
                  CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)
                  >gi_2285800_dbj_BAA21650_ (D78172) 26S proteasome beta
                  subunit [Spinacia oleracea]
                  233891
Seq. No.
Seq. ID
                  LIB3272-023-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q3068809
BLAST 'score
                  536
E value
                  6.0e-55
Match length
                  127
% identity
NCBI Description (AF059295) Skpl homolog [Arabidopsis thaliana]
Seq. No.
                  233892
                  LIB3272-023-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3157951
BLAST score
                  201
E value
                  8.0e-17
Match length
                  86
% identity
                  67
NCBI Description
                  (AC002131) Contains similarity to vesicle trafficking
                  protein gb U91538 from Mus musculus. ESTs gb F15494 and
                  gb F14097 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  233893
Seq. ID
                  LIB3272-023-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g1172002
BLAST score
                  591
E value
                  2.0e-61
Match length
                  143
                  76
% identity
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 556424 (L36822)
                  phenylalanine ammonia lyase [Stylosanthes humilis]
                  233894
Seq. No.
Seq. ID
                  LIB3272-023-P1-K1-E2
                  BLASTX
Method
NCBI GI
                  g2462931
BLAST score
                  157
E value
                  2.0e-10
Match length
                  88
```

NCBI Description (Z83833) UDP-glucose:sterol glucosyltransferase



# [Arabidopsis thaliana]

```
Seq. No.
                  233895
Seq. ID
                  LIB3272-023-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g2586127
BLAST score
                  363
E value
                  1.0e-34
                  138
Match length
% identity
                  52
NCBI Description (U89510) b-keto acyl reductase [Hordeum vulgare]
```

Seq. No. 233896

Seq. ID LIB3272-023-P1-K1-E4
Method BLASTX
NCBI GI g2507421
BLAST score 451
E value 6.0e-45
Match length 95
% identity 91

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi 1800277

(U81042) translation initiation factor [Arabidopsis thaliana] >gi\_4490709\_emb\_CAB38843.1\_ (AL035680) translation initiation factor [Arabidopsis thaliana]

 Seq. No.
 233897

 Seq. ID
 LIB3272-023-P1-K1-E6

 Method
 BLASTX

 NCBI GI
 g131015

NCBI GI g131015 BLAST score 470 E value 4.0e-47 Match length 123 % identity 68

NCBI Description PATHOGENESIS-RELATED PROTEIN R MAJOR FORM PRECURSOR

(THAUMATIN-LIKE PROTEIN E22) >gi\_100385\_pir\_\_JH0230 pathogenesis-related protein R precursor - common tobacco >gi\_19855\_emb\_CAA33293\_ (X15224) thaumatin-like protein [Nicotiana tabacum] >gi\_19980\_emb\_CAA31235\_ (X12739) pathogenesis-related protein R (AA 1 - 226) [Nicotiana

tabacum]

Seq. No. 233898

Seq. ID LIB3272-023-P1-K1-E7

Method BLASTX
NCBI GI g2213583
BLAST score 468
E value 6.0e-47
Match length 126

% identity 73

NCBI Description (AC000348) T7N9.3 [Arabidopsis thaliana]

Seq. No. 233899

Seq. ID LIB3272-023-P1-K1-E8

Method BLASTX
NCBI GI g2651303
BLAST score 531
E value 2.0e-54



```
Match length
                  87
% identity
                 (AC002336) putative potassium transporter [Arabidopsis
NCBI Description
                  thaliana]
                  233900
Seq. No.
                  LIB3272-023-P1-K1-F1
Seq. ID
Method
                  BLASTX
                  g1477428
NCBI GI
BLAST score
                  777
                  4.0e-83
E value
Match length
                  146
                  99
% identity
NCBI Description (X99623) alpha-tubulin 1 [Hordeum vulgare]
                  233901
Seq. No.
                  LIB3272-023-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263712
BLAST score
                  463
E value
                  2.0e-46
Match length
                  108
                  77
% identity
NCBI Description (AC006223) putative ribosomal protein S12 [Arabidopsis
                  thaliana]
                  233902
Seq. No.
                  LIB3272-023-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662343
                  233
BLAST score
                  5.0e-20
E value
Match length
                  48
                  94
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                   233903
Seq. No.
Seq. ID
                  LIB3272-023-P1-K1-F2
                  BLASTX
Method
                   g2677828
NCBI GI
                  483
BLAST score
                   1.0e-48
E value
Match length
                  135
                   67
% identity
NCBI Description (U93166) cysteine protease [Prunus armeniaca]
                   233904
Seq. No.
Seq. ID
                  LIB3272-023-P1-K1-F4
                   BLASTX
Method
                   g629858
NCBI GI
BLAST score
                   565
                   3.0e-58
E value
Match length
                  129
```

Seq. No. 233905

% identity

82

NCBI Description protein kinase C inhibitor - maize

E value

Match length

1.0e-15



```
Seq. ID
                  LIB3272-023-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q3643602
BLAST score
                  332
                  5.0e-31
E value
Match length
                  114
                  62
% identity
                  (AC005395) putative tonoplast intrinsic protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  233906
                  LIB3272-023-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4558659
BLAST score
                  586
                  8.0e-61
E value
Match length
                  140
                  74
% identity
NCBI Description (AC007063) unknown protein [Arabidopsis thaliana]
                  233907
Seq. No.
                  LIB3272-023-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3759184
BLAST score
                  139
E value
                   4.0e-15
Match length
                  70
                   61
% identity
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
                   233908
                  LIB3272-023-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g542157
BLAST score
                  480
E value
                   2.0e-48
                  127
Match length
                  72
% identity
NCBI Description ribosomal 5S RNA-binding protein - Rice
Seq. No.
                   233909
Seq. ID
                  LIB3272-023-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g2407790
BLAST score
                   455
E value
                   2.0e-45
Match length
                  145
                   15
% identity
NCBI Description (AF019910) grr1 [Glycine max]
Seq. No.
                   233910
Seq. ID
                  LIB3272-023-P1-K1-G12
                  BLASTX
Method
NCBI GI
                   g2160166
BLAST score
                  197
```

E value

Match length

% identity

2.0e-37

NCBI Description (AF055850) unknown [Arabidopsis thaliana]

146



```
% identity
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.
                   233911
                   LIB3272-023-P1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1710530
BLAST score
                   666
E value
                   4.0e-70
Match length
                   134
% identity
                   89
                   60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256
NCBI Description
                   ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein
                   L27a [Arabidopsis thaliana]
Seq. No.
                   233912
Seq. ID
                   LIB3272-023-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   q2245108
BLAST score
                   197
E value
                   3.0e-15
Match length
                   45
% identity
                   87
NCBI Description (Z97343) EREBP-4 homolog [Arabidopsis thaliana]
                   233913
Seq. No.
                   LIB3272-023-P1-K1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4558659
BLAST score
                   603
E value
                   9.0e-63
Match length
                   145
% identity
                   73
NCBI Description (AC007063) unknown protein [Arabidopsis thaliana]
Seq. No.
                   233914
Seq. ID
                   LIB3272-023-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   g3355468
BLAST score
                   543
E value
                   1.0e-55
Match length
                   123
                   91
% identity
NCBI Description (AC004218) putative ribosomal protein L35 [Arabidopsis
                   thaliana]
                   233915
Seq. No.
Seq. ID
                   LIB3272-023-P1-K1-H11
                   BLASTX
Method
NCBI GI
                   g3695023
BLAST score
                   387
```



```
Seq. No.
                   233916
Seq. ID
                  LIB3272-023-P1-K1-H2
Method
                  BLASTX
NCBI GI
                   g3493172
BLAST score
                   738
E value
                   1.0e-78
Match length
                   148
% identity
                   51
NCBI Description (U89609) fiber annexin [Gossypium hirsutum]
Seq. No.
                  233917
Seq. ID
                  LIB3272-023-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q629670
BLAST score
                  297
E value
                   7.0e-27
Match length
                  101
% identity
                   59
NCBI Description hypothetical protein - tomato
Seq. No.
                  233918
Seq. ID
                  LIB3272-023-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  q3158474
BLAST score
                  454
E value
                  3.0e-45
Match length
                  111
% identity
                  80
NCBI Description (AF067184) aquaporin 1 [Samanea saman]
Seq. No.
                  233919
Seq. ID
                  LIB3272-023-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g4580389
BLAST score
                  576
E value
                  1.0e-59
Match length
                  129
% identity
                  82
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]
Seq. No.
                  233920
Seq. ID
                  LIB3272-024-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g112697
BLAST score
                  227
E value
                  8.0e-19
Match length
                  67
                  70
% identity
NCBI Description 14 KD PROLINE-RICH PROTEIN DC2.15 PRECURSOR
                  >gi_486809_pir__S35714 proline-rich protein, 14K, embryonic
                  - carrot >gi_18316_emb_CAA33476_ (X15436) 14 kD protein (AA
                  1-137) [Daucus carota]
```

Seq. No. 233921

Seq. ID LIB3272-024-P1-K1-A10

Method BLASTX NCBI GI g1709498

Seq. No.

Seq. ID

Method

NCBI GI

233926

BLASTX

g125606

LIB3272-024-P1-K1-A6



```
BLAST score
- E value
                     3.0e-53
  Match length
                     114
  % identity
                     82
  NCBI Description
                     OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                     >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis
                     thaliana >gi_887390_emb_CAA61411 (X89008) osmotin
                     [Arabidopsis thaliana]
  Seq. No.
                     233922
  Seq. ID
                     LIB3272-024-P1-K1-A12
  Method
                     BLASTX
  NCBI GI
                     g1724100
  BLAST score
                     541
  E value
                     1.0e-55
  Match length
                     123
  % identity
  NCBI Description (U79765) porin [Mesembryanthemum crystallinum]
  Seq. No.
                     233923
  Seq. ID
                     LIB3272-024-P1-K1-A2
  Method
                     BLASTX
  NCBI GI
                     q2130073
  BLAST score
                     580
  E value
                     4.0e-60
  Match length
                     140
  % identity
                     80
                    fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
  NCBI Description
                     cytosolic - rice >gi_786178_dbj_BAA08845 (D50307) aldolase
                     C-1 [Oryza sativa] >gi_790970_dbj_BAA08830 (D50301)
                     aldolase C-1 [Oryza sativa]
  Seq. No.
                     233924
  Seq. ID
                    LIB3272-024-P1-K1-A4
  Method
                    BLASTX
  NCBI GI
                    g2980793
  BLAST score
                     553
  E value
                     6.0e-57
  Match length
                    138
  % identity
                    72
  NCBI Description (AL022197) putative protein [Arabidopsis thaliana]
  Seq. No.
                    233925
  Seq. ID
                    LIB3272-024-P1-K1-A5
  Method
                    BLASTX
  NCBI GI
                    g3360289
                    535
  BLAST score
  E value
                    8.0e-55
  Match length
                    127
  % identity
                    73
  NCBI Description
                    (AF023164) leucine-rich repeat transmembrane protein kinase
                    1 [Zea mays]
```



BLAST score 8.0e-18 E value Match length 66 % identity 62 PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 100463\_pir\_ S12248 NCBI Description pyruvate kinase (EC 2.7.1.40) - potato >gi 22576\_emb\_CAA37727 (X53688) pyruvate kinase [Solanum tuberosum] Seq. No. 233927 LIB3272-024-P1-K1-A8 Seq. ID Method BLASTX NCBI GI q167367 BLAST score 196 E value 4.0e-28 Match length 115 % identity 68 NCBI Description (L08199) peroxidase [Gossypium hirsutum] Seq. No. 233928 LIB3272-024-P1-K1-A9 Seq. ID BLASTX Method NCBI GI q508304 BLAST score 207 E value 2.0e-16 Match length 51 78 % identity NCBI Description (L22305) corC [Medicago sativa] 233929 Seq. No. LIB3272-024-P1-K1-B1 Seq. ID Method BLASTX NCBI GI g542058 BLAST score 497 E value 2.0e-50 Match length 131 % identity 68 NCBI Description HSR203J protein - common tobacco >gi\_444002\_emb\_CAA54393\_ (X77136) HSR203J [Nicotiana tabacum] Seq. No. 233930 Seq. ID LIB3272-024-P1-K1-B12 Method BLASTX NCBI GI g575603 BLAST score 324

E value 4.0e-30 109 Match length 57 % identity

NCBI Description (D42064) cationic peroxidase isozyme 38K precursor

[Nicotiana tabacum]

233931 Seq. No.

Seq. ID LIB3272-024-P1-K1-B2

BLASTX Method NCBI GI g464986 BLAST score 523 E value 2.0e-53

84



```
Match length
                    98
% identity
                    98
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                   >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
6.3.2.19) UBC9 - Arabidopsis thaliana
                   >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                   ubiquitin conjugating enzyme [Arabidopsis thaliana]
                   >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating
                    enzyme E2 [Arabidopsis thaliana]
                   >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein
                    ligase UBC9 [Arabidopsis thaliana]
Seq. No.
                    233932
Seq. ID
                   LIB3272-024-P1-K1-B3
Method
                   BLASTX
NCBI GI
                    q710626
BLAST score
                    153
E value
                    5.0e-10
Match length
                    43
% identity
NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi 3241941
                    (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                    thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis
                   thaliana]
                    233933
Seq. No.
Seq. ID
                    LIB3272-024-P1-K1-B4
Method
                    BLASTX
NCBI GI
                    g2677828
BLAST score
                    469
E value
                    4.0e-47
Match length
                    134
% identity
                    66
NCBI Description (U93166) cysteine protease [Prunus armeniaca]
                   233934
Seq. No.
Seq. ID
                   LIB3272-024-P1-K1-B5
Method
                   BLASTX
NCBI GI
                    g3122673
BLAST score
                    265
E value
                    9.0e-24
Match length
                    53
                    92
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_
                    (Z97341) ribosomal protein [Arabidopsis thaliana]
                    233935
Seq. No.
Seq. ID
                   LIB3272-024-P1-K1-B6
Method
                   BLASTX
                    g3915847
NCBI GI
BLAST score
                    373
                    7.0e-36
E value
Match length
                    87
```

33783

NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative



# 40S ribosomal protein S2 [Arabidopsis thaliana]

```
Seq. No.
                   233936
Seq. ID
                  LIB3272-024-P1-K1-B7
Method
                  BLASTX
NCBI GI
                   q629483
BLAST score
                   331
E value
                   7.0e - 31
Match length
                  125
% identity
                   54
NCBI Description
                  gene 1-Sc3 protein - European white birch
                  >gi 534898 emb CAA54696 (X77601) 1 Sc-3 [Betula pendula]
                  >gi 1584322_prf __2122374C allergen Bet v 1-Sc3 [Betula
                  pendula]
Seq. No.
                  233937
                  LIB3272-024-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3158376
BLAST score
                   488
E value
                  2.0e-49
Match length
                  131
                   75
% identity
NCBI Description (AF035385) unknown [Arabidopsis thaliana]
                  233938
Seq. No.
Seq. ID
                  LIB3272-024-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g2252836
BLAST score
                   300
E value
                   2.0e-27
Match length
                  86
% identity
                   67
NCBI Description
                  (AF013293) contains weak similarity to S. cerevisiae BOB1
                  protein (PIR:S45444) [Arabidopsis thaliana]
Seq. No.
                   233939
                  LIB3272-024-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1730109
                   475
BLAST score
E value
                   7.0e-48
Match length
                   112
% identity
                   82
                  LEUCOANTHOCYANIDIN DIOXYGENASE (LDOX) (LEUCOANTHOCYANIDIN
NCBI Description
                  HYDROXYLASE) >gi_499022_emb_CAA53580_ (X75966)
                  leucoanthocyanidin dioxygenase [Vitis vinifera]
Seq. No.
                   233940
Seq. ID
                  LIB3272-024-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g3980393
BLAST score
                  399
E value
                  7.0e-39
Match length
                  122
```

% identity 61
NCBI Description (AC004561) putative glutathione S-transferase [Arabidopsis



#### thaliana]

233941 Seq. No. LIB3272-024-P1-K1-C5 Seq. ID Method BLASTX g2160166 NCBI GI BLAST score 319 E value 2.0e-29 Match length 136 51 % identity NCBI Description (AC000132) No definition line found [Arabidopsis thaliana] 233942 Seq. No. LIB3272-024-P1-K1-D11 Seq. ID Method BLASTX NCBI GI q4510430 518 BLAST score 8.0e-53 E value 108 Match length % identity 86 (AC006929) unknown protein, 3' partial [Arabidopsis NCBI Description thaliana] 233943 Seq. No. Seq. ID LIB3272-024-P1-K1-D12 Method BLASTX NCBI GI q508304 BLAST score 212 6.0e-17E value Match length 51 80 % identity NCBI Description (L22305) corC [Medicago sativa] 233944 Seq. No. LIB3272-024-P1-K1-D3 Seq. ID Method BLASTX NCBI GI q464707 BLAST score 570 E value 6.0e-59 Match length 116 96 % identity NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi\_405613\_emb\_CAA80684\_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi\_434343\_emb\_CAA82273\_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi\_434345\_emb\_CAA82274\_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi\_434906\_emb\_CAA82275\_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi\_2505871\_emb\_CAA72909\_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi\_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb\_Z28701, DNA gb\_Z23165 from A. thaliana. ESTs gb\_T21121, gb\_Z17755, gb\_R64776 and gb\_R30430 come from this gene. [Arabidopsis thaliana] >gi\_4538910\_emb\_CAB39647.1\_ (AL049482) S18.A ribosomal

protein [Arabidopsis thaliana]



```
Seq. No.
                  233945
Seq. ID
                  LIB3272-024-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g2529683
BLAST score
                  343
E value
                  2.0e-32
Match length
                  129
                  57
% identity
NCBI Description (AC002535) unknown protein [Arabidopsis thaliana]
Seq. No.
                  233946
Seq. ID
                  LIB3272-024-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q2791804
BLAST score
                  186
E value
                  6.0e-14
Match length
                  62
% identity
                  58
NCBI Description (AF041432) bet3 [Homo sapiens] >gi 3413800 emb CAA11902
                  (AJ224335) hBET3 protein [Homo sapiens]
Seq. No.
                  233947
Seq. ID
                  LIB3272-024-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q1408471
BLAST score
                  468
E value
                  6.0e-47
Match length
                  106
% identity
                  79
NCBI Description
                  (U48938) actin depolymerizing factor 1 [Arabidopsis
                  thaliana] >gi 3851707 (AF102173) actin depolymerizing
                  factor 1 [Arabidopsis thaliana]
Seq. No.
                  233948
Seq. ID
                  LIB3272-024-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q464981
BLAST score
                  465
E value
                  1.0e-46
Match length
                  87
% identity
                  97
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 388207 (L23762)
                  ubiquitin carrier protein [Lycopersicon esculentum]
Seq. No.
                  233949
Seq. ID
                  LIB3272-024-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q2501578
```

BLAST score 502 E value 2.0e-55

Match length 124 % identity 97

NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi\_2129913\_pir\_\_\$60047

ethylene-responsive protein 1 - Para rubber tree

>gi 1209317 (M88254) ethylene-inducible protein [Hevea

brasiliensis



```
233950
  Seq. No.
  Seq. ID
                     LIB3272-024-P1-K1-E2
  Method
                     BLASTX
  NCBI GI
                     q3142294
  BLAST score
                     656
  E value
                     5.0e-69
  Match length
                     137
  % identity
                     91
  NCBI Description
                     (AC002411) Strong similarity to initiation factor eIF-2,
                     gb_U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and
                     gb N37529 come from this gene. [Arabidopsis thaliana]
  Seq. No.
                     233951
  Seq. ID
                     LIB3272-024-P1-K1-E4
  Method
                     BLASTX
  NCBI GI
                     q730241
  BLAST score
                     258
  E value
                     2.0e-22
  Match length
                     103
  % identity
                     51
                     DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN
  NCBI Description
                     GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (OLIGOSACCHARYL
                     TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115)
                     (HA0643) > gi\_473947\_dbj\_BAA06126\_ (D29643) \ similar \ to \ Canis
                     oligosaccharyltransferase 48 kDa subunit (M98392). [Homo
                     sapiens]
                     233952
  Seq. No.
  Seq. ID
                     LIB3272-024-P1-K1-E5
  Method
                     BLASTX
  NCBI GI
                     g2286153
  BLAST score
                     507
  E value
                     1.0e-51
  Match length
                     105
  % identity
                     96
  NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
  Seq. No.
                     233953
  Seq. ID
                     LIB3272-024-P1-K1-E6
  Method
                     BLASTX
  NCBI GI
                     g2499945
  BLAST score
                     167
  E value
                     7.0e-12
                     79
  Match length
  % identity
                     47
NCBI Description
                     URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
                     PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
```

DECARBOXYLASE >gi\_1076363\_pir\_\_S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) /

orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi\_443818\_emb\_CAA50686\_ (X71842)

pyrE-F [Arabidopsis thaliana]

Seq. No. 233954

Seq. ID LIB3272-024-P1-K1-E7

Method BLASTX



```
NCBI GI
                     g3913413
                     268
 BLAST score
                     2.0e-23
 É value
                     58
 Match length
                     90
% % identity
                     S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME 1 (ADOMETDC 1)
 NCBI Description
                     (SAMDC 1) (SAMDC9) >gi 1155240 (U38526)
                     S-adenosylmethionine decarboxylase 1 [Dianthus
                     caryophyllus] >gi 2406585 (U94786) S-adenosylmethionine
                     decarboxylase [Dianthus caryophyllus]
                     233955
 Seq. No.
                     LIB3272-024-P1-K1-E8
 Seq. ID
                     BLASTX
 Method
 NCBI GI
                     g1168727
 BLAST score
                     386
 E value
                     2.0e-37
 Match length
                     105
                     67
  % identity
                   CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD)
 NCBI Description
                     >gi 474300 dbj BAA03099 (D13991) cinnamyl alcohol
                     dehydrogenase [Aralia cordata] >gi 745086 prf_2015401A
                    cinnamoyl alcohol dehydrogenase [Aralia cordata]
                     233956
  Seq. No.
                     LIB3272-024-P1-K1-E9
  Seq. ID
                     BLASTX
 Method
 NCBI GI
                     g2129739
                     302
 BLAST score
 E value
                     1.0e-27
                     70
 Match length
                     89
  % identity
  NCBI Description shaggy-like kinase etha - Arabidopsis thaliana
                     >gi_1161512_emb_CAA64409_ (X94939) shaggy-like kinase etha [Arabidopsis thaliana] >gi_1627516_emb_CAA70144_ (Y08947)
                     shaggy-like kinase etha [Arabidopsis thaliana]
                     233957
  Seq. No.
  Seq. ID
                     LIB3272-024-P1-K1-F10
  Method
                     BLASTX
  NCBI GI
                     q2760837
  BLAST score
                     199
  E value
                     2.0e-15
  Match length
                     89
  % identity
  NCBI Description (AC003105) putative cytochrome P450 [Arabidopsis thaliana]
  Seq. No.
                     233958
  Seq. ID
                     LIB3272-024-P1-K1-F11
                     BLASTX
  Method
                     q4314355
  NCBI GI
  BLAST score
                     323
```

6.0e-30 E value Match length 97 % identity

NCBI Description (AC006340) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                   233959
                  LIB3272-024-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3850778
                  434
BLAST score
                   5.0e-43
E value
                  106
Match length
                   76
% identity
NCBI Description (Y18346) gluaredoxin [Lycopersicon esculentum]
                  233960
Seq. No.
                  LIB3272-024-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q120669
BLAST score
                   476
E value
                   6.0e-48
                  105
Match length
% identity
                   86
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                   233961
                   LIB3272-024-P1-K1-F6
Seq. ID
Method
                   BLASTX
                   q4567249
NCBI GI
                   509
BLAST score
E value
                   9.0e-52
Match length
                   133
% identity
NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]
                   233962
Seq. No.
Seq. ID
                   LIB3272-024-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   g585241
                   165
BLAST score
E value
                   2.0e-11
Match length
                   64
% identity
                   56
                   HISTONE H1 >gi 629668 pir S45662 histone H1 - tomato
NCBI Description
                   >gi_424100 (U03391) histone H1 [Lycopersicon esculentum]
Seq. No.
                   233963
                   LIB3272-024-P1-K1-G10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1076660
BLAST score
                   526
E value
                   9.0e-54
Match length
                   135
                   78
```

D13F(MYBST1) protein - potato >gi\_786426\_bbs\_159122 NCBI Description (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]

NCBI Description

61

```
Seq. No.
                   233964
Seq. ID
                   LIB3272-024-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g2253411
BLAST score
                   194
E value
                   8.0e-15
Match length
                   65
                   48
% identity
NCBI Description
                  (AF007219) PP2A inhibitor [Tetraodon fluviatilis]
Seq. No.
                   233965
Seq. ID
                  LIB3272-024-P1-K1-G3
Method
                   BLASTX
NCBI GI
                  g1922938
BLAST score
                   220
E value
                   8.0e-18
Match length
                   129
                   36
% identity
NCBI Description
                  (AC000106) Similar to Caenorhabditis hypothetical protein
                  CO7A9.11 (gb Z29094). [Arabidopsis thaliana]
Seq. No.
                   233966
                  LIB3272-024-P1-K1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                  g2267567
BLAST score
                   403
E value
                   2.0e-39
Match length
                   87
% identity
                   87
NCBI Description
                  (AF009003) glycine-rich RNA binding protein 1 [Pelargonium
                   x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding
                  protein 2 [Pelargonium x hortorum]
Seq. No.
                   233967
Seq. ID
                   LIB3272-024-P1-K1-G6
Method
                  BLASTX
NCBI GI
                   q3023847
BLAST score
                   555
E value
                   4.0e-57
Match length
                   116
% identity
NCBI Description
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                   PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta
                   subunit-like [Medicago sativa]
Seq. No.
                   233968
Seq. ID
                  LIB3272-024-P1-K1-G7
Method
                  BLASTX
NCBI GI
                   q2129915
BLAST score
                  299
E value
                   4.0e-27
                   97
Match length
```

33790

>gi 1360725 emb CAA87068 (Z46944) non-photosynthetic

ferredoxin precursor - sweet orange

ferredoxin [Citrus sinensis]

NCBI Description

84



```
Seq. No.
                   233969
Seq. ID
                  LIB3272-024-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q1762933
BLAST score
                   458
E value
                   9.0e-46
Match length
                   116
% identity
                   78
NCBI Description
                  (U66263) tumor-related protein [Nicotiana tabacum]
                  233970
Seq. No.
Seq. ID
                  LIB3272-024-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q2832708
BLAST score
                  280
E value
                   6.0e-25
Match length
                  107
% identity
                   50
NCBI Description
                  (AL021713) beta-1, 3-glucanase-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  233971
Seq. ID
                  LIB3272-024-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q1706326
BLAST score
                < 497
E value
                  2.0e-50
Match length
                  114
% identity
                  82
NCBI Description
                  PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC)
                  >gi_2146786_pir__S65470 pyruvate decarboxylase (EC 4.1.1.1)
                   (clone PDC1) - Garden pea >gi_1177603_emb_CAA91444_
                   (Z66543) pyruvate decarboxylase [Pisum sativum]
Seq. No.
                  233972
Seq. ID
                  LIB3272-024-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q267082
BLAST score
                  620
E value
                  9.0e-65
Match length
                  119
% identity
                  95
                  TUBULIN BETA-8 CHAIN >gi 320189 pir JQ1592 tubulin beta-8
NCBI Description
                  chain - Arabidopsis thalīana >gī 166908 (M84705) beta-8
                  tubulin [Arabidopsis thaliana]
Seq. No.
                  233973
Seq. ID
                  LIB3272-024-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g131385
BLAST score
                  542
E value
                  1.0e-55
Match length
                  134
```

33791

OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD



## THYLAKOID MEMBRANE PROTEIN)

```
233974
Seq. No.
Seq. ID
                  LIB3272-024-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g1170747
BLAST score
                  221
                  9.0e-27
E value
                  78
Match length
                  78
% identity
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
NCBI Description
                   (M88324) late embryogenesis-abundant protein [Gossypium
                  hirsutum] >gi_167347 (M37697) Lea5-A late
                  embryogenesis-abundant protein [Gossypium hirsutum]
                  233975
Seq. No.
                  LIB3272-024-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170747
BLAST score
                  348
E value
                  7.0e-33
Match length
                  82
                  83
% identity
                 LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
NCBI Description
                   (M88324) late embryogenesis-abundant protein [\overline{G}ossypium]
                  hirsutum] >gi_167347 (M37697) Lea5-A late
                  embryogenesis-abundant protein [Gossypium hirsutum]
                  233976
Seq. No.
Seq. ID
                  LIB3272-026-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  q3184098
BLAST score
                  143
                   6.0e-09
E value
                  101
Match length
% identity
                   36
NCBI Description
                  (AL023777) coenzyme a synthetase [Schizosaccharomyces
                  pombe]
                  233977
Seq. No.
Seq. ID
                  LIB3272-026-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  q549063
BLAST score
                   497
E value
                  2.0e-50
Match length
                  114
% identity
                  82
NCBI Description
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                  >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
                   factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                  21kd polypeptide [Oryza sativa]
Seq. No.
                   233978
```

LIB3272-026-P1-K1-A12 Seq. ID

Method BLASTX NCBI GI g730583 BLAST score 242



```
2.0e-20
E value
Match length
                  114
                  47
% identity
                  60S ACIDIC RIBOSOMAL PROTEIN P2 >qi 551267 emb CAA55047
NCBI Description
                   (X78213) 60s acidic ribosomal protein P2 [Parthenium
                  argentatum]
                  233979
Seq. No.
                  LIB3272-026-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2984709
                   402
BLAST score
                  3.0e-39
E value
                  82
Match length
                  91
% identity
                 (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
                  233980
Seq. No.
                  LIB3272-026-P1-K1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2984709
BLAST score
                   468
                   6.0e-47
E value
                  97
Match length
% identity
                   90
                 (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
Seq. No.
                  233981
                  LIB3272-026-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1166450
                   294
BLAST score
                   1.0e-26
E value
                   63
Match length
% identity
                   83
NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]
Seq. No.
                   233982
                   LIB3272-026-P1-K1-B12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4481934
BLAST score
                   163
E value
                   3.0e-11
Match length
                   105
% identity
                   14
                  (AL035640) CDA peptide synthetase I [Streptomyces
NCBI Description
                   coelicolor]
Seq. No.
                   233983
                   LIB3272-026-P1-K1-B3
Seq. ID
```

Method BLASTX
NCBI GI g3319921
BLAST score 242
E value 2.0e-20
Match length 94
% identity 57

NCBI Description (AJ223388) Hev b 3 [Hevea brasiliensis]